

TEXAS WATER JOURNAL

Volume 6 Number 1
2015



TEXAS WATER JOURNAL

Volume 6, Number 1

2015

ISSN 2160-5319

texaswaterjournal.org

THE TEXAS WATER JOURNAL is an online, peer-reviewed journal devoted to the timely consideration of Texas water resources management and policy issues. The journal provides in-depth analysis of Texas water resources management and policies from a multidisciplinary perspective that integrates science, engineering, law, planning, and other disciplines. It also provides updates on key state legislation and policy changes by Texas administrative agencies.

For more information on TWJ as well as TWJ policies and submission guidelines, please visit *texaswaterjournal.org*.

Editorial Board

Todd H. Votteler, Ph.D.
Editor-in-Chief
Guadalupe-Blanco River Authority

Kathy A. Alexander, Ph.D.

Robert L. Gulley, Ph.D.
Texas Comptroller of Public Accounts

Robert E. Mace, Ph.D.
Texas Water Development Board

Ken A. Rainwater, Ph.D.
Texas Tech University

Ralph A. Wurbs, Ph.D.
Texas A&M University

Managing Editor

Kathy Wythe
Texas Water Resources Institute
Texas A&M Institute of Renewable Natural Resources

Layout Editor

Leslie Lee
Texas Water Resources Institute
Texas A&M Institute of Renewable Natural Resources

Website Editor

Ross Anderson
Texas Water Resources Institute
Texas A&M Institute of Renewable Natural Resources

The Texas Water Journal is published in cooperation with the Texas Water Resources Institute, part of Texas A&M AgriLife Research, the Texas A&M AgriLife Extension Service, and the College of Agriculture and Life Sciences at Texas A&M University.



Estimating *E. coli* and *Enterococcus* loads in a coastal Texas watershed

Kyna Borel¹, R. Karthikeyan², Troy A. Berthold³, Kevin Wagner⁴

Abstract: Pathogens are the principal cause of water body impairment for 303(d) listed waters in Texas and across the United States with 10,654 impairments nationally (TCEQ 2012; USEPA 2013). In Texas, 45% of 568 total impairments are caused by elevated bacteria levels (TCEQ 2012). Models such as the Soil and Water Assessment Tool (SWAT) and Hydrological Simulation Program-FORTRAN (HSPF) have been used for assessing bacterial sources and loading. Other simplistic microbial models, such as the Potential Nonpoint Pollution Index (PNPI), Spatially Explicit Delivery MODEL (SEDMOD), and Spatially Explicit Load Enrichment Calculation Tool (SELECT), have been developed to rank potential pollution impacts from nonpoint sources and identify critical areas primarily using land use and geomorphology.

Keywords: water quality modeling, TMDL, GIS, coastal watershed protection

¹ Former Graduate Research Assistant, Department of Biological and Agricultural Engineering, Texas A&M University, College Station, Texas 77843

² Associate Professor, Department of Biological and Agricultural Engineering, Texas A&M University, College Station, Texas 77843

³ Research Scientist, Texas Water Resources Institute, College Station, Texas 77843

⁴ Associate Director, Texas Water Resources Institute, College Station, Texas 77843

* Corresponding author: kynaborel@gmail.com

Citation: Borel K, Karthikeyan R, Berthold TA, Wagner K. 2014. Estimating *E. coli* and *Enterococcus* loads in a coastal Texas watershed. Texas Water Journal. 6(1):33-44. Available from: <https://doi.org/10.21423/twj.v6i1.7008>.

© 2015 Kyna Borel, R. Karthikeyan, Troy A. Berthold, Kevin Wagner. This work is licensed under the Creative Commons Attribution 4.0 International License. To view a copy of this license, visit <https://creativecommons.org/licenses/by/4.0/> or visit the TWJ [website](#).

Terms used in paper

Short name of acronym	Descriptive name
AU	animal unit
BMPs	best management practices
CFU	colony forming units
HSPF	Hydrological Simulation Program-FORTRAN
HUC	hydrologic unit code
MGD	million gallons per day
OSSFs	on-site sewage facilities
PNPI	Potential Nonpoint Pollution Index
SEDMOD	Spatially Explicit Delivery MODel
SELECT	Spatially Explicit Load Enrichment Calculation Tool
SWAT	Soil and Water Assessment Tool
TPWD	Texas Parks and Wildlife Department
USEPA	U.S. Environmental Protection Agency
USGS	U.S. Geological Survey
USDA-NRCS	U.S. Department of Agriculture-Natural Resources Conservation Service
WWTFs	wastewater treatment facilities

INTRODUCTION

Pathogens are the principal cause of water body impairment for 303(d) listed waters in Texas and across the United States with 10,654 impairments nationally (TCEQ 2012; USEPA 2013). In Texas, 45% of 568 total impairments are caused by elevated bacteria levels (TCEQ 2012). Models such as the Soil and Water Assessment Tool (SWAT) and Hydrological Simulation Program-FORTRAN (HSPF) have been used for assessing bacterial sources and loading. Other simplistic microbial models, such as the Potential Nonpoint Pollution Index (PNPI), Spatially Explicit Delivery MODEL (SEDMOD), and Spatially Explicit Load Enrichment Calculation Tool (SELECT), have been developed to rank potential pollution impacts from nonpoint and point sources and identify critical areas primarily using land use, geomorphology, and potential sources in the watershed (Borel et al. 2012; Fraser et al. 1998; Munafo et al. 2005; Riebschleager et al. 2012; Teague et al. 2009).

The SELECT methodology was developed to characterize *E. coli* sources from point and nonpoint pollution in watersheds where watershed protection plans or total maximum daily loads (TMDLs) are developed to address bacterial contamination (Teague et al. 2009). Automated SELECT contains a

graphic user interface within ArcGIS, whereby the user can adjust project parameters to develop watershed-specific pollutant loading scenarios using source and area characteristics (Riebschleager et al. 2012).

STUDY WATERSHED

The Copano Bay watershed (Figure 1) is located in the San Antonio-Nueces Coastal Basin and contains 3 water bodies impaired for bacteria: the tidal classified segments of the Aransas and Mission rivers and Aransas Creek, an unclassified water body. Both the rivers discharge to Copano Bay. This 485,073-hectare (1,198,641 acre) rural watershed contains both fresh and tidal waters. The Aransas River watershed totals 217,068 hectares (536,387 acres), of which 45% is used for cultivated crops (Figure 2). The largest municipality within the Aransas River watershed is Beeville with a population of 13,101 (USCB 2013). The Aransas River watershed encompasses portions of Bee, San Patricio, and Refugio counties with less than 1% of the watershed within Aransas and Live Oak counties. The Mission River watershed is predominantly comprised of range and pasture land – 73% shrub/scrub and pasture hay out of the total 267,807 hectare (661,765 acre) land area (Figure 2). The watershed contains only 2 municipi-

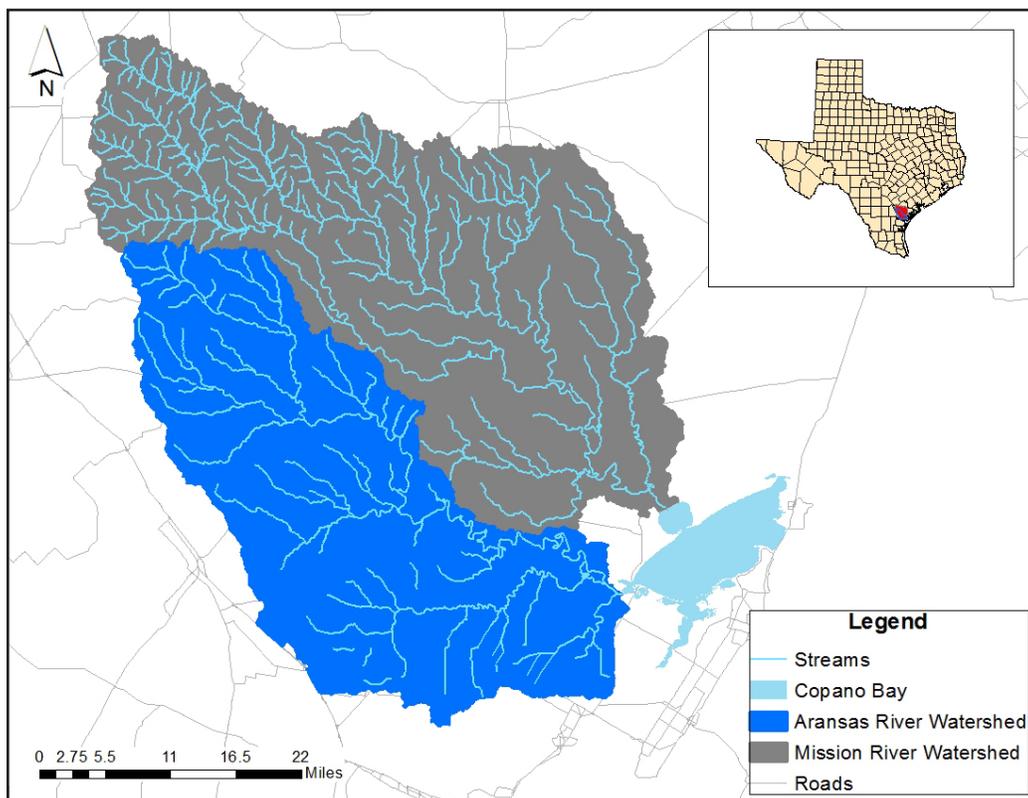


Figure 1. Copano Bay watershed location in Texas.

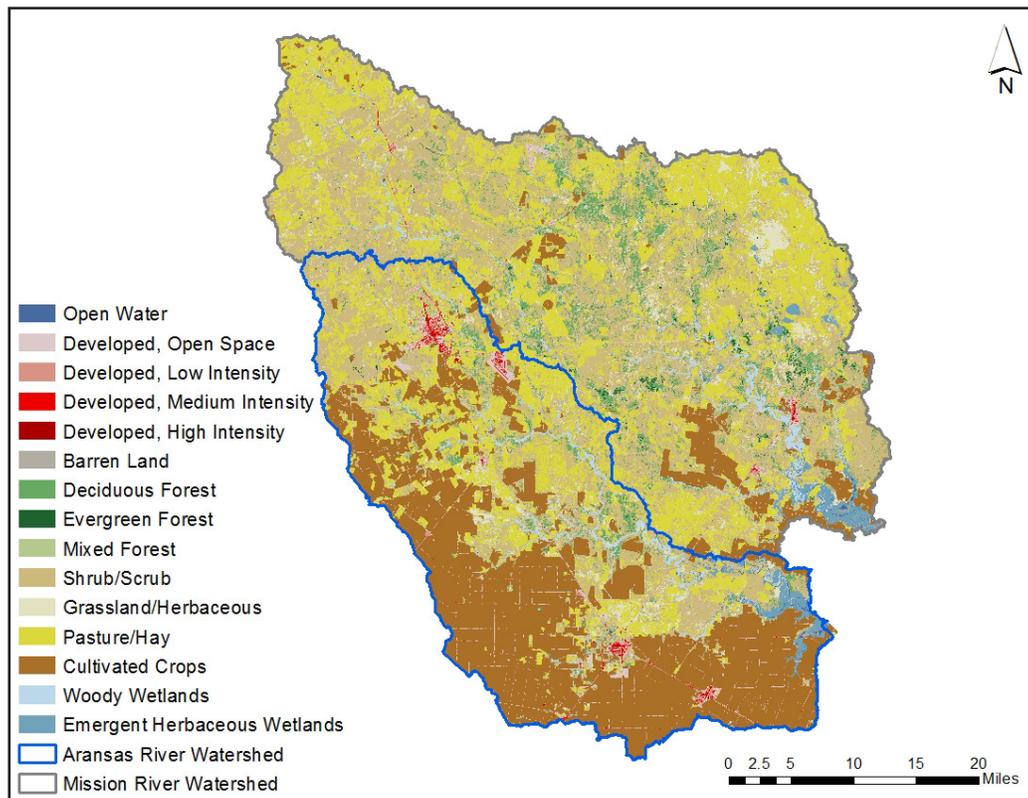


Figure 2. Copano Bay watershed land use.

palities, Refugio, population 2,840, and Woodsboro, population 1,484 (USCB 2013), spanning across portions of Karnes, Goliad, Bee, and Refugio counties.

SPATIAL ANALYSES

The spatially explicit methodology, developed at Texas A&M University by the Department of Biological and Agricultural Engineering and Spatial Sciences Laboratory, was used to identify contributing potential bacteria sources and to estimate daily potential from indicator bacteria, *E. coli* and *Enterococcus*, loads in the Aransas River and Mission River watersheds. All birds and mammals are potential sources of bacteria, and those present in the watershed contribute *E. coli* or *Enterococcus* to the tidal and freshwater portion of the Aransas and Mission rivers. However, each watershed is different and not all sources are likely to contribute significant amounts of bacteria to the water bodies. Additionally, sufficient information on species populations, *E. coli* and *Enterococcus* concentrations, and feces production rates are often unavailable, thus precluding the ability to effectively assess potential *E. coli* or *Enterococcus* contributions from respective sources. Data from government agencies and local stakeholders on the number and distribution of contributing sources, in combination with National Land Cover Database 2006 (NLCD 2006) land use

classification data were entered into a GIS software program. Each watershed was also divided into 4,047 to 16,187 hectares (10,000 and 40,000 acres) 12-digit hydrologic unit code (HUC) subwatersheds acquired from U.S. Geological Survey (USGS) and U.S. Department of Agriculture-Natural Resources Conservation Service (USDA-NRCS) (2012). Bacterial sources were examined at this subwatershed level, as opposed to the entire watershed of each river, to identify and target the areas in each subwatershed where the sources were likely to impact water quality.

The 2 factors considered when determining the potential contribution for each source were the abundance of a particular source in the watershed and whether sufficient information is available to effectively predict bacteria loadings from that source. The methodology developed by Wagner and Moench (2009) to estimate animal population was applied here to update population densities. Wagner and Moench (2009) included cattle, horses, goats, sheep, domestic hogs, poultry, deer, and feral hogs in their estimation protocol. With the exception of domestic hogs and poultry, all of these sources, with the addition of on-site sewage facilities (OSSFs), wastewater treatment facilities (WWTFs), and pet dogs, warranted modeling and had sufficient information to model using SELECT.

POTENTIAL *E. COLI* AND *ENTEROCOCCUS* LOAD ESTIMATION

The analysis was performed at a 30 meter by 30 meter resolution. Each source was distributed to appropriate land uses in the watershed, and then the potential *E. coli* and *Enterococcus* loads were calculated using the equations in Tables 1 and 2, respectively. *E. coli* and *Enterococcus* bacte-

ria are indicator bacteria and are generally not pathogenic but indicators of potential fecal contamination. The daily fecal coliform production rates for the livestock, wildlife, and feral hog sources were estimated per animal unit (AU) from Wagner and Moench (2009). The highest fecal coliform production values in U.S. Environmental Protection Agency (USEPA) guidelines document (2001) were used for OSSF and dog sources. *E. coli* and *Enterococcus* loads were calculated

Table 1. Calculation of potential *E. coli* loads from various sources.

Source	<i>E. coli</i> load calculation
Cattle	$EC = \# \text{ Cattle} * 1 \text{ AU} * 8.55 \times 10^9 \text{ cfu/AU/day} * 0.63$
Horses	$EC = \# \text{ Horses} * 1.25 \text{ AU} * 2.91 \times 10^9 \text{ cfu/AU/day} * 0.63$
Goats	$EC = \# \text{ Goats} * 0.17 \text{ AU} * 2.54 \times 10^{10} \text{ cfu/AU/day} * 0.63$
Sheep	$EC = \# \text{ Sheep} * 0.2 \text{ AU} * 2.90 \times 10^{11} \text{ cfu/AU/day} * 0.63$
Deer	$EC = \# \text{ Deer} * 0.112 \text{ AU} * 1.50 \times 10^{10} \text{ cfu/AU/day} * 0.63$
Feral Hogs	$EC = \# \text{ Hogs} * 0.125 \text{ AU} * 1.21 \times 10^9 \text{ cfu/AU/day} * 0.63$
OSSFs	$EC = \# \text{ OSSFs} * \text{ Failure Rate} * \frac{10 * 10^6}{100 \text{ mL}} * \frac{70 \text{ gal}}{\text{person day}} * \frac{\text{Avg \#}}{\text{Household}} * \frac{3758.2 \text{ mL}}{\text{gal}} * 0.63$
Dogs	$EC = \# \text{ Households} * \frac{1 \text{ dog}}{\text{household}} * 5 \times 10^9 \text{ cfu/day} * 0.63$
WWTFs	$EC = \text{ Permitted MGD} * \frac{126 \text{ cfu}}{100 \text{ mL}} * \frac{10^6 \text{ gal}}{\text{MGD}} * \frac{3758.2 \text{ mL}}{\text{gal}}$

Table 2. Calculation of potential *Enterococcus* loads from various sources.

Source	<i>Enterococcus</i> load calculation
Cattle	$EC = \# \text{ Cattle} * 1 \text{ AU} * 8.55 \times 10^9 \text{ cfu/AU/day} * 0.175$
Horses	$EC = \# \text{ Horses} * 1.25 \text{ AU} * 2.91 \times 10^9 \text{ cfu/AU/day} * 0.175$
Goats	$EC = \# \text{ Goats} * 0.17 \text{ AU} * 2.54 \times 10^{10} \text{ cfu/AU/day} * 0.175$
Sheep	$EC = \# \text{ Sheep} * 0.2 \text{ AU} * 2.90 \times 10^{11} \text{ cfu/AU/day} * 0.175$
Deer	$EC = \# \text{ Deer} * 0.112 \text{ AU} * 1.50 \times 10^{10} \text{ cfu/AU/day} * 0.175$
Feral Hogs	$EC = \# \text{ Hogs} * 0.125 \text{ AU} * 1.21 \times 10^9 \text{ cfu/AU/day} * 0.175$
OSSFs	$EC = \# \text{ OSSFs} * \text{ Failure Rate} * \frac{10 * 10^6}{100 \text{ mL}} * \frac{70 \text{ gal}}{\text{person day}} * \frac{\text{Avg \#}}{\text{Household}} * \frac{3758.2 \text{ mL}}{\text{gal}} * 0.175$
Dogs	$EC = \# \text{ Households} * \frac{1 \text{ dog}}{\text{household}} * 5 \times 10^9 \text{ cfu/day} * 0.175$
WWTFs	$EC = \text{ Permitted MGD} * \frac{35 \text{ cfu}}{100 \text{ mL}} * \frac{10^6 \text{ gal}}{\text{MGD}} * \frac{3758.2 \text{ mL}}{\text{gal}}$

from fecal coliform loads using a ratio of 0.63 fecal coliform to *E. coli* and 0.175 fecal coliform to *Enterococcus*, based on 2010 Texas Surface Water Quality regulatory standards in recreational waters. The geometric mean regulatory standard for primary contact recreational use for freshwater (Segments 2002 and 2004) is 126 organisms per 100 milliliter for *E. coli*, and for high saline inland waters (Segments 2001 and 2003) 35 organisms per 100 milliliter for *Enterococcus* (TCEQ 2010). After the potential *E. coli* or *Enterococcus* loads were calculated, the results were aggregated to the subwatershed level to identify areas of potential concern.

Cattle

Cattle were uniformly applied according to 4 separate stocking rates derived from 2004 to 2008 *Texas Agricultural Statistics* (USDA-NASS 2004–2008) and USDA-NRCS estimates from Wagner and Moench (2009). The 4 stocking rates were: 20 acre/AU for the land use classifications of deciduous forest, evergreen forest, and mixed forest, 30 acre/AU for the shrub/scrub land use classification, 15.4 acre/AU for the land use classification grasslands/herbaceous, and 7.7 acre/AU for the pasture/hay classification. A total of 3,152 AUs were evenly distributed to all of the forested lands. 13,153 AUs of cattle were uniformly applied over shrub/scrub classifications. 3,148 AUs were evenly distributed over grassland/herbaceous land use classifications and 40,052 AUs were distributed over pasture/hay lands. The total cattle potential loads were estimated by adding together the results from the 4 separate stocking rate distributions. A fecal coliform production rate of 8.55×10^9 colony forming units (CFU) per AU per day (Wagner and Moench 2009) was used in the model and converted from fecal coliform to *E. coli* using a conversion ratio. The total potential *E. coli* and *Enterococcus* loads for cattle were estimated using the distributed cattle density production rate, fecal coliform production rate, and conversion ratios.

Horses

A total of 2,772 AUs of horses were evenly distributed over developed open space, grassland/herbaceous, and pasture/hay. This number was derived from the 2007 USDA Census of Agriculture (USDA-NASS 2007) county estimates multiplied by the percentage of the county in the Aransas River and Mission River watersheds and the AU conversion of 1.25 (Wagner and Moench 2009). The percentage of a county in a watershed was adjusted from Wagner and Moench (2009) because the watershed boundary differed from the original report, causing the estimated animal populations to adjust as well. The fecal coliform production rate used in the model was 2.91×10^8 CFU per AU per day (Wagner and Moench 2009). The total potential *E. coli* and *Enterococcus* loads for horses were

estimated using the distributed horse density, fecal coliform production rate, and conversion ratios.

Goats

A total of 565 AUs of goats were evenly distributed over developed open space, shrub/scrub grassland/herbaceous, and pasture/hay. Wagner and Moench (2009) estimated the goat numbers by using the 2005–2008 *Texas Agricultural Statistics* for Bee, Goliad, and Karnes counties and district numbers for Aransas, Refugio, and San Patricio counties. The numbers were updated from Wagner and Moench (2009) by using an adjusted percent in watershed number because the Aransas River and Mission River watersheds boundaries differed from the original report. The fecal coliform production rate used in the model was 2.54×10^{10} CFU per AU per day (Wagner and Moench 2009), and total potential *E. coli* and *Enterococcus* loads for goats were estimated using the distributed goat density, fecal coliform production rate, and conversion ratios.

Sheep

A total of 111 AUs of sheep were evenly distributed over developed open space, shrub/scrub, grassland/herbaceous, and pasture/hay. This number was derived from the 2007 *USDA Census of Agriculture* county estimates multiplied by the percentage of the county in the watershed and the AU conversion of 0.2 (USDA-NASS 2007; Wagner and Moench 2009). The fecal coliform production rate used in the model was 2.90×10^{11} CFU per AU per day (Wagner and Moench 2009) and total potential *E. coli* and *Enterococcus* loads for sheep were estimated using the distributed sheep density, fecal coliform production rate, and conversion ratios.

Deer

A total of 9,951 deer AUs were evenly applied over the entire watershed. This is the population estimate produced by applying Wagner and Moench (2009) county densities calculated from Texas Parks and Wildlife Department (TPWD) surveys. Deer were evenly distributed across the Aransas River and Mission River watersheds to best reflect the surveying techniques used by the TPWD. The densities were multiplied by the number of acres of the county in the watershed and the AU conversion of 0.112 to determine the number of deer AUs in each county. The fecal coliform production rate used was 1.50×10^{10} CFU per AU per day (Yagow 2001; Cox et al. 2005; Wagner and Moench 2009), and total potential *E. coli* and *Enterococcus* loads for deer were estimated using the distributed deer density, fecal coliform production rate, and conversion ratios.

Feral hogs

A total of 4,198 feral hog AUs were applied uniformly across deciduous forest, evergreen forest, mixed forest, shrub/scrub, grassland/herbaceous, pasture/hay, cultivated crops, and woody wetlands. This population estimate was derived by Reidy (2007) using a density of 33.3 acre/hog and an AU conversion of 0.125 (Wagner and Moench 2009). The fecal coliform production rate used was 1.21×10^9 CFU per AU per day (Cox et al. 2005; Mukhtar 2007; Wagner and Moench 2009), and total potential *E. coli* and *Enterococcus* loads for feral hogs were estimated using the distributed feral hog density, fecal coliform production rate, and conversion ratios.

On-site sewage facilities

OSSFs were modeled using spatially distributed point data of each household obtained from residential 911 address data gathered from the Coastal Bend Council of Governments and the Golden Crescent Regional Planning Commission. 2010 census data (USCB 2010) was used for Karnes County because 911 address data was unavailable for this county. Households within Certificate of Convenience and Necessity areas (PUC 2013) were removed to exclude households being serviced by a WWTF. The total number of households with OSSFs in the watershed was estimated to be 10,047, and the average persons per household for a census block were calculated by using 2010 Census data (USCB 2010). A fecal coliform concentration of raw sewage 10×10^6 CFU per 100 milliliters (USEPA 2001) was used to model failing OSSFs with a constant sewage discharge of 70 gallons per person per day. OSSF failure rate was estimated by applying the soil drainfield limitation classes as follows: very limited with 15% failing, somewhat limited with 10% failing, not limited with 5% failing, and not rated with 15% failing (USDA-NRCS 2004). The percentage of *E. coli* and *Enterococcus* contributing to the Aransas River and Mission River watersheds due to OSSF failures were calculated by multiplying the OSSF household densities, average person per household, fecal coliform concentration of raw sewage, sewage discharge, failure rate, and conversion ratios.

Dogs

A dog density of 1 dog per household was an updated density as reported by the American Veterinarian Medical Association and used in the Geronimo Creek watershed analysis (AVMA 2002; Geronimo and Alligator Creeks Watershed Partnership 2012). The density was applied to the residential 911 addresses, resulting in an estimated dog population of 10,065. The fecal coliform production rate of 5×10^9 CFU per dog per day (USEPA 2001) multiplied by the conversion ratios was

used to determine the potential *E. coli* and *Enterococcus* loads resulting from dogs.

Wastewater treatment facilities

There are 12 WWTFs in the Aransas River and Mission River watersheds. Three WWTFs are within the Mission River watershed: town of Refugio, town of Woodsboro, and Pettus Municipal Utility District with permitted discharges of 0.576, 0.25, and 0.105 million gallons per day (MGD) respectively. Nine WWTFs are within the Aransas River watershed including 2 for the city of Beeville with permitted discharges of 3 and 2.5 MGD as well as, 2 for the city of Sinton with permitted discharges of 0.015 and 0.8 MGD. The remaining WWTFs in the Aransas River watershed are: city of Taft, Skidmore Water Supply Corporation, St. Paul Water Supply Corporation, Tynan Water Supply Corporation, and Texas Department of Transportation with permitted discharges of 0.9, 0.131, 0.05, 0.045, and 0.00038 MGD, respectively. Each WWTF was modeled at its daily maximum permitted discharge and, if applicable, its effluent limitation of either an *E. coli* concentration of 126 CFU or most probable number per 100 milliliters or an *Enterococcus* concentration of 35 CFU per 100 milliliters, to estimate the potential bacteria loads from WWTFs.

In total, 9 potential sources were modeled using SELECT in both the Aransas River and Mission River watersheds. Since the 2 watersheds are part of the entire Copano Bay watershed, the potential source contribution population densities applied were the same for both the Aransas River and Mission River watersheds.

RESULTS AND DISCUSSION

The watershed spatial analysis performed by SELECT highlights subwatersheds within the individual Aransas River and Mission River watersheds that have the highest potential to contribute *E. coli* and *Enterococcus* based on land use distribution and potential source contributions. The analysis highlights subwatersheds of concern for particular sources and for total potential *E. coli* and *Enterococcus* loads, taking into account all of the potential sources modeled. Conclusions can be made about which sources have the highest potential to contribute *E. coli* and *Enterococcus* and pinpoint subwatersheds where those contributions are in the Aransas River and Mission River watersheds by using SELECT results.

Spatially explicit *E. coli* and *Enterococcus* load estimation

Tables 3 and 4 illustrate the source specific *E. coli* and *Enterococcus* ranges used to estimate the contribution of each source

Table 3. Daily potential *E. coli* load ranges.

Potential Sources	Daily Potential <i>E. coli</i> Load (cfu/day)	
	Mission River Watershed	Aransas River Watershed
Cattle	$7.42 \times 10^{11} - 1.81 \times 10^{13}$	$2.86 \times 10^{11} - 1.25 \times 10^{13}$
Horses	$1.43 \times 10^9 - 2.39 \times 10^{10}$	$3.47 \times 10^9 - 2.17 \times 10^{10}$
Goats	$7.13 \times 10^9 - 5.43 \times 10^{11}$	$2.14 \times 10^{10} - 5.43 \times 10^{11}$
Sheep	$0 - 1.68 \times 10^{12}$	$0 - 1.68 \times 10^{12}$
Deer	$8.56 \times 10^{11} - 3.23 \times 10^{12}$	$8.56 \times 10^{11} - 4.25 \times 10^{12}$
Feral Hogs	$1.87 \times 10^{10} - 1.15 \times 10^{11}$	$9.87 \times 10^{10} - 1.15 \times 10^{11}$
OSSF	$0 - 5.13 \times 10^{12}$	$0 - 5.13 \times 10^{12}$
Dogs	$3.15 \times 10^9 - 3.39 \times 10^{12}$	$3.15 \times 10^9 - 3.39 \times 10^{12}$
WWTF	$0 - 1.43 \times 10^{10}$	$0 - 1.43 \times 10^{10}$

Table 4. Daily potential *Enterococcus* load ranges.

Potential Sources	Daily Potential <i>Enterococcus</i> Load (cfu/day)	
	Mission River Watershed	Aransas River Watershed
Cattle	$2.08 \times 10^{11} - 5.06 \times 10^{12}$	$8.00 \times 10^{10} - 3.51 \times 10^{12}$
Horses	$3.99 \times 10^8 - 6.70 \times 10^9$	$9.71 \times 10^8 - 6.05 \times 10^9$
Goats	$2.00 \times 10^9 - 1.52 \times 10^{11}$	$5.98 \times 10^9 - 1.52 \times 10^{11}$
Sheep	$0 - 4.72 \times 10^{11}$	$0 - 4.72 \times 10^{11}$
Deer	$2.40 \times 10^{11} - 9.06 \times 10^{11}$	$9.98 \times 10^{11} - 1.19 \times 10^{12}$
Feral Hogs	$5.23 \times 10^9 - 3.23 \times 10^{10}$	$8.90 \times 10^9 - 3.23 \times 10^{10}$
OSSF	$0 - 1.44 \times 10^{12}$	$0 - 1.44 \times 10^{12}$
Dogs	$8.82 \times 10^8 - 9.50 \times 10^{11}$	$8.82 \times 10^8 - 9.50 \times 10^{11}$
WWTF	$0 - 3.99 \times 10^9$	$0 - 3.99 \times 10^9$

for both the Mission River and Aransas River watersheds. The source-specific ranges for both watersheds are identical or similar because sources were distributed similarly. The source exhibiting highest daily potential *E. coli* and *Enterococcus* loads in both the Aransas River and Mission River watersheds was cattle, while OSSFs, dogs, and deer were the next highest contributors, respectively. Sources with moderate potential contributions were sheep, feral hogs, and goats. The lowest contributors were horses and WWTFs.

Figures 3 and 4 illustrate the total potential *E. coli* and *Enterococcus* loads, or combined load, which includes the loading potentials of all of the modeled sources applied in the Mission and Aransas River watersheds. Subwatersheds in red indicate areas with the highest potential for *E. coli* contributions to the river, while the darkest green represents areas with the lowest potential. The highest contributing subwatersheds either had a dominant land use of pasture/hay or urban land uses generally due to the high numbers of cattle, OSSFs, and dogs associated with these land uses. The lowest contributing subwatersheds contained areas of mostly cultivated crop land.

Potential Issues

SELECT provides a daily snapshot of fecal and bacterial deposition based on conditions inputted into the model, and as such, fecal buildup or bacteria die-off and re-growth are not taken into account. Fecal buildup over the land surface before a rainfall event as well as bacteria die-off can cause the actual *E. coli* or *Enterococcus* production rates to vary widely compared to those in the model.

SELECT does not take into account direct deposition of fecal material into the stream. Direct deposition significantly affects the bacteria concentrations present in a water body more so than land deposition. Larsen et al. (1994) found that manure deposited 0.6 meters (2 feet) from a stream contributed 83% less bacteria and manure deposited at 2.1 meters (7 feet) contributed 95% less than manure deposited directly into a stream. The timing of fecal deposition is also not taken into account. If fecal matter is deposited shortly before a rain event, then the bacteria will more likely end up in the water body

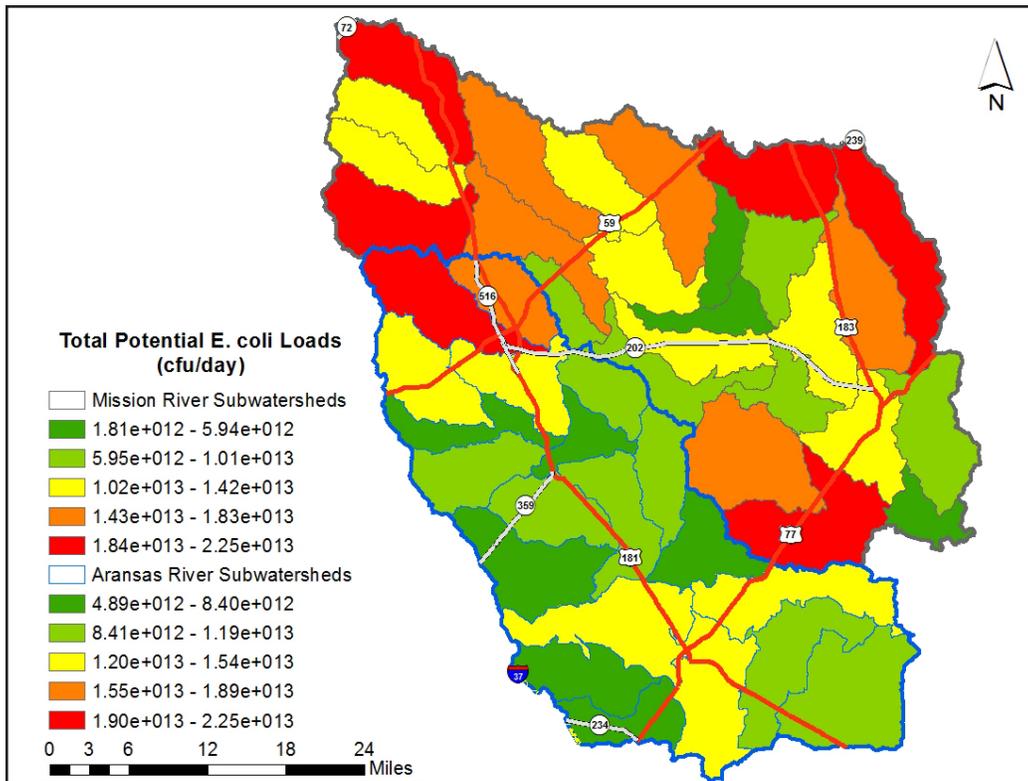


Figure 3. Total daily potential *E. coli* loads from all considered sources in the Mission River and Aransas River watersheds.

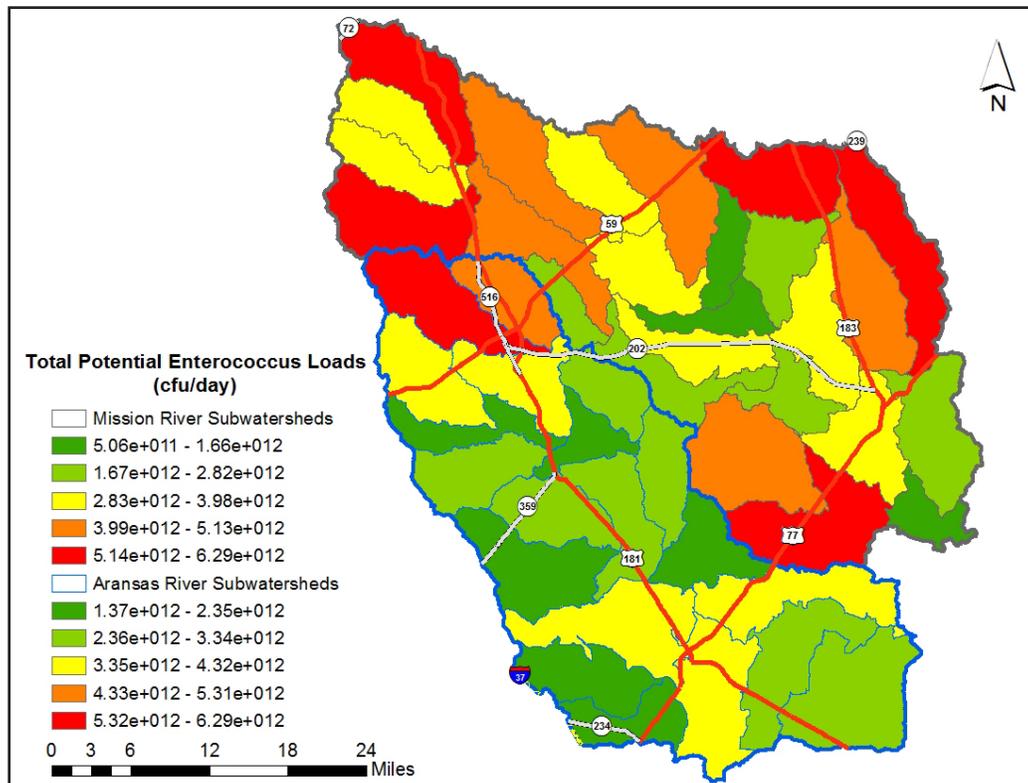


Figure 4. Total daily potential *Enterococcus* loads from all considered sources in the Mission River and Aransas River watersheds.

via surface runoff. A significant factor found by Wagner et al. (2012) is when runoff occurred more than 2 weeks following grazing (and fecal matter deposition), *E. coli* levels were 88% lower compared to runoff during or soon after grazing. SELECT does not take into account the distance of the fecal deposition from the water body. As found by Larsen et al. (1994), bacteria from fecal deposition have a much higher potential to impact water quality when deposited at closer distances compared to farther distances from a water body.

In addition, the animal densities used in the model can vary. Animal densities can change drastically from season to season and from year to year, particularly in response to worsening drought conditions that often affect many areas of Texas. Further, with the exception of feral hogs and deer, estimates of wildlife numbers are impracticable to evaluate. These issues can impact the watershed planning process, particularly because SELECT results show cattle as the top contributors of bacteria into the water bodies. In comparison, bacterial source tracking conducted in the Buck Creek, Little Brazos River, and Big Cypress Creek watersheds suggest that wildlife contributions range from 42–65%, while cattle and other domestic animal contributions range from only 14–29% (Di Giovanni et al. 2013). The fecal material from cattle may not be reaching and contaminating the water body, but other sources could be contaminating the water more directly or not integrated into the model. As a result, the best management practices (BMPs) chosen to be implemented would be influenced by these issues with the model, and their overall impact of projected loadings would be greatly affected.

CONCLUSIONS

The SELECT methodology was applied to the entire Copano Bay watershed, comprised of the Aransas River and Mission River watersheds, to calculate potential *E. coli* and *Enterococcus* loads occurring in the watersheds and identify priority areas for implementing management practices. The SELECT methodology was adapted to the Copano Bay watershed to include the perceived potential contributors with data availability. The model is unable to reflect the true potential loading of the watershed as not all contributing sources are taken into account due to the availability of data. Once data is collected, the SELECT model can be adapted and additional sources can easily be added to the model. In both the Aransas River and Mission River watersheds, cattle were determined to be the largest potential contributor. This suggests that BMPs supporting good grazing management will yield the most improvements and be the most effective at lowering the bacteria contamination in the water body. The SELECT methodology was able to highlight areas of highest concern, which provides guidance for individuals and entities that implement BMPs

where practices would be the most effective. The SELECT methodology can easily be adapted and applied to watersheds to reflect stakeholder concerns.

The next steps for the SELECT methodology are to account for sources that are currently not able to be modeled, such as mesomammals, birds, and other background sources. Potential integration of bacterial source tracking results with SELECT could also be evaluated to address these issues. Future SELECT methodology could also include fecal buildup and bacteria die-off and re-growth to improve the model. SELECT outputs could be combined with another model to determine the *E. coli* and *Enterococcus* loads reaching the water bodies either through surface runoff or through soils.

REFERENCES

- [AVMA] American Veterinary Medical Association. 2002. U.S. pet ownership and demographics source book. Schaumburg (Illinois): Center for Information Management American Veterinary Medical Association.
- Borel KE, Karthikeyan R, Smith PK, Gregory LF, Srinivasan R. 2012. Estimating daily potential *E. coli* loads in rural Texas watersheds using spatially explicit load enrichment calculation tool (SELECT). *Texas Water Journal*. 3(1):42-58.
- Cox P, Griffith M, Angles M, Deere D, Ferguson C. 2005. Concentrations of pathogens and indicators in animal feces in the Sydney watershed. *Applied and Environmental Microbiology*. 71(10):5929-34.
- Di Giovanni GD, Casarez EA, Gentry TJ, Martin EC, Gregory L, Wagner K. 2013. Support analytical infrastructure and further development of a statewide bacterial source tracking library [Internet]. College Station (Texas): Texas Water Resources Institute. TR-448. 74 p. Available from: <http://twri.tamu.edu/reports/2013/tr448.pdf>
- Fraser RH, Barten PK, Pinney DA. 1998. Predicting stream pathogen loading from livestock using a geographical information system-based delivery model. *Journal of Environmental Quality*. 27:935-945.
- Geronimo and Alligator Creeks Watershed Partnership. 2012. Geronimo and Alligator Creeks watershed protection plan [Internet]. College Station (Texas): Texas AgriLife Extension Service; [cited 2015 January 11]. 174 p. Available from: <http://www.geronimocreek.org/documents/wpp/FinalDraftGACWPP.pdf>
- Larsen R, Miner J, Buckhouse J, Moore JA. 1994. Water-quality benefits of having cattle manure deposited away from streams. *Bioresource Tech*. 48(2):113-118.
- Mukhtar S. 2007. Manure production and characteristics: Its importance to Texas and animal feeding operations [Internet]. College Station (Texas): Texas AgriLife Extension Service, Texas A&M System; [cited 2015 January

- 11]. L-5489. Available from: <http://agrifecdn.tamu.edu/tammi/files/2014/04/manureproductionSM-5489.pdf>
- Munafa M, Cecchi G, Baiocco F, Mancini L. 2005. River pollution from non-point sources: a new simplified method of assessment. *Journal of Environmental Management*. 77:93-98.
- [NLCD] National Land Cover Database. 2006. NLCD 2006 land cover (2011 edition) [Internet]. Washington (District of Columbia); National Land Cover Database Multi-Resolution Land Characteristics Consortium; [cited 2015 January 11]. Available from: http://www.mrlc.gov/nlcd06_data.php
- [PUC] Public Utility Commission of Texas. 2013. Water & Sewer Certificates of Convenience and Necessity Service Areas & Facility Lines [Internet]. Austin (Texas): Public Utility Commission of Texas; [cited 2015 January 11]. Available from: <https://www.puc.texas.gov/industry/water/utilities/gis.aspx>
- Reidy MM. 2007. Efficacy of electric fencing to inhibit feral pig movements and evaluation of population estimation techniques [thesis]. [Kingsville (Texas)]: Texas A&M University-Kingsville.
- Riebschleager KJ, Karthikeyan R, Srinivasan R, McKee K. 2012. Estimating potential *E. coli* sources in a watershed using spatially explicit modeling techniques. *Journal of the American Water Resources Association*. 48(4):745-761.
- Teague A, Karthikeyan R, Babbar-Sebens M, Srinivasan R, Persyn RA. 2009. Spatially explicit load enrichment calculation tool to identify potential *E. coli* sources in watersheds, *Transactions of the ASABE*. 52(4):1109-1120.
- [TCEQ] Texas Commission on Environmental Quality. 2012. 2012 Texas integrated report [Internet]. Austin (Texas): Texas Commission on Environmental Quality; [cited 2015 January 11]. Available from: <http://www.tceq.texas.gov/waterquality/assessment/waterquality/assessment/12twqi/twqi12>
- [TCEQ] Texas Commission on Environmental Quality. 2010. Chapter 307 – Texas surface water quality standards [Internet]. Austin (Texas): Texas Commission on Environmental Quality; [cited 2015 January 30]. 217 p. Available from: https://www.tceq.texas.gov/assets/public/waterquality/standards/TSWQS2010/TSWQS2010_rule.pdf
- [USCB] U.S. Census Bureau. 2010. 2010 TIGER/Line Shapefiles [Internet]. Washington (District of Columbia): U.S. Census Bureau; [cited 2015 January 11]. Available from: <ftp://ftp2.census.gov/geo/pvs/tiger2010st/>
- [USCB] U.S. Census Bureau. 2013. Annual estimates of the resident population: April 1, 2010 to July 1, 2012 [Internet]. Washington (District of Columbia): U.S. Census Bureau, Population Division; [cited 2015 January 11]. Available from: http://factfinder.census.gov/faces/tableservices/jsf/pages/productview.xhtml?pid=PEP_2012_PEPANNRES&prodType=table
- [USDA-NASS] U.S. Department of Agriculture National Agricultural Statistics Service. 2004–2008. Texas agricultural statistics [Internet]. Austin (Texas): U.S. Department of Agriculture National Agricultural Statistics Service Texas Field Office; [cited 2015 January 11]. Available from: http://www.nass.usda.gov/Statistics_by_State/Texas/Publications/Annual_Statistical_Bulletin/
- [USDA-NASS] U.S. Department of Agriculture National Agricultural Statistics Service. 2007. 2007 Census of agriculture [Internet]. Washington (District of Columbia): U.S. Department of Agriculture National Agricultural Statistics Service; [cited 2015 January 11]. Available from: <http://www.agcensus.usda.gov/Publications/2007/index.php>
- [USDA-NRCS] U.S. Department of Agriculture-Natural Resources Conservation Survey. 2004. Soil Survey Geographic (SSURGO) Database [Internet]. Washington (District of Columbia): U. S. Department of Agriculture National Resource Conservation Service; [cited 2015 January 11] Available from: <http://websoilsurvey.sc.egov.usda.gov/App/WebSoilSurvey.aspx>
- [USEPA] U.S. Environmental Protection Agency. 2001. Protocol for developing pathogen TMDLs: Source Assessment, 5-1-5-18 1st edition [Internet]. Washington (District of Columbia): U.S. Environmental Protection Agency; [cited 2015 January 11]. 132 p. Available from: http://www.epa.gov/owow/tmdl/pathogen_all.pdf
- [USEPA] U.S. Environmental Protection Agency. 2013. Causes of impairment for 303(d) listed waters [Internet]. Washington (District of Columbia): U.S. Environmental Protection Agency; [cited 2015 January 11]. Available from: http://iaspub.epa.gov/waters10/attains_nationcy.control?p_report_type=T#status_of_data
- [USGS and USDA-NRCS] U.S. Geological Survey and U.S. Department of Agriculture Natural Resources Conservation Service. 2012. Federal standards and procedures for the national watershed boundary dataset (WBD) (3rd edition): U.S. Geological Survey Techniques and Methods 11-A3 [Internet]. Reston (Virginia): U.S Geological Survey; [cited 2015 January 11]. 63 p. Available from: <http://pubs.usgs.gov/tm/tm11a3/>
- Wagner K, Moench E. 2009. Education program for improved water quality in Copano Bay: Task two report [Internet]. College Station (Texas): Texas Water Resources Institute; [cited 2015 January 11]. TR-347. 33 p. Available from: <http://twri.tamu.edu/reports/2009/tr347.pdf>

- Wagner K, Redmon L, Gentry T, Harmel R. 2012. Assessment of cattle grazing effects on *E. coli* runoff. Transactions of the ASABE. 55(6):2111-2122.
- Yagow G. 2001. Fecal coliform TMDL, Mountain Run watershed, Culpeper County, Virginia [Internet]. Richmond (Virginia): Virginia Tech Department of Biological Systems Engineering, Department of Environmental Quality, and Department of Conservation and Recreation; [cited 2015 January 11]. Available from: <http://www.deq.virginia.gov/portals/0/DEQ/Water/TMDL/apptmdls/rapprvr/mtrnfec.pdf>