TEXAS WATERSHED COORDINATOR ROUNDTABLE

- Welcome to the Roundtable!
- Please be sure you signed-in on your way in the door.
- Coffee and snacks at the back of the room.
- Restrooms outside in hallway on the right.

The Texas Watershed Planning Program is managed by the Texas Water Resources Institute and is funded through a Clean Water Act Section 319(h) nonpoint source grant provided by the Texas State Soil and Water Conservation Board and U.S. Environmental Protection Agency.

INTRODUCTIONS

- Name
- Employer
- Role / Position Title
- Watershed(s) you work in

Texas Watershed Coordinator Roundtable

May 20, 2025 | 9:00 am – 4:00 pm

Texas A&M University Hildebrand Equine Center

3240 F&B Rd, College Station, TX 77845

8:30 a.m.	**Event Sign In**
9:00 a.m.	**Welcome, Introductions and Roundtable Overview** - Lucas Gregory, *Associate Director, TWRI*
9:15 a.m.	**Setting the Stage: History of the Texas Bacteria TMDL Task Force** - Lucas Gregory, *Associate Director, TWRI*
9:30 a.m.	**Microbial Source Tracking: State of the Science, Approaches and Applications in Texas** - Terry Gentry, *Professor, Department of Soil & Crop Sciences – Texas A&M University*
10:30 a.m.	**Networking Break**
11:00 am	**MST and Quantitative Microbial Risk Assessments in Texas** - Anna Gitter, *Assistant Professor, Env. & Occupational Health Sciences – UT Health*
11:45 a.m.	**Networking Lunch Break**
12:45 p.m.	**MST Marker and QMRA Applications to Inform Local Water Quality Standards** - Jeff Soller, *Founder and Principal Scientist, Soller Environmental LLC*
2:00 p.m.	**Networking Break**
2:15 p.m.	**Panel Discussion on Managing Risks In Recreational Waters** - Jason Pinchback, *Water Resources Manager, Texas General Land Office* - Terry Gentry, *Professor, Department of Soil & Crop Sciences – Texas A&M University* - Anna Gitter, *Assistant Professor, Env. & Occupational Health Sciences – UT Health* - Jeff Soller, *Founder and Principal Scientist, Soller Environmental LLC*
3:30 p.m.	**Brief Agency Updates** - EPA, TCEQ, TSSWCB
3:50 p.m.	**Wrap-Up & Program Evaluation** - Next Roundtable – Fall 2025

TEXAS BACTERIA TMDL TASK FORCE

TERMINOLOGY

- CWA: Clean Water Act
- 303(d) List:
  - 1992-1998: Texas Clean Water Act Section 303(d) List
  - 2000-2008: Texas Water Quality Inventory and 303(d) List
  - 2010-present: Texas Integrated Report and 303(d) List
- BST: bacteria source tracking (aka: microbial source tracking)
- TMDL: Total Maximum Daily Load
- I-Plan: TMDL Implementation Plan
- WPP: Watershed Protection Plan
  - (Watershed Based Plans in other states)

HISTORY

- Bacteria concentrations in the 1990s led to 303d List inclusion
- 1998 303d List added TMDL development priorities and completion schedule to meet the CWA Section 303(d) 13-year resolution timeline
  - 8 TMDLs developed prior to this prioritization
  - Work underway in 8 other watersheds
- Then – 2006: Stakeholder feedback in some watersheds suggested little engagement in the planning process
  - Little or no local input for model development
  - Limited local vetting of assumptions
- Approaches used varied widely across the state

BACTERIA TMDL TASK FORCE – SEPTEMBER 2006

- TCEQ & TSSWCB charged a 7-person Task Force with:
  - Examining approaches that other states use to develop and implement bacteria TMDLs
  - Recommend cost-effective and time-efficient methods to develop TMDLs
  - Recommend effective approaches for developing TMDL Implementation Plans (I-Plans)
  - Evaluate various models and bacteria source tracking (BST) methods available for TMDL and I-Plan development and recommend conditions for appropriate use of certain methods
  - Develop a roadmap for further research needed to reduce uncertainty about how bacteria behave under different water conditions in Texas
- Engaged roughly 50 stakeholders and agency staff in meetings and draft report review

BACTERIA TMDL TASK FORCE REPORT – JUNE 2007

- Described characteristics, strengths, and weaknesses of models/tools used/under development to assist bacteria TMDL and I-Plan analysis
  - Load duration curves
  - Spatial Models
    - Arc Hydro → SPARROW → SELECT
  - Mass Balance Models
    - BLEST → BIT
  - Mechanistic Hydrologic/Water Quality Models
    - HSPF → SWAT → SWMM → WASP
- Describes and recommends effective use of BST methods
  - ERIC-PCR → Ribotyping → PFGE → KB-ARA → CSU → *Bacteriodales* PCR

BACTERIA TMDL TASK FORCE REPORT – JUNE 2007

- Recommended 3-Tier Approach to Developing/Implementing TMDLs & I-Plans
  - Tier 1 – 1 year process to form stakeholder group, develop GIS, survey potential bacteria sources, calculate LDCs from existing data
    - Outcome: Develop TMDL or proceed to Tier 2
  - Tier 2 – 1 to 2 year effort to collect targeted water quality monitoring data to fill gaps, conduct library independent BST to determine major sources, and develop simple spatial or mass balance bacteria models
    - Outcome: Develop TMDL, request UAA, or proceed to Tier 3
  - Tier 3 – 2 to 3 year process to continue strong stakeholder involvement, continue extensive monitoring, conduct library dependent BST, develop detailed watershed model
    - Outcome: Information needed for TMDL and I-Plan development in complex watersheds

BACTERIA TMDL TASK FORCE REPORT – JUNE 2007

- Charted course for addressing bacteria impairments in Texas
- Provided toolbox approach
- Used for TMDLs, I-Plans, and WPPs
- Led to expanded use of BST in Texas

Microbial Source Tracking: State of the Science, Approaches and Applications in Texas

Terry Gentry

Department of Soil and Crop Sciences
Texas A&M University

May 20, 2025

Photo: Texas Beach Watch, Texas General Land Office

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Don't leave your mark at the pool this summer!

It only takes one person with diarrhea to contaminate the entire pool.

Learn more at www.cdc.gov/healthyswimming

What is Microbial Source Tracking?

- Used to determine the sources of fecal contamination
- Based on uniqueness of bacteria or other targets from individual sources
- A variety of different methods used
- Often works best as part of a "toolbox approach"

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MST Target Organisms

- Microbial v. Bacterial Source Tracking
- Different targets:
    - *E. coli*
    - *Bacteroidales*
    - Bacteriophage
    - Human viruses
    - Animal cells
    - Chemicals

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Evolution of Microbial Source Tracking Technologies

Timeframe	Category	
	Library Dependent	Library Independent
Traditional technologies **1970's - 1990's**	**Phenotyping** Antibiotic resistance profiling Biochemical profiling Carbon source utilization	**Chemical detection** Caffeine Coprostanol Optical brighteners **Source-specific microorganisms** Coliphage Bifidobacterium
PCR-based technologies **1990's - 2010's**	**Genotyping** ERIC-PCR Rep-PCR PFGE Ribotyping	**Source-specific PCR/qPCR** Human: Bacteroides Norovirus crAssphage Swine: Bacteroides Bovine: Bacteroides Gull: Bacteroides Poultry: Bacteroides
Emerging sequencing-based technologies **2010's - Present**	**16S rRNA gene/Shotgun sequencing** Shared-OTUs SourceTracker Meta-SourceTracker	**Shotgun sequencing** crAssphage genome

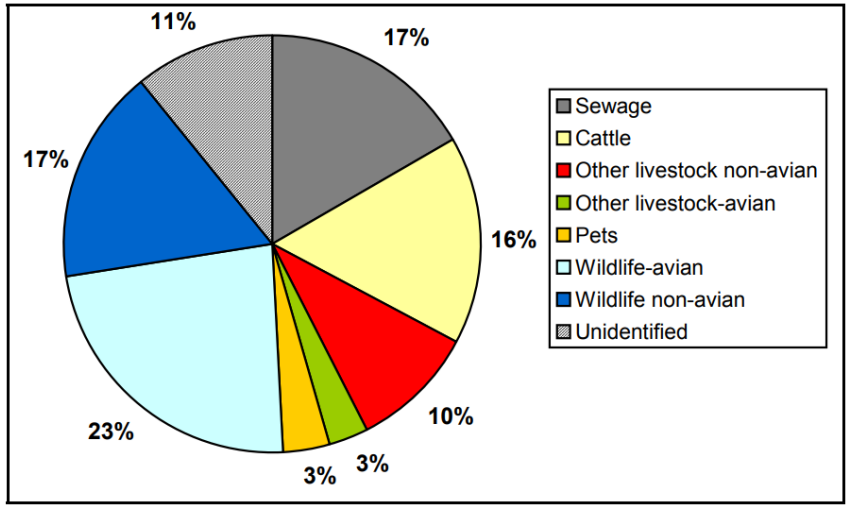
Adapted from Raza *et al.* (2021)

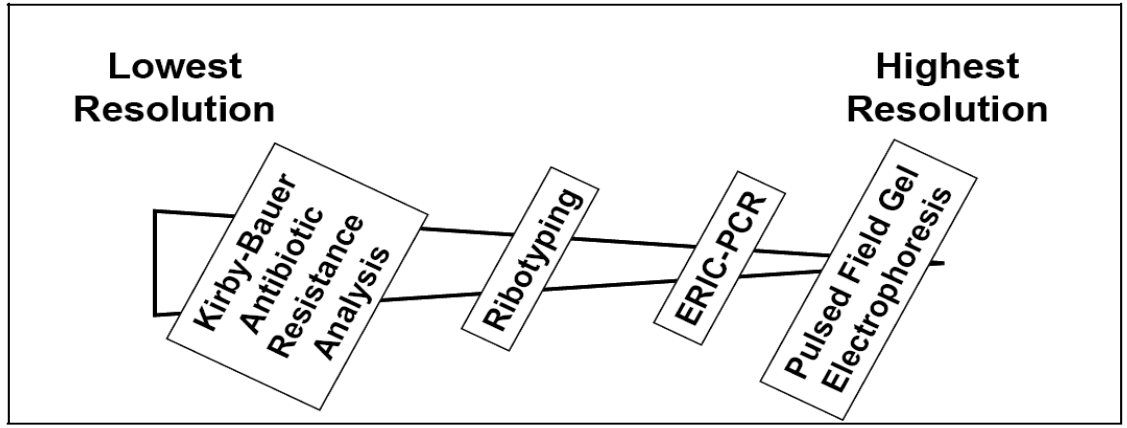
MST Approaches

- **Culture-based**
  - Isolate microorganisms (bacteria)
  - Phenotypic/genotypic characterization
  - Compare to isolates from known-source samples
- **Marker-based**
  - Extract DNA from samples
  - Use PCR-based methods to detect/quantify source-specific markers
- **Sequencing-based**
  - Extract DNA from samples
  - DNA sequencing, compare to known-sources

Lake Waco/Belton Project

- Initiated Sep. 2002 with funding from TSSWCB
- 4-method composite performed better than individual methods
- 2-method composites appeared promising
  - ERIC-ARA = lower cost but more processing
  - ERIC-RP = higher cost but automated





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Bacteria TMDL Task Force

- Evaluated a variety of models and bacteria source tracking (BST) methods available for developing TMDLs and I-Plans
- Methods included ERIC-PCR, Ribotyping, PFGE, KB-ARA, CSU and *Bacteroidales* PCR
- Recommended:
  - Library independent methods like *Bacteroidales* PCR for preliminary qualitative analyses
  - Library-dependent methods if more quantitative data needed
  - Confirmed ERIC-RP as a recommended method

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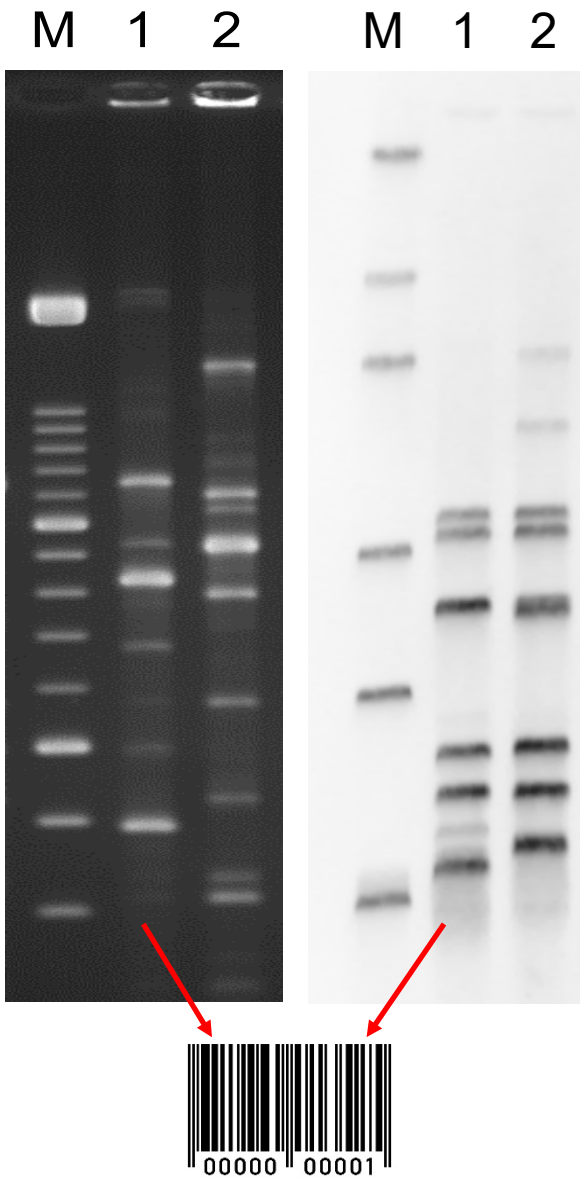
Culture-Based MST Methods

Methods:

- **DNA fingerprinting**
  - **Enterobacterial repetitive intergenic consensus sequence-polymerase chain reaction (ERIC-PCR)**
  - **RiboPrinting® (RP)**



Advantages/Disadvantages:

- **More discriminating**
- **Allows ranking of sources**
- **Relatively expensive**

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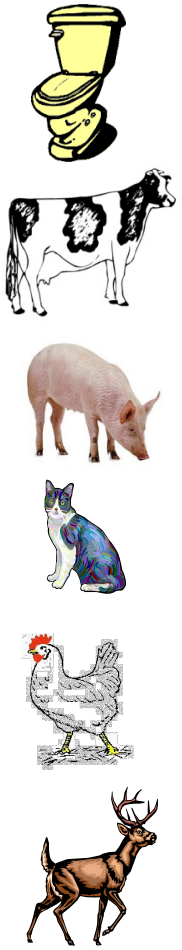
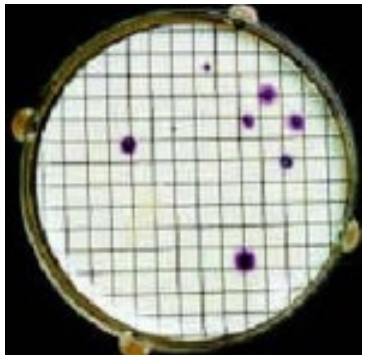
Development of Texas *E. coli* BST Library

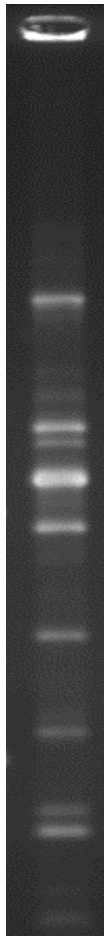
Sources



Isolate *E. coli* →



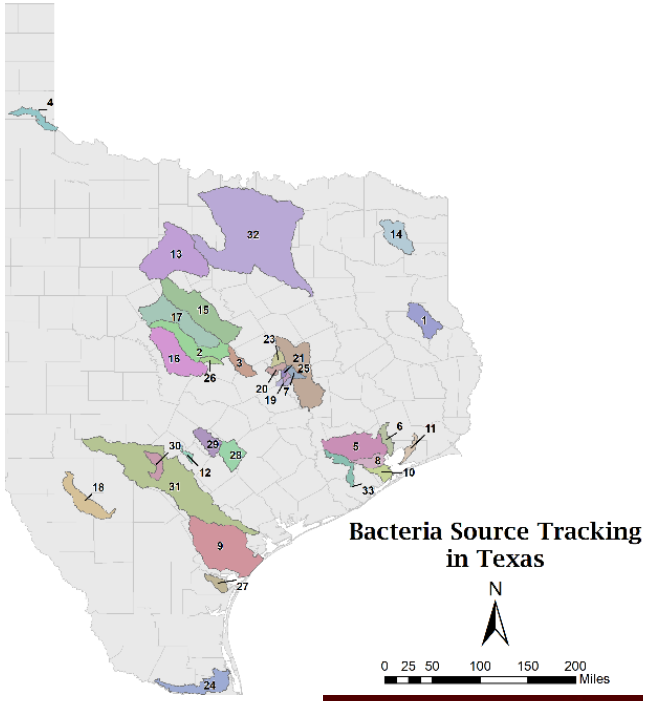
DNA Fingerprint →



Add to Library →

Texas *E. coli* BST Library (v. 03-20)

- Contains 1,912 *E. coli* isolates from 1,653 different human and animal samples
- Developed by collecting over 4,000 domestic sewage, wildlife, livestock, and pet fecal samples and screening over 7,000 isolates for clones and host specificity
- Samples from >20 watersheds across Texas for MST including:
  - Plum Creek
  - San Antonio
  - Lake Granbury
  - Oyster Creek / Trinity River
  - Waco / Belton Lake
  - Little Brazos River Tributaries
  - Attoyac Bayou
- Additional isolates added from future MST projects



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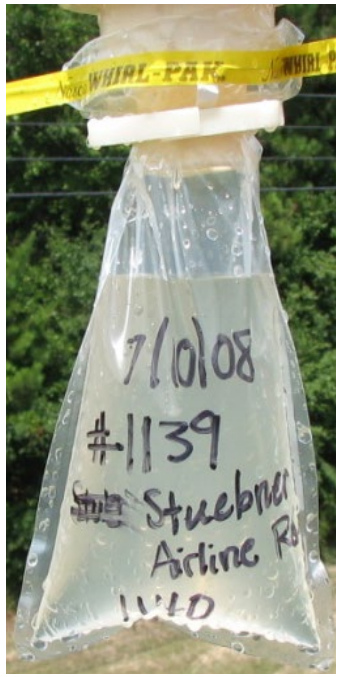
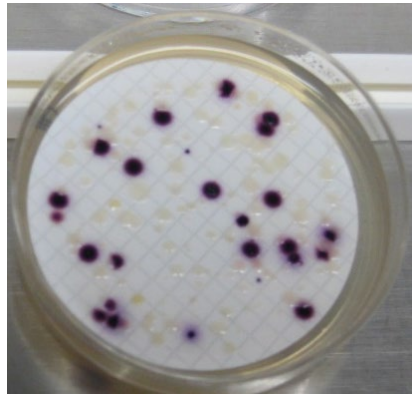
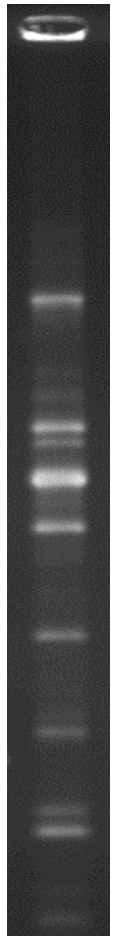
Use of Texas *E. coli* BST Library for Identifying Water Isolates



Isolate *E. coli* →



DNA Fingerprint →



Compare to Library →

Source ID

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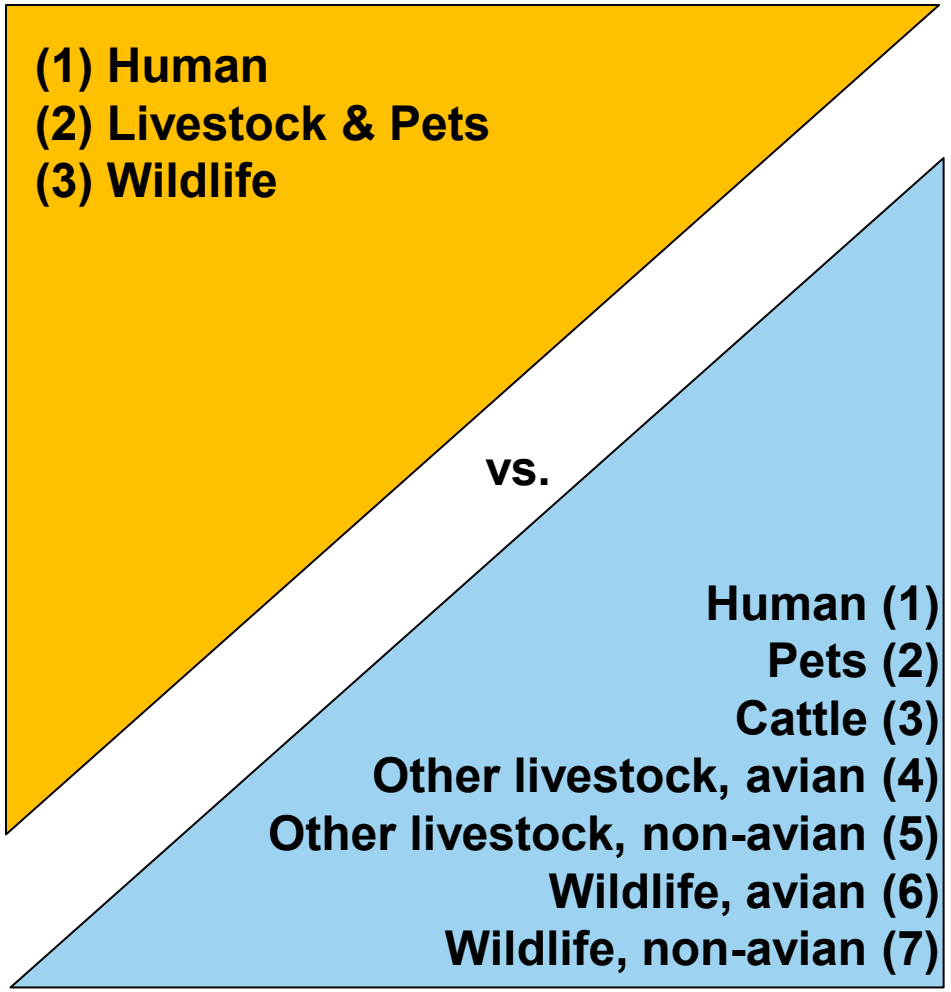
Three-way v. Seven-way Split of Results

- **Using the results**
  - Is it from human sources?
  - Is it from livestock?
  - Is it from wildlife?
- **Biology**
  - Large variety of wildlife
  - Geographical and temporal differences
  - Cosmopolitan strains
- **Statistics**
  - Number of isolates collected
  - May only use three-way split for limited studies



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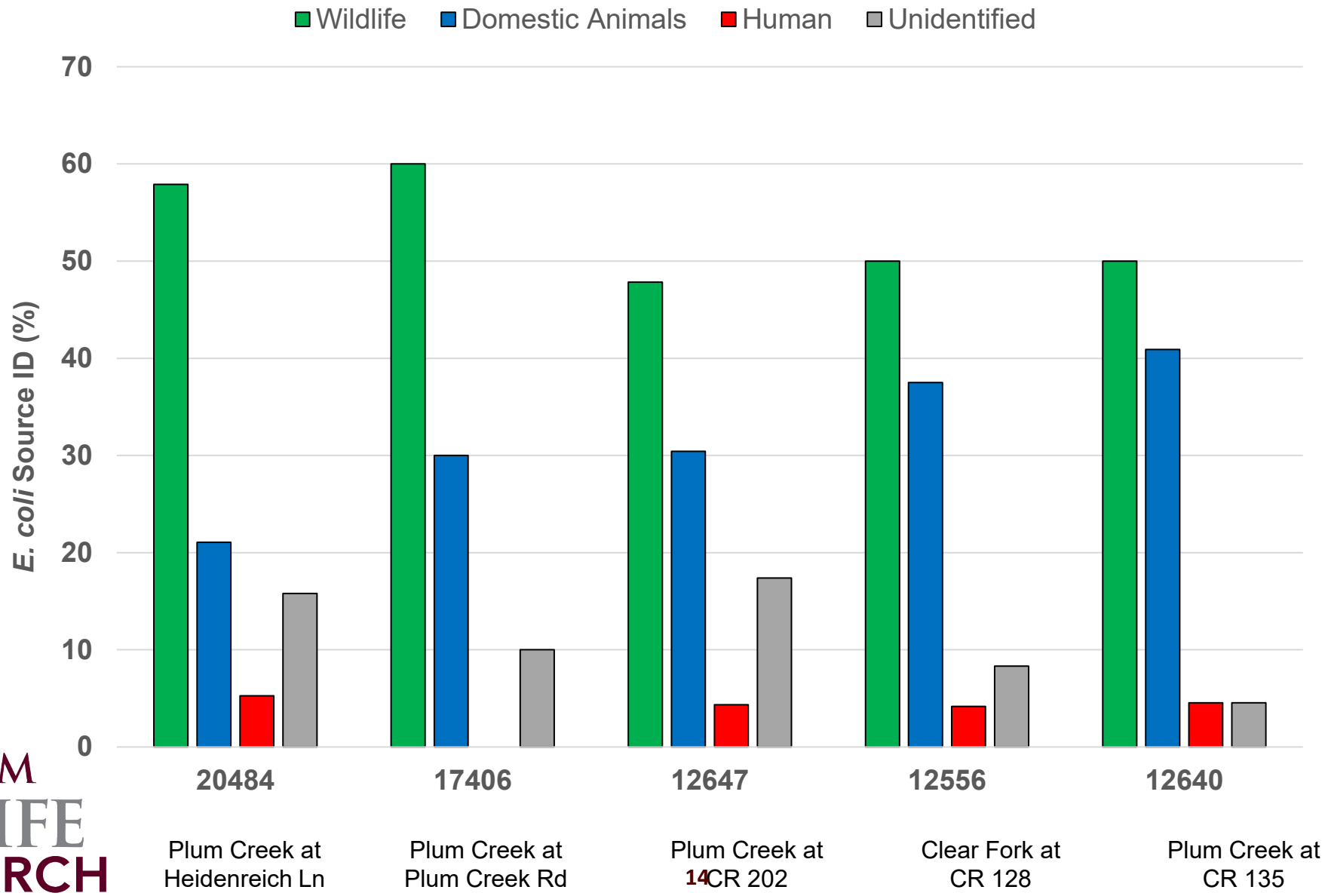
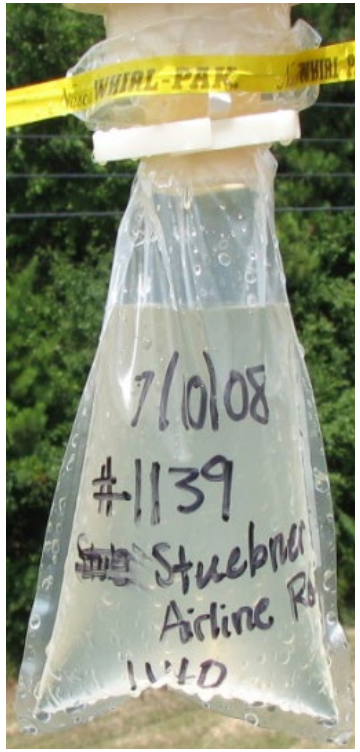
Plum Creek MST Results

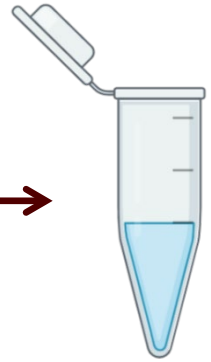
5 Sampling Sites (3-Way Split)



Marker-Based MST

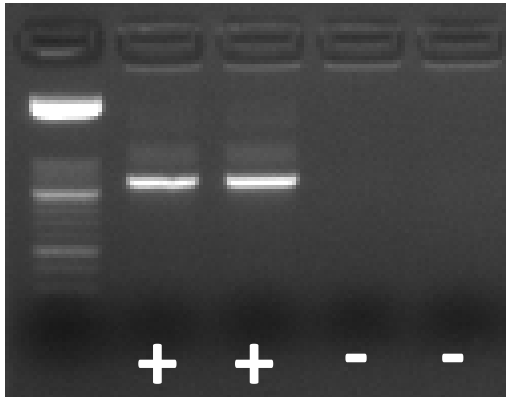


Extract DNA →

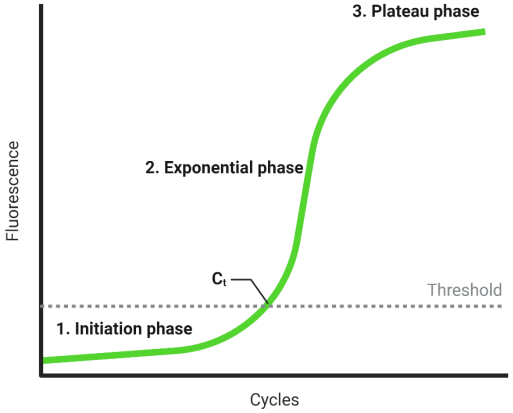


PCR amplify target sequence →

Presence/Absence →



Quantitative →



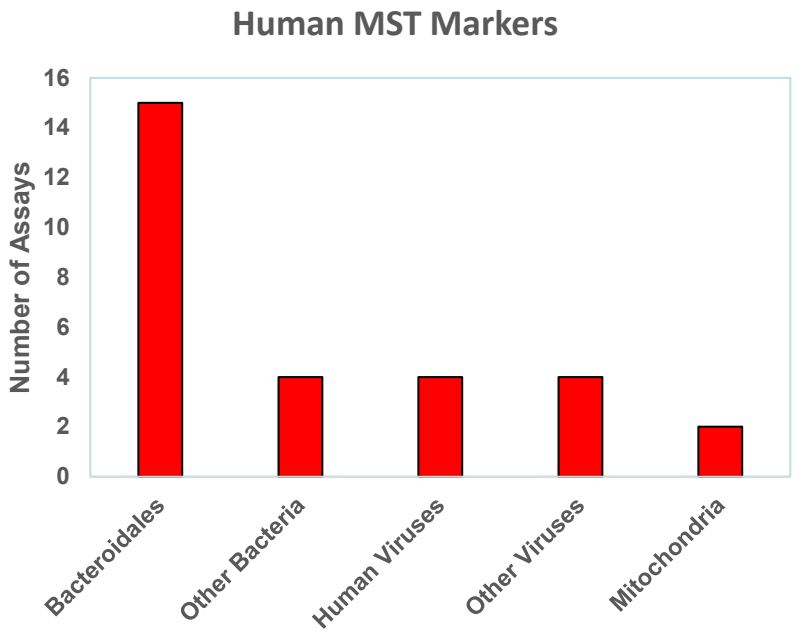
Advantages:

- Cost
- Time

TEXAS A&M AGRILIFE RESEARCH

Marker-Based MST

- Most common approach targets *Bacteroidales*
- *Bacteroidales* – human and animal fecal bacteria, more abundant than *E. coli*
- Markers available for
  - Ruminants (cattle, deer, elk, sheep)
  - Humans
  - Horses
  - Birds
  - Hogs
- Limited markers for wildlife
- Relationship to *E. coli,* enterococci, and pathogens uncertain
- Some highly specific, but tradeoff with sensitivity



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Examples of Marker-Based MST Methods

Host	Marker	Microorganism	Advantages	Disadvantages
Human	HF183	*Bacteroides dorei*	High level in sewage aids sensitivity in environmental samples	Not completely specific, e.g., deer, dogs, chickens
Human	HPyVs	Human polyomaviruses	Complete specificity	Low concentration in sewage restricts sensitivity in environmental samples
Poultry	LA35	*Brevibacterium*	High level in poultry litter aids sensitivity in environmental samples	Some cross-reactivity with other bird species
Ruminant	CF128	*Bacteroidales*	Detects a variety of ruminants, e.g., cattle, deer, goats, sheep	May not be specific enough depending on the application

Teaf *et al*. (2018)

- **Often a tradeoff between sensitivity and specificity**

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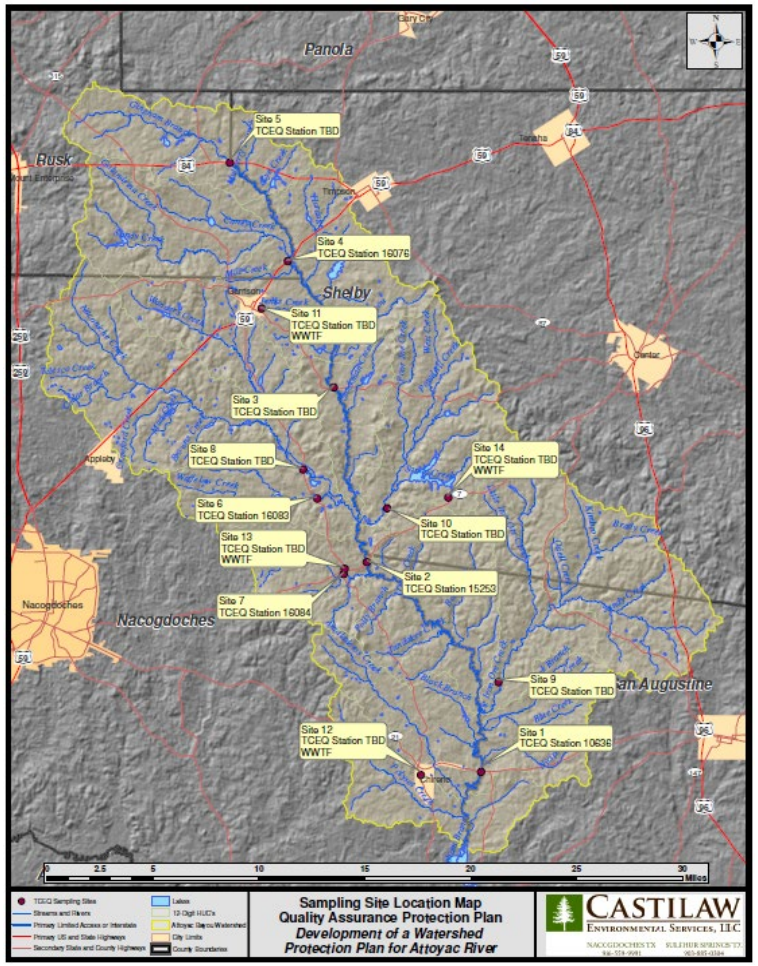
Marker-Based MST in Texas

- Several watersheds in Texas
  - Lake Granbury (UT)
  - Buck Creek (UT)
  - Little Brazos River Tributaries (TAMU)
  - Big Cypress (TAMU)
  - Attoyac Bayou (TAMU)
  - Leona River (TAMU)
  - Galveston (TAMU)
  - Beaumont (TAMU)
  - Nueces County (TAMU)
- Edge-of-field runoff (BMP evaluation)
  - Dairy manure (UT)
  - Grazing systems (TAMU)
- Oklahoma City (UT; waterborne disease outbreak)

TEXAS A&M AGRILIFE RESEARCH

Attoyac Bayou MST

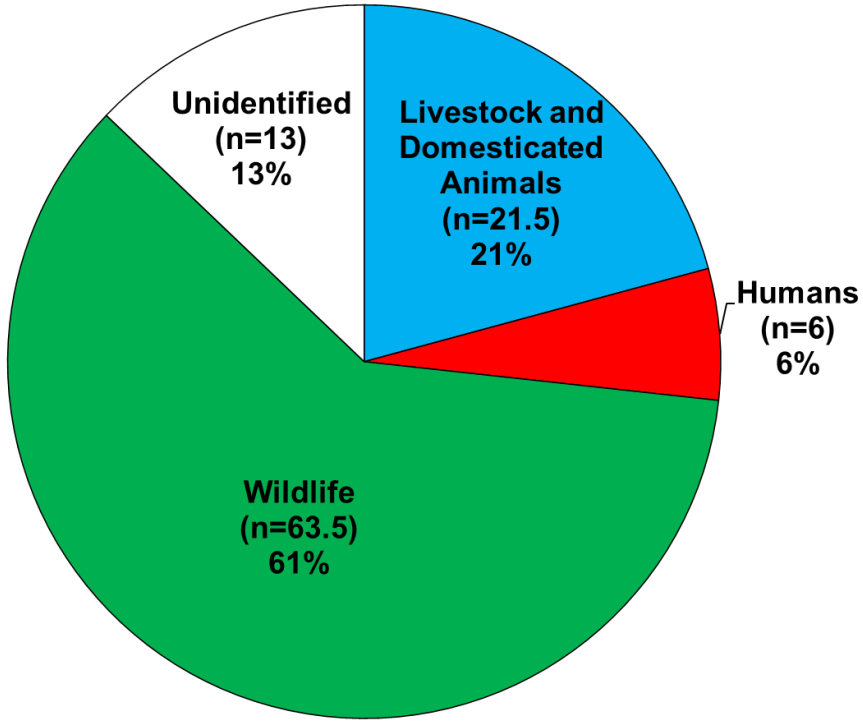
- Limited library-dependent
  - Analyze *E. coli* from ~100 water samples from across the study area using both ERIC-PCR and RP fingerprinting
- Library-independent
  - Analyze ~250 water samples
  - *Bacteroidales* PCR (+/-)
    - Human (HF183)
    - Ruminant (CF128F)
    - Hog (PF163F)
    - Horse (Ho597F)



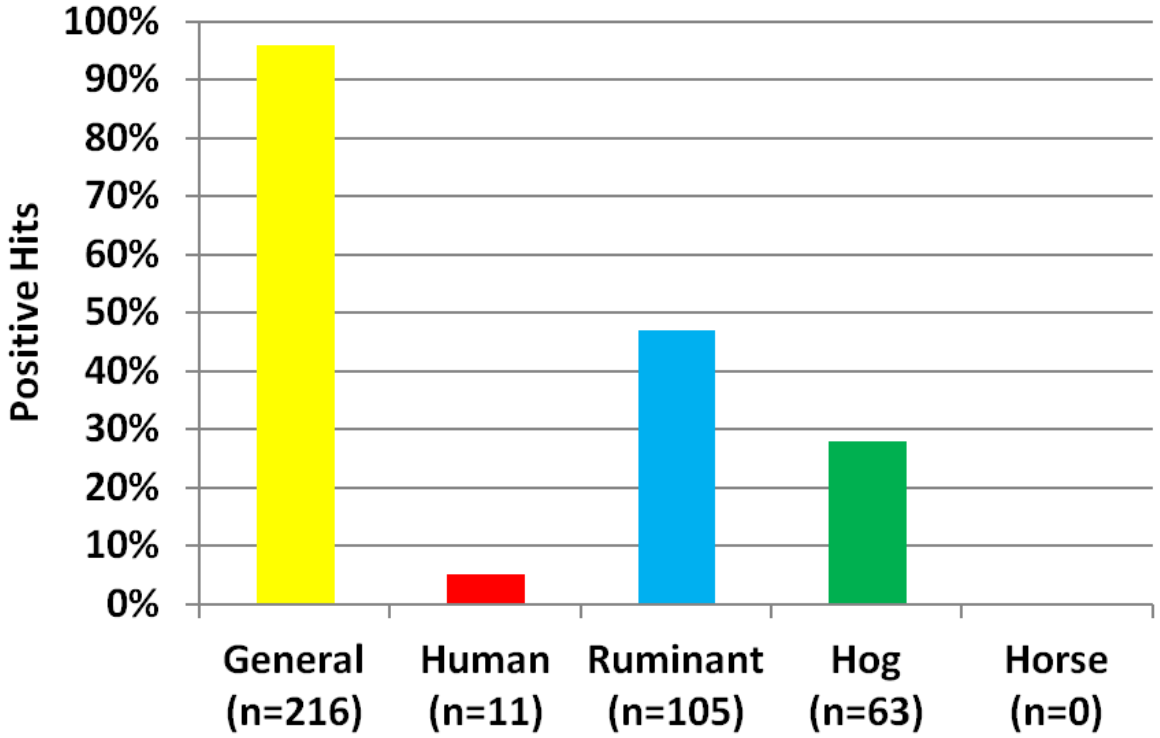
TEXAS A&M AGRILIFE RESEARCH

Attoyac Bayou *Bacteroidales*
Base Flow Samples (n=225)

Culture-Based



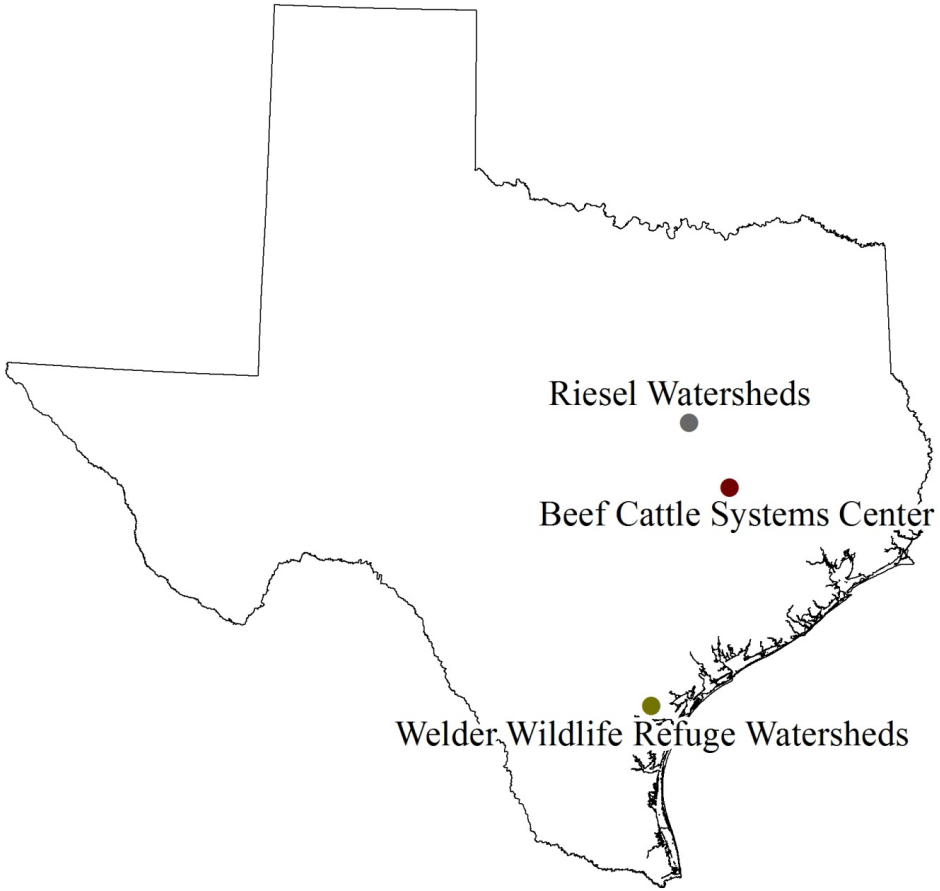
Marker-Based



TEXAS A&M AGRILIFE RESEARCH

Grazing Management Evaluation

- Runoff collected over three years
- *E. coli* - EPA Method 1603
- *Bacteroides* (Layton et al., 2006)
  - Total *Bacteroides* spp. (AllBac)
  - Bovine-associated *Bacteroides* spp. (BoBac)



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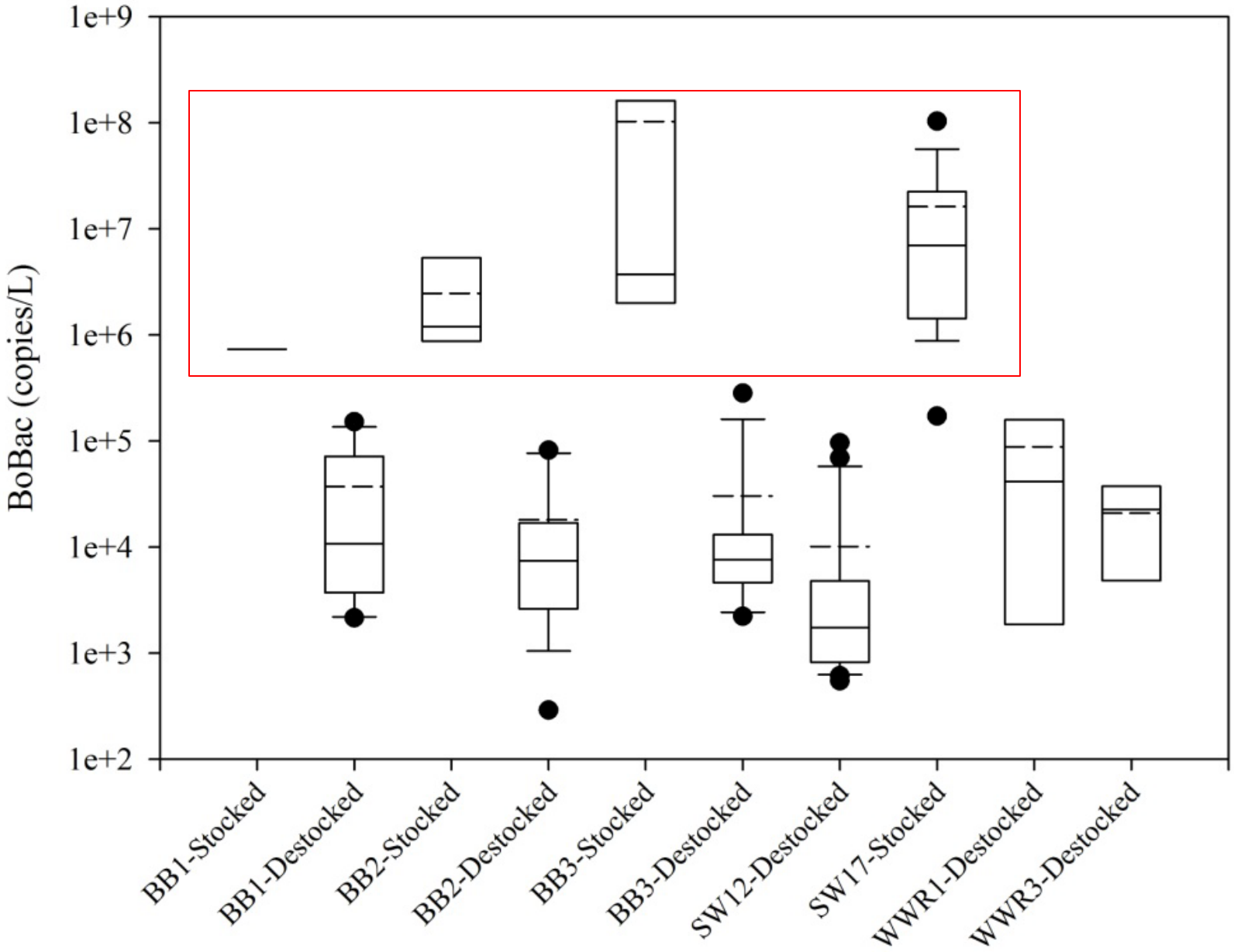

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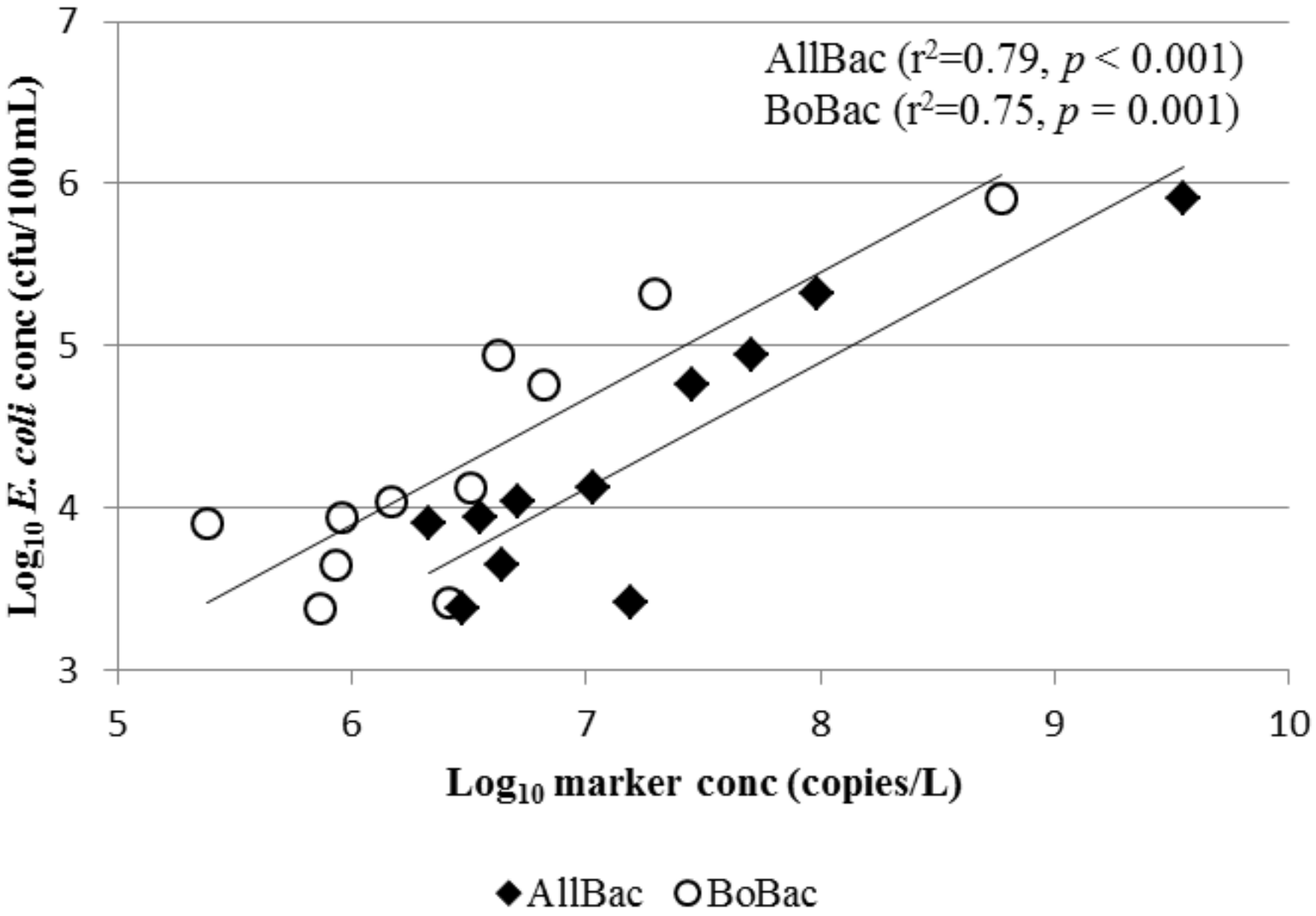

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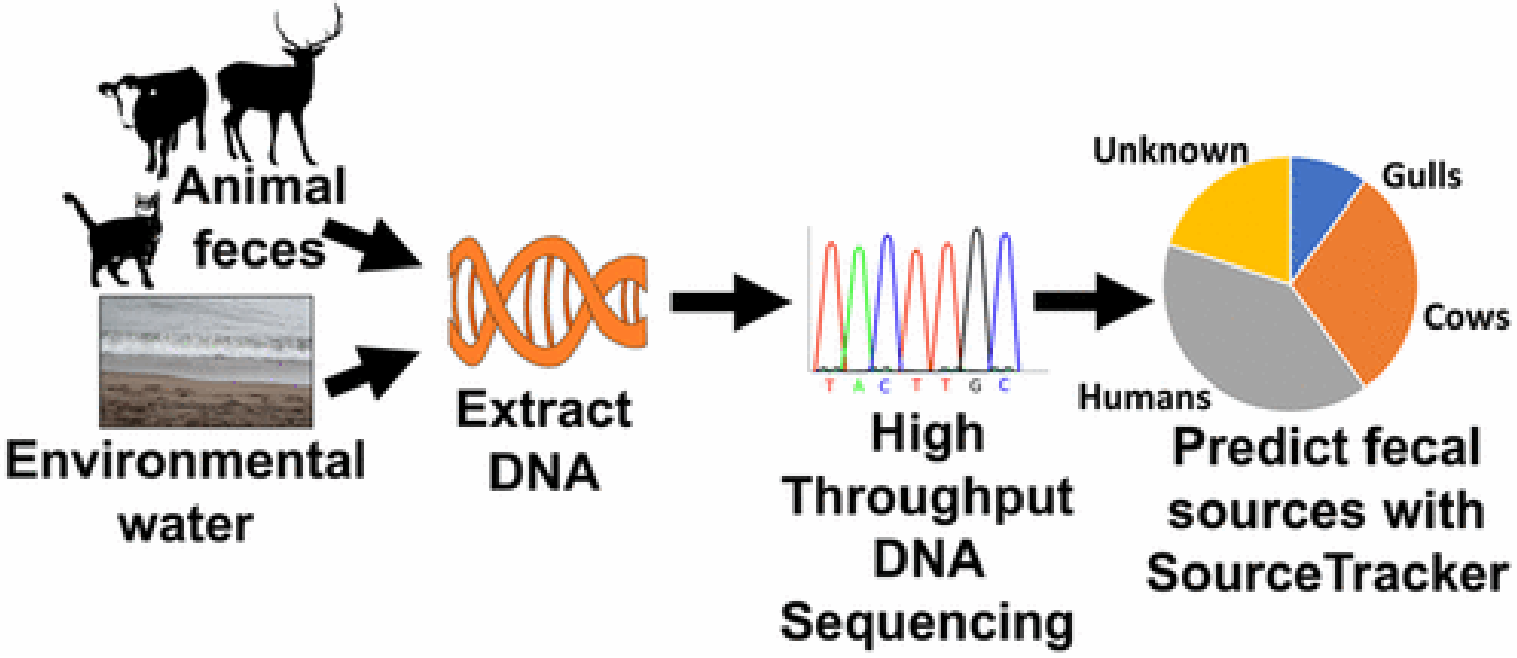
Sequencing-Based MST

- High-throughput DNA sequencing (HTS) to identify microbiome in water samples
- Compare to microbiomes in known-source samples using programs such as SourceTracker (Knights et al., 2011)

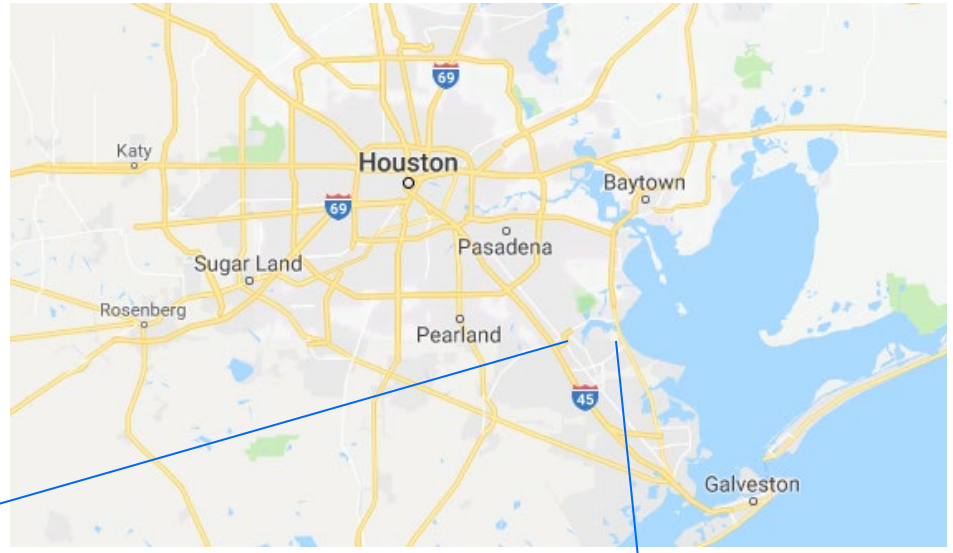


Brown et al. (2017)

Texas A&M AgriLife Research

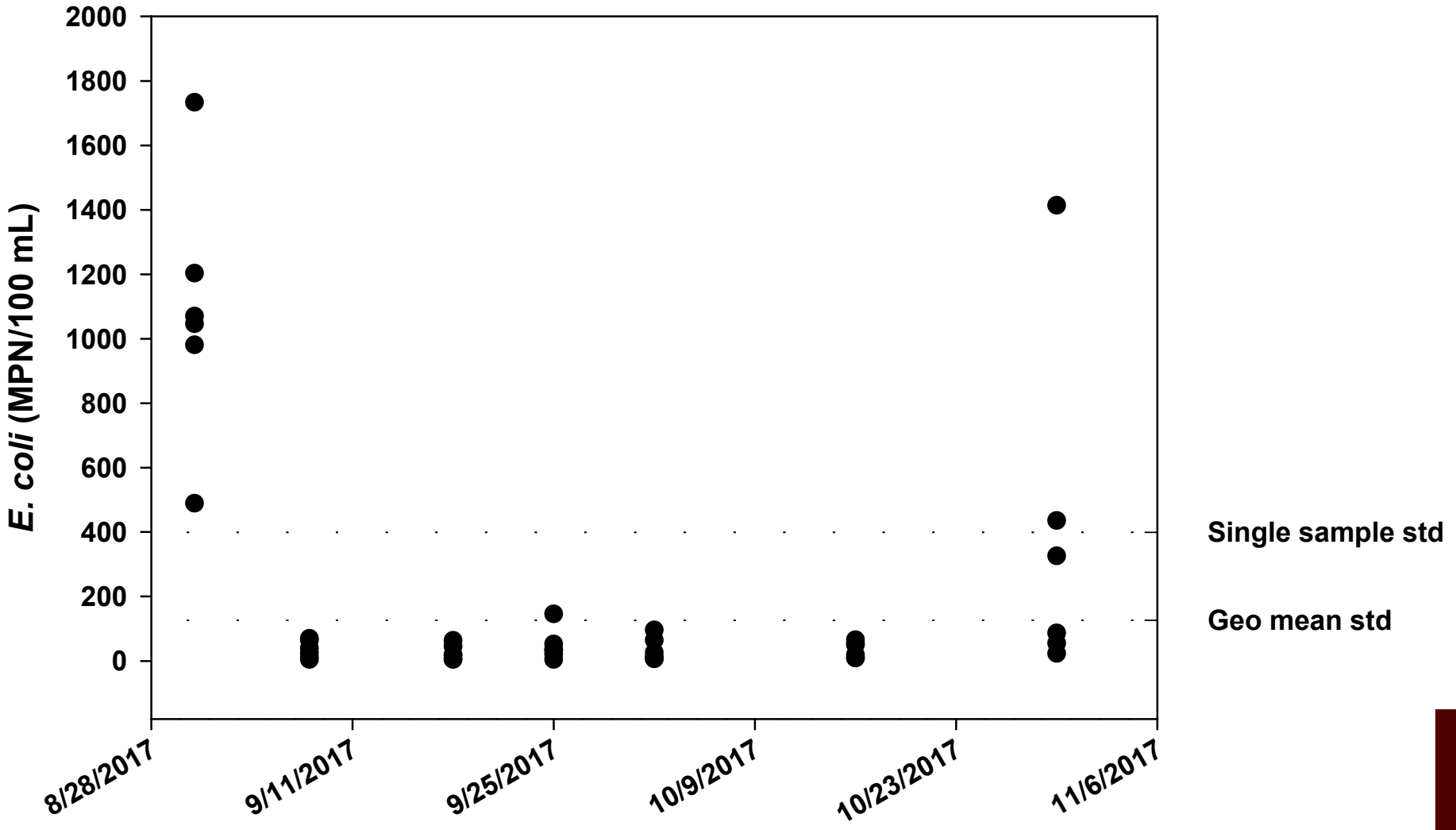
Hurricane Harvey Flooding

- Six locations in the southeastern Houston area around Clear Lake
- Surface water samples collected as soon as sites accessible following the hurricane and then every 1-2 weeks for ~2 months
- Measured *E. coli* and used qPCR for general and human markers



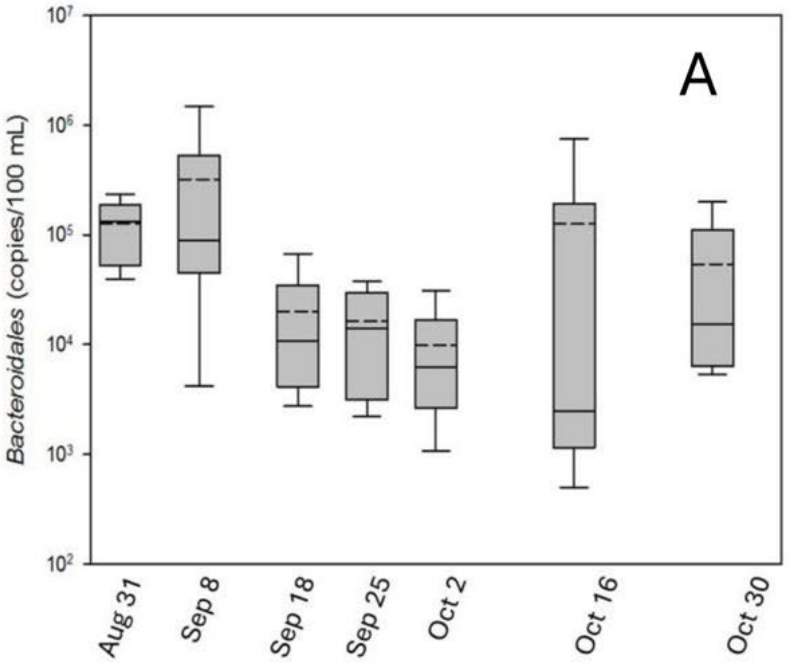
Texas A&M AgriLife Research

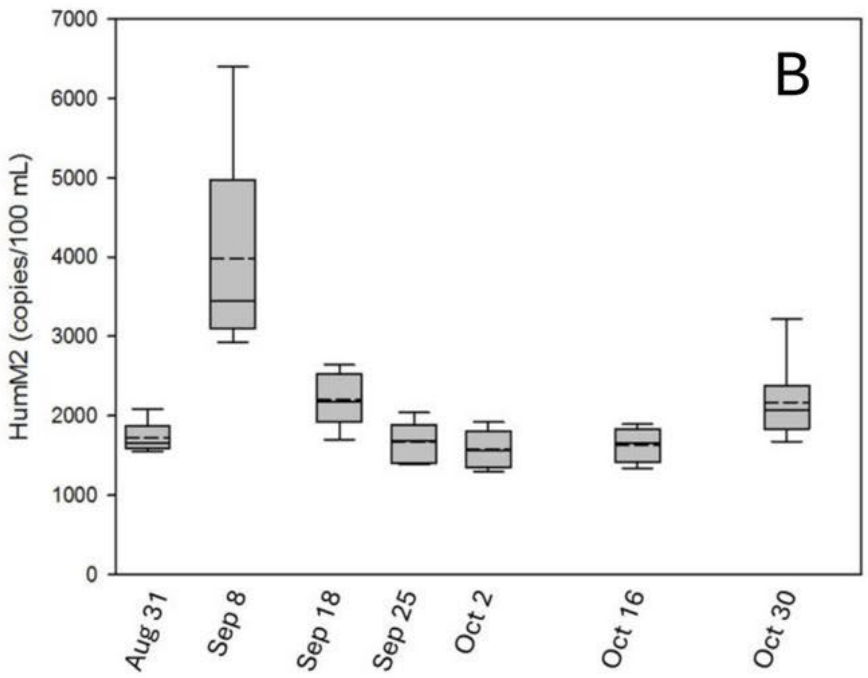
E. coli Levels

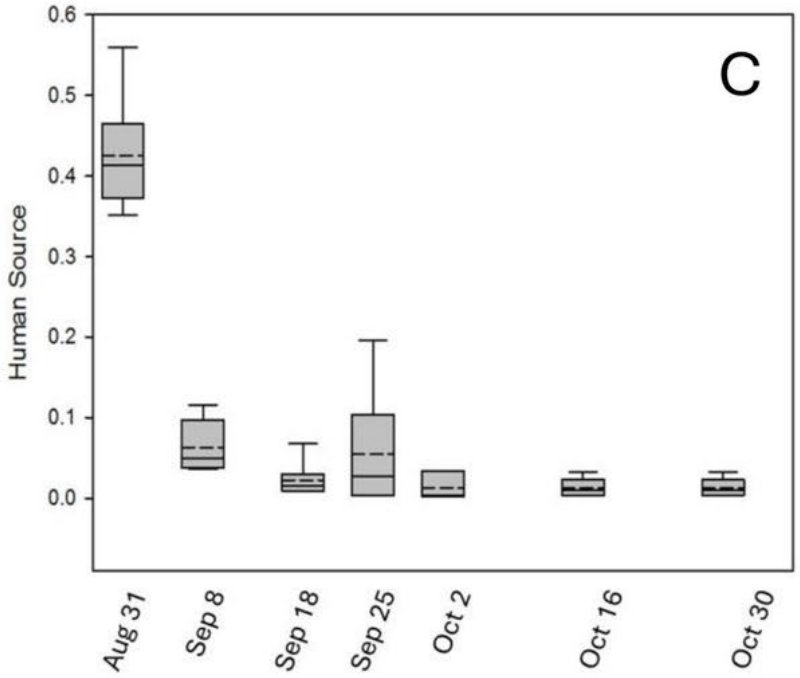


TEXAS A&M AGRILIFE RESEARCH

MST Results







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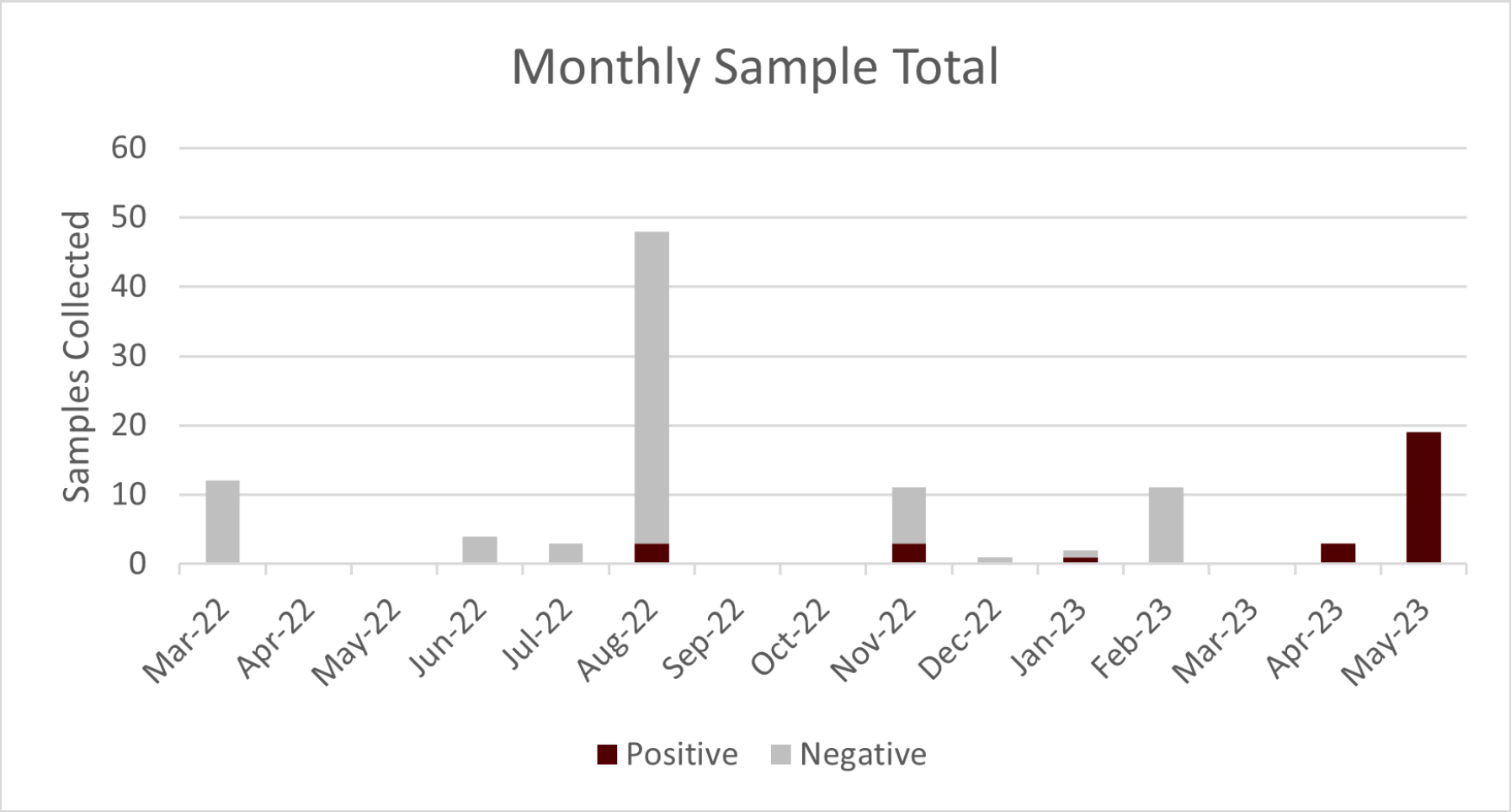
Galveston MST

- TBW samples with enterococci levels >104 MPN/100 mL
- A total of 114 samples from 2022-2023
  - Quantitative PCR markers for specific sources
    - Human (HF183)
    - Dog (DogBact)
    - Gull (LeeSeaGull)
  - Microbiome-based BST (select 2022 samples)
    - Human (WWTF & Septic)
    - Dog & Coyote
    - Gull

Texas A&M AgriLife Research

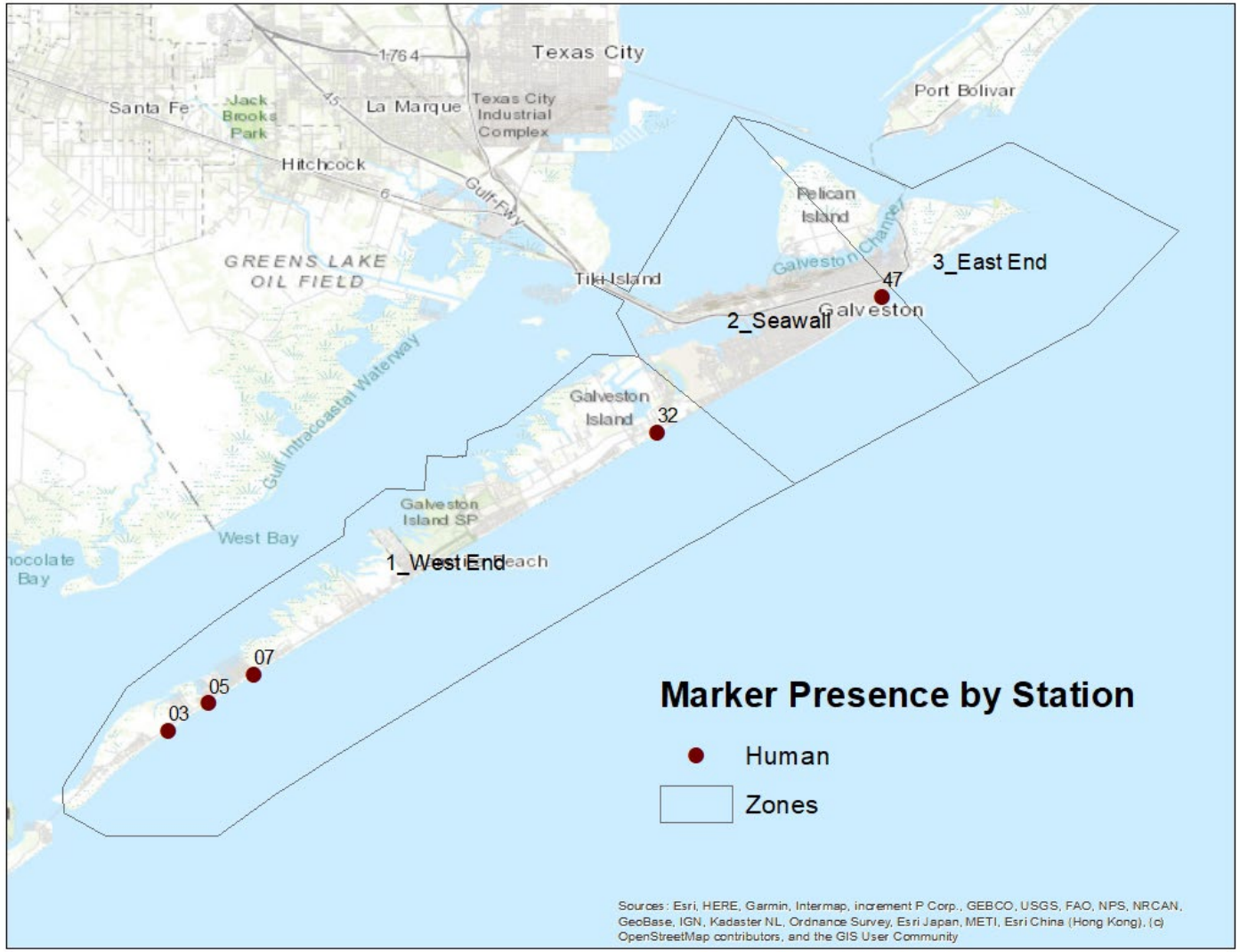
Overall Marker Results



- ~25% of samples positive for at least one of the source markers
- Markers more prevalent in 2023 samples

Texas A&M AgriLife Research

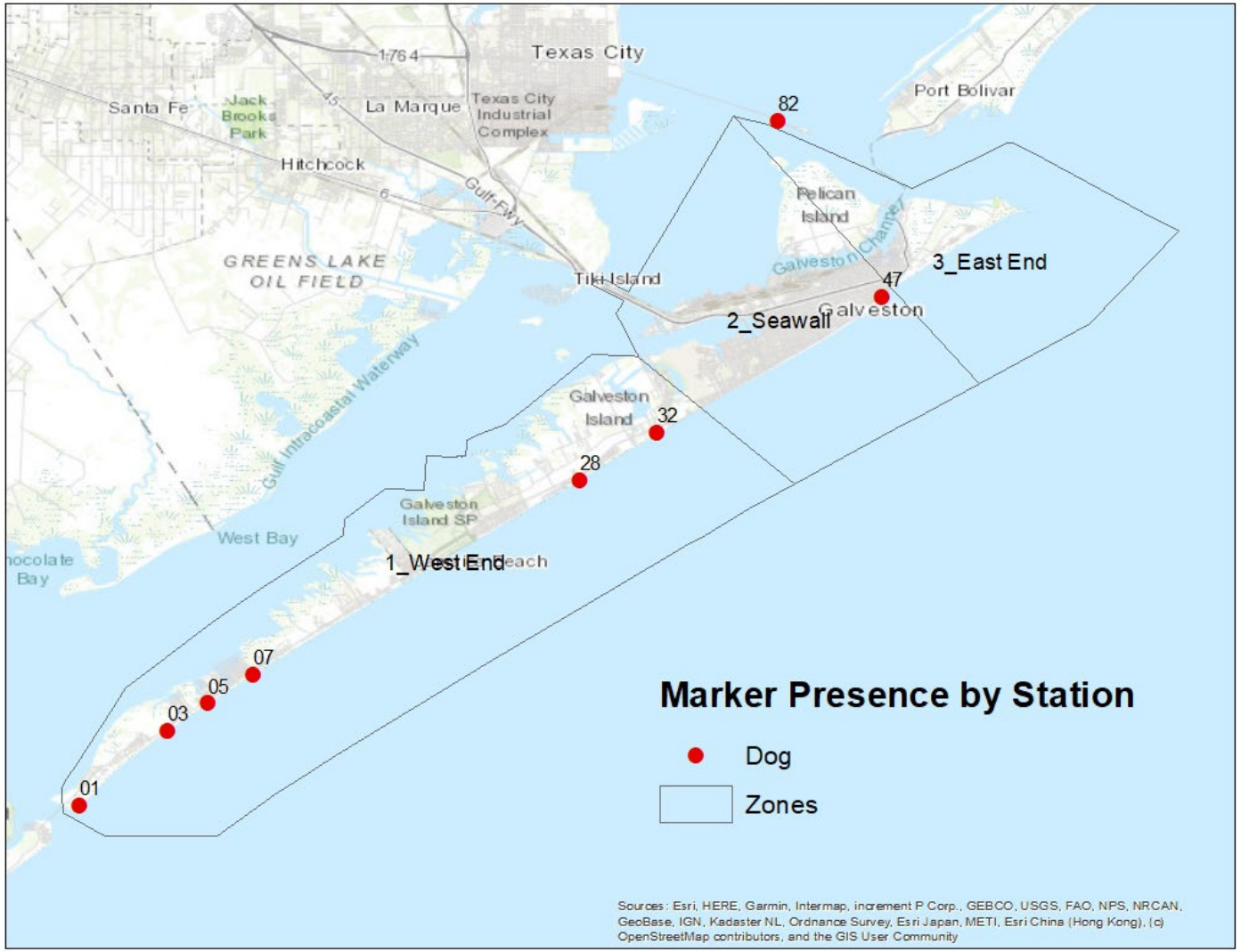
Human Marker



- **Detected in 4% of samples**
- **Highest level (1,138 copies/100 ml) in GAL032 sample from 5/23/2023**

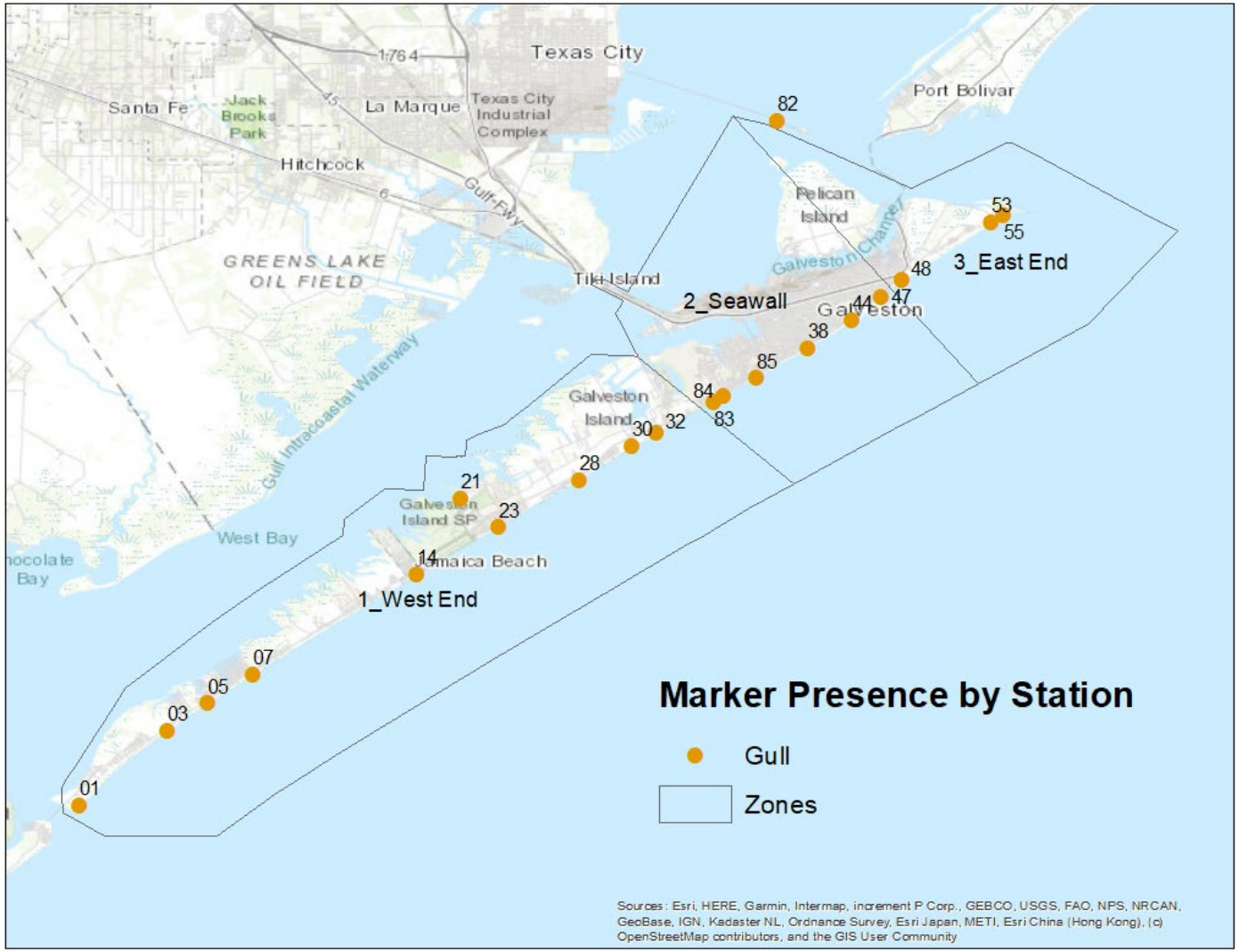
Texas A&M AgriLife Research

Dog Marker



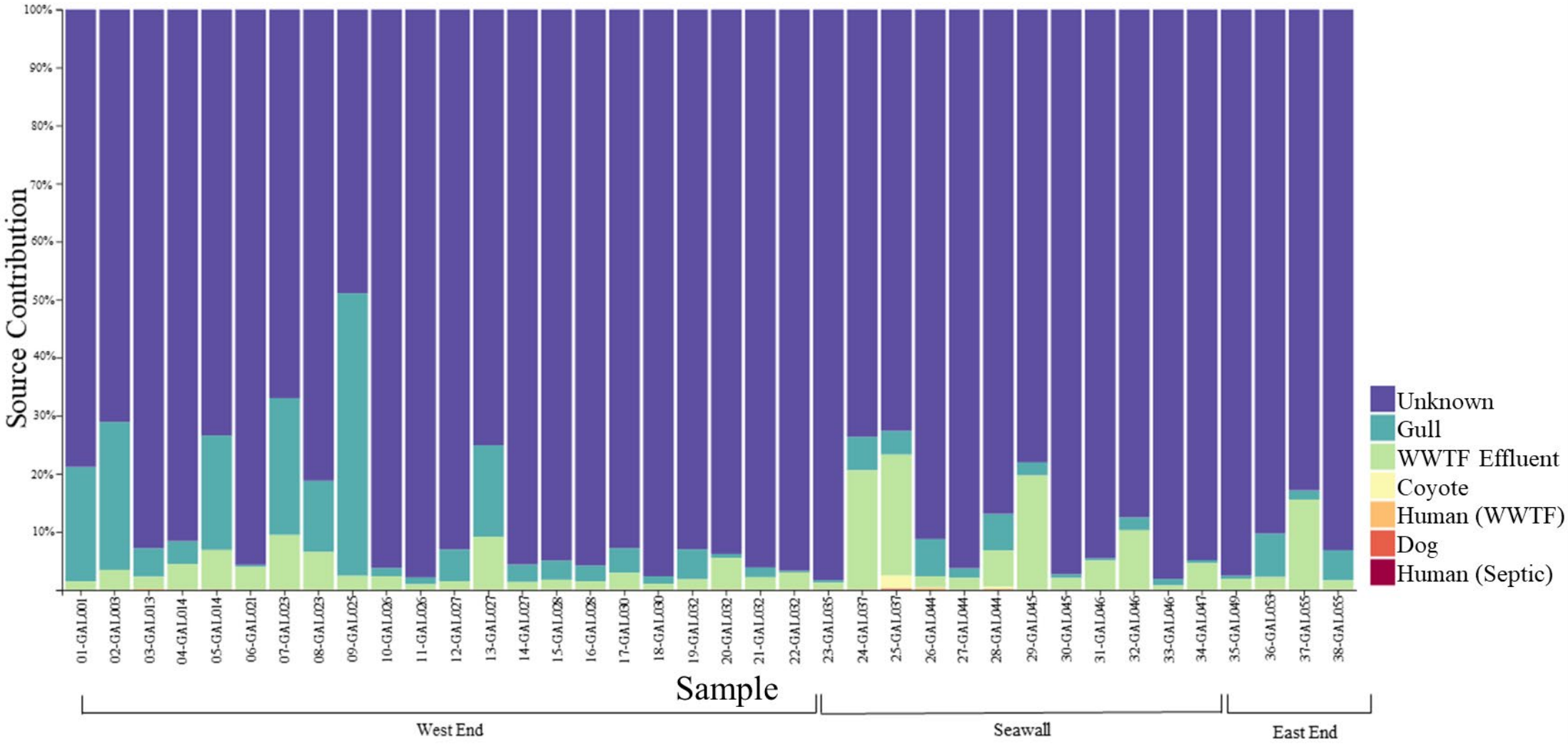
- **Detected in 7% of samples**
- **Wider distribution but tended to overlap with human marker-positive sites**

Gull Marker



- **Detected in 24% of samples**
- **Widest distribution of tested markers**

Microbiome MST (2022 samples)



TEXAS A&M AGRILIFE RESEARCH

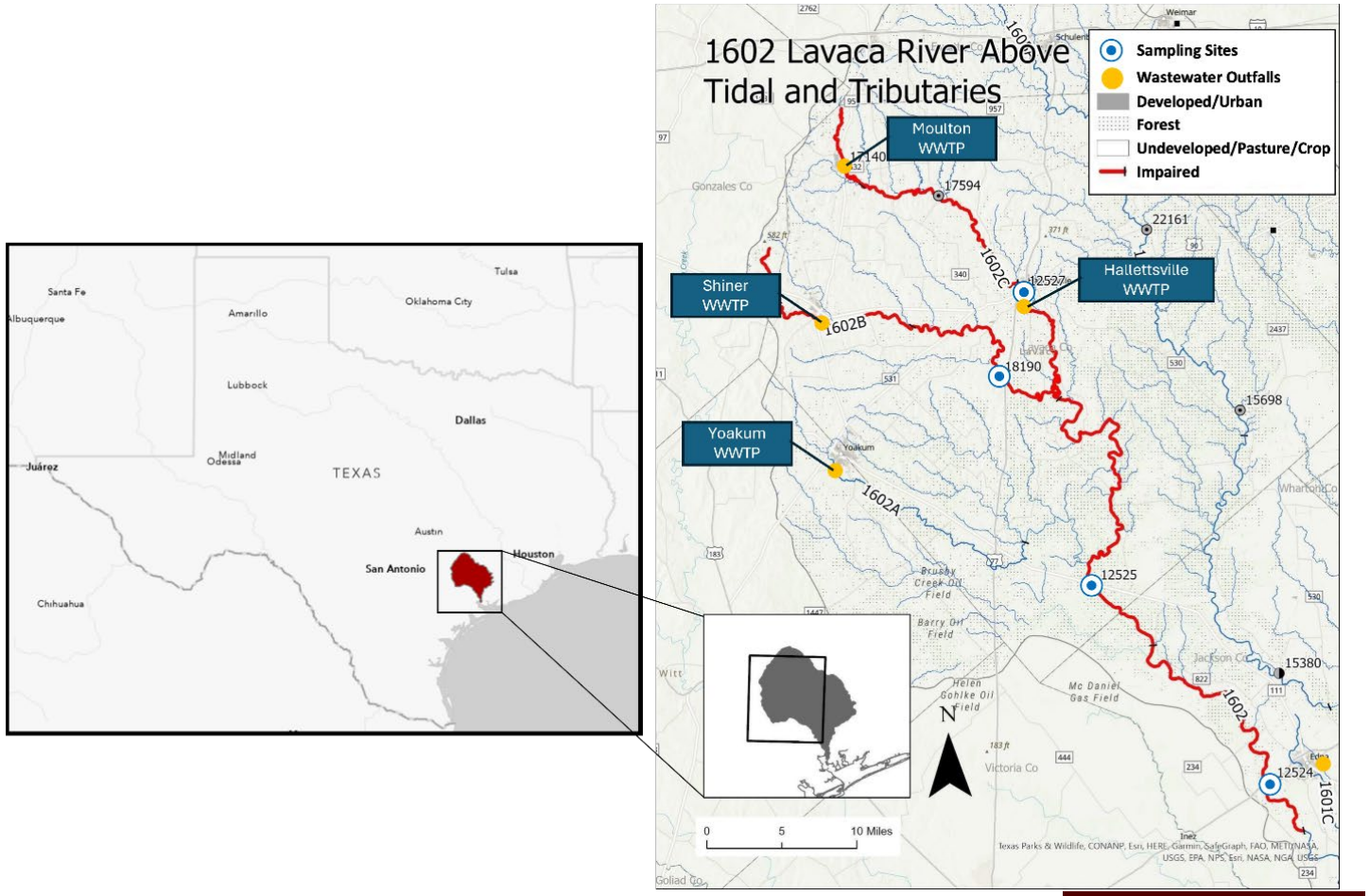
Conclusions

- Results likely impacted by study design and 2022 water quality
- Markers for humans, dogs, and gulls detected at sites throughout the island
- Possible impact of WWTP effluent on aquatic microbiome
- Additional analyses and targeted sampling may help identify major sources of risk
- Using QMRA to estimate risk using current data

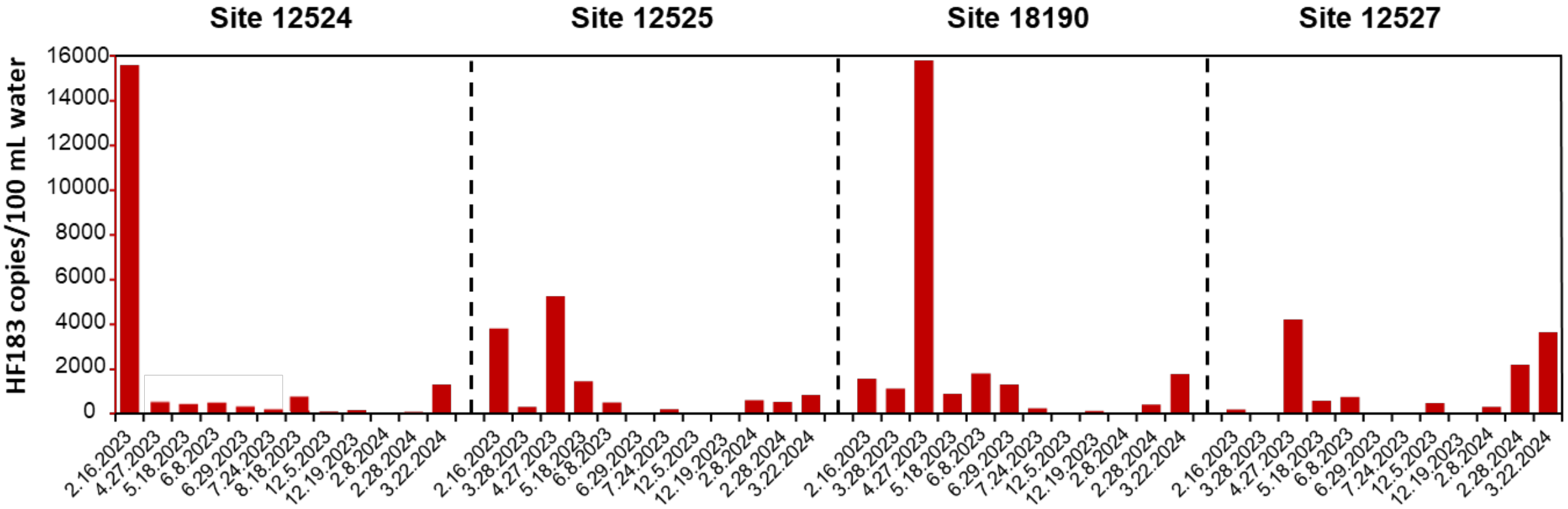
Texas A&M AgriLife Research

Lavaca River MST

- Monthly (12) grab samples from four sites
- Marker-based MST – human (HF183)
- Sequencing-based MST
  - Microbiome
    - 16S rRNA gene
    - SourceTracker
  - Shotgun sequencing



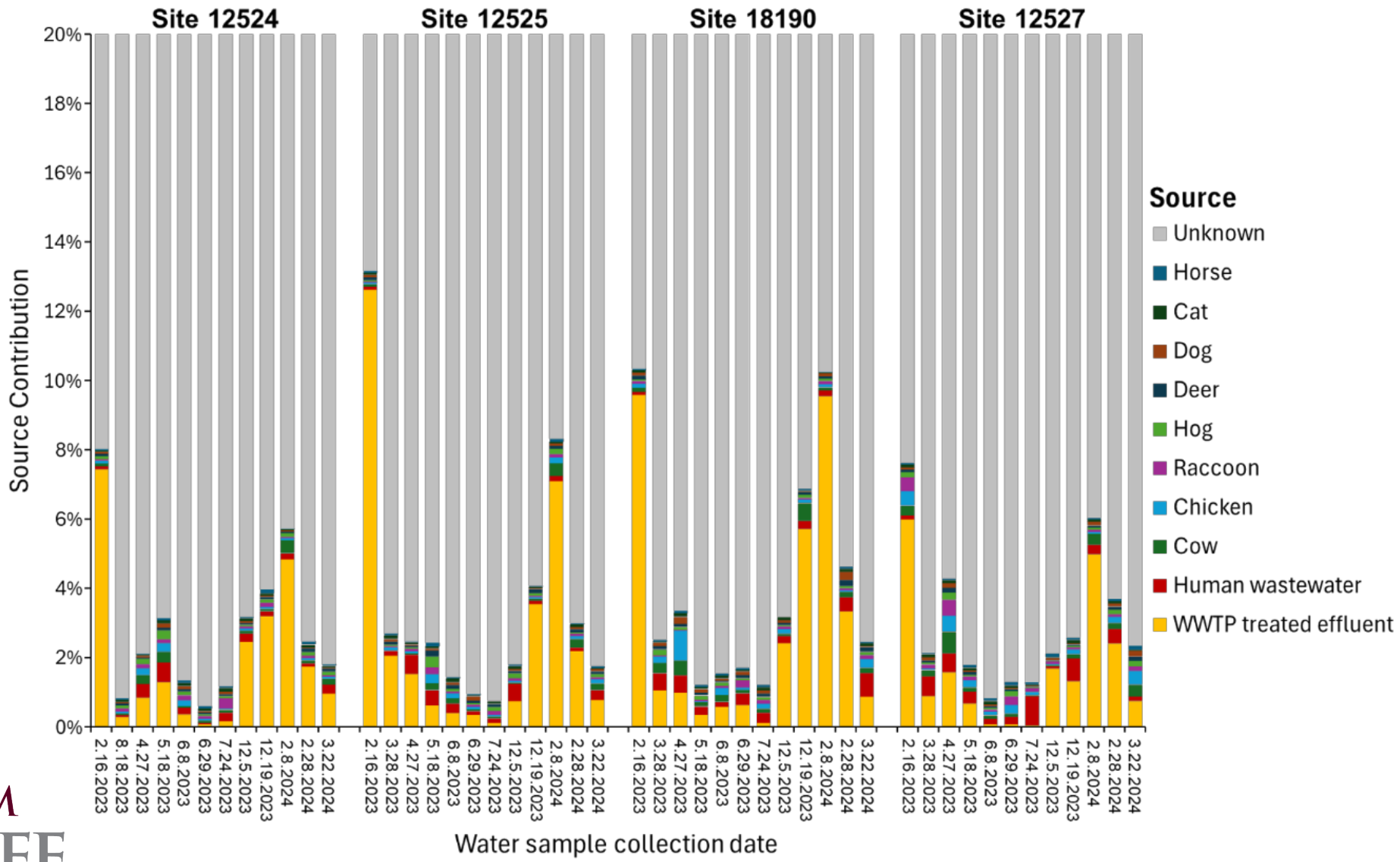
Lavaca River Watershed MST



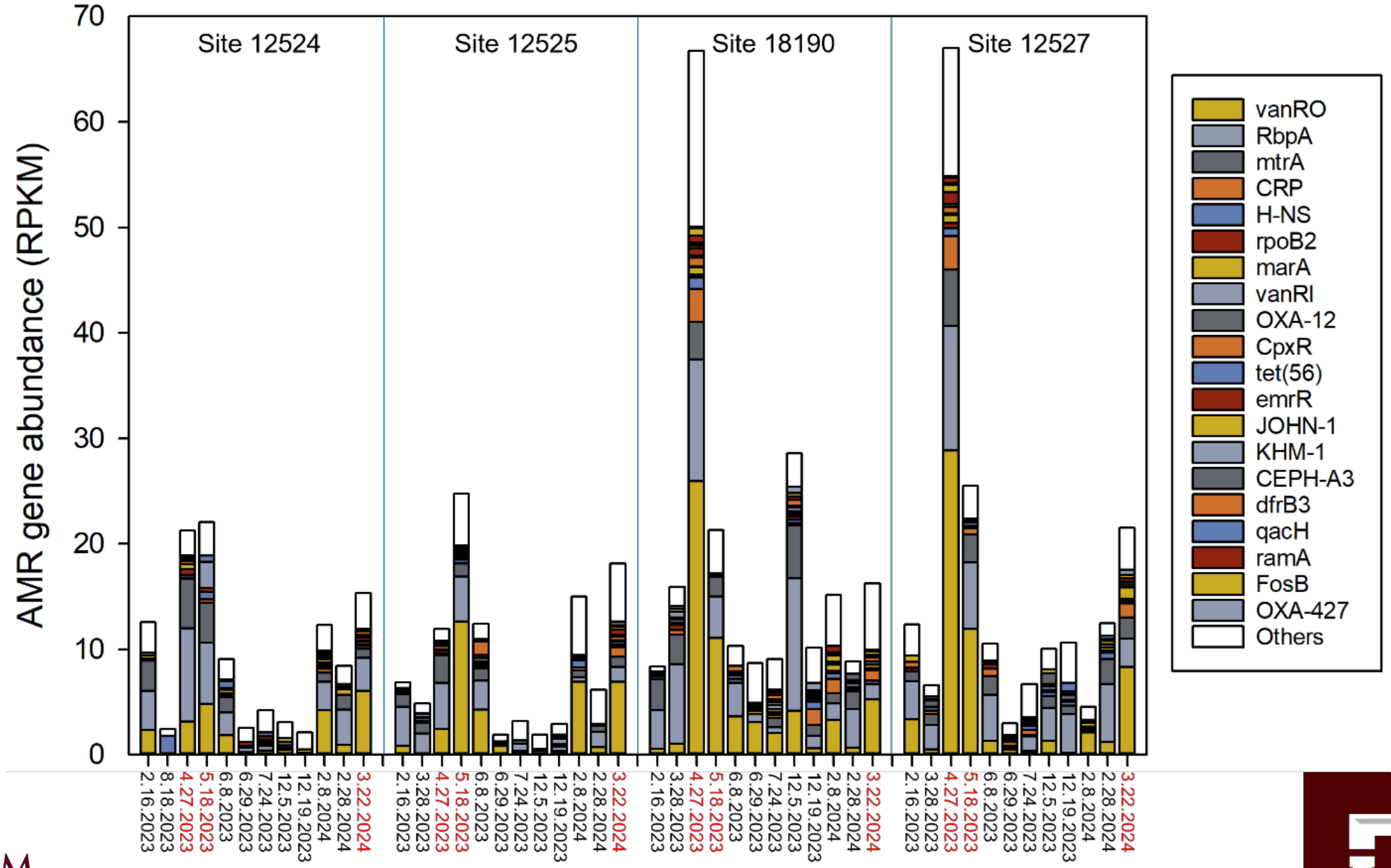
- **Human marker consistently detected at all four sites**
- **Precipitation significantly correlated with HF183**

TEXAS A&M AGRILIFE RESEARCH

Lavaca River Watershed MST



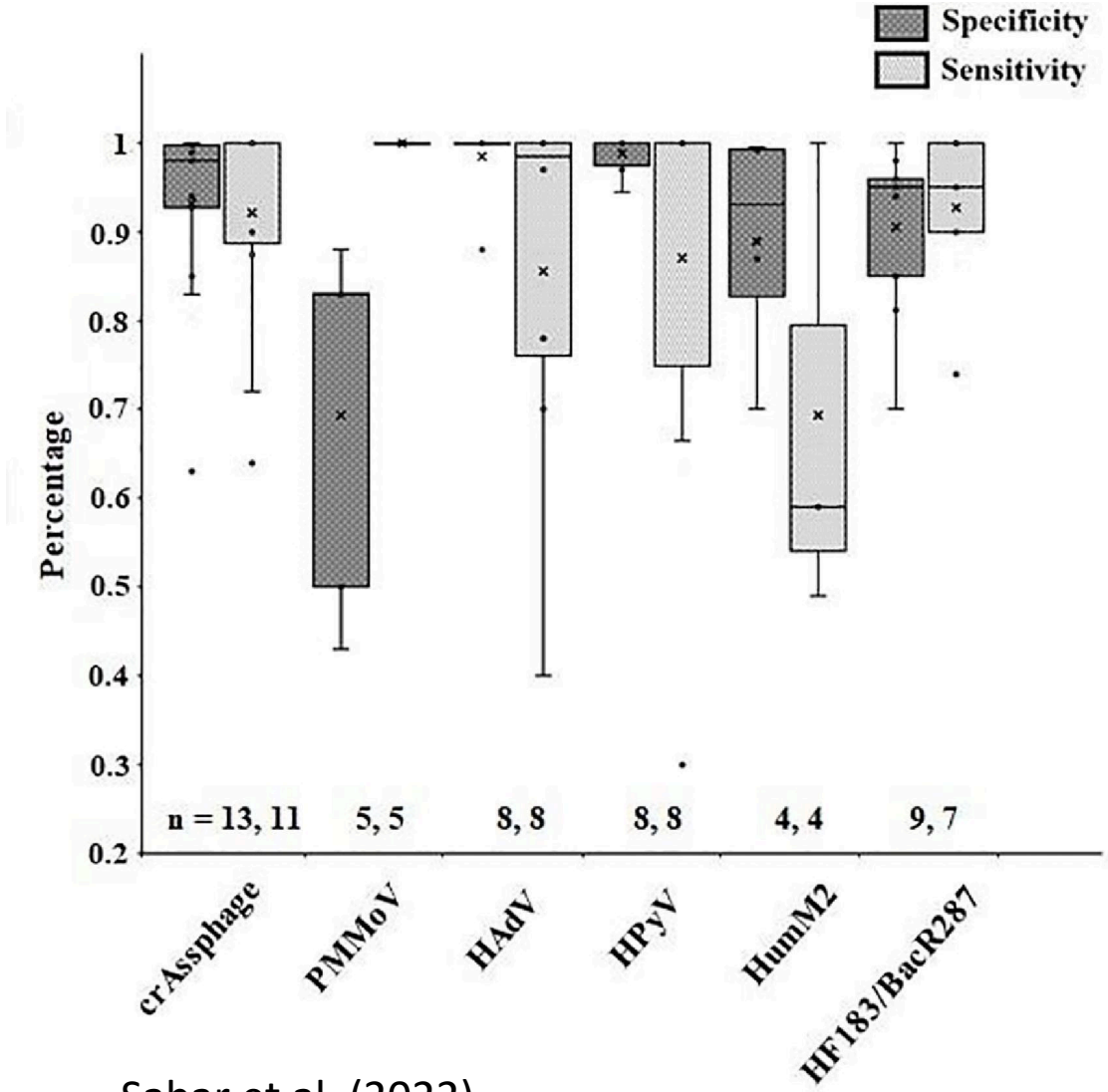
TEXAS A&M AGRILIFE RESEARCH



TEXAS A&M AGRILIFE RESEARCH

New Markers?

- CrAssphage
  - Discovered by cross assembling human fecal metagenomes (cross-assembly phage)
  - Viruses that infect *Bacteroides*
  - Among most numerous organisms in human feces
  - Potential for marker- and sequencing-based MST



Sabar et al. (2022)

Summary

- Continual evolution in MST methods
- Other Texas MST researchers
- Important to reconcile with:
  - *E. coli,* enterococci enumeration data
  - Land use, modeling
  - Stakeholder input, common sense
- Combine with QMRA and other approaches?

Texas A&M AgriLife Research

Acknowledgements

- Texas State Soil & Water Conservation Board
- Texas General Land Office
- NSF
- Texas A&M University
  - Jialin Hu
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  - Gabriele Bonaiti
- UTHealth Houston
  - Anna Gitter
  - George Di Giovanni
- U Houston - Clear Lake
  - Michael LaMontagne

TEXAS A&M AGRILIFE RESEARCH

Questions?

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Texas A&M AgriLife Research

Evaluating Source-Specific Health Risks in Texas Recreational Waters

Anna Gitter, PhD
Assistant Professor
UTHealth Houston School of Public Health

UTHealth Houston
School of Public Health

D.C., Md. & Va. The District Maryland Virginia Crime & Public Safety Local Education Obituaries Transportation Capital Weather Gang

Lake Anna bacteria levels safe, Va. says; E.coli outbreak cause unclear

Tests show Lake Anna water meets benchmarks for safe swimming, Virginia health officials said, after at least 25 recent visitors were diagnosed with E. coli infections.

4 min 49

Star Advertiser

Sunday, April 27, 2025 83° Today's Paper

BREAKING NEWS

Kauai's

TRAVEL & OUTDOORS

Are Texas Waters Clean Enough for Swimming? (Short Answer: Yes)

The bad news: Texas beaches really do have a fecal pollution problem. The good news: it's complicated.

By Peter Holley June 2024 1

CALIFORNIA

L.A. County fire-affec health officials say

SPORTS

Claire Michel, Ol fell ill after swim in virus made her sick

AMES OBITUARIES FINANCE CLASSIFIEDS BEST OF BILOXI

e of this exclusive limited-time offer. SUBS

ng in the water at these 2 nes

ter is polluting

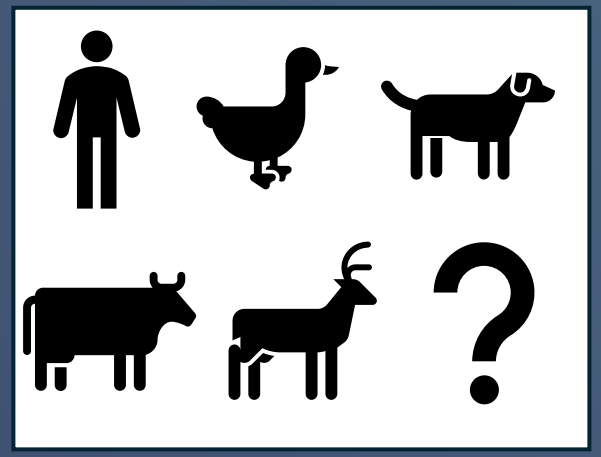
pristine watersheds in Texas. But for years, previous ful homebuilders.

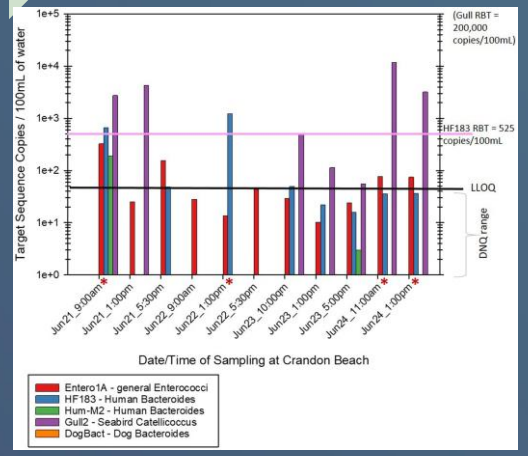
BY DYLAN BADDOUR, INSIDE CLIMATE NEWS APRIL 28, 2025 5 AM CENTRAL SHARE REPUBLISH

Recreational water quality and public health safety is still a concern in 2025

Measuring recreational water quality

Water sampling → Measure FIB → MST Quantification → Data analysis





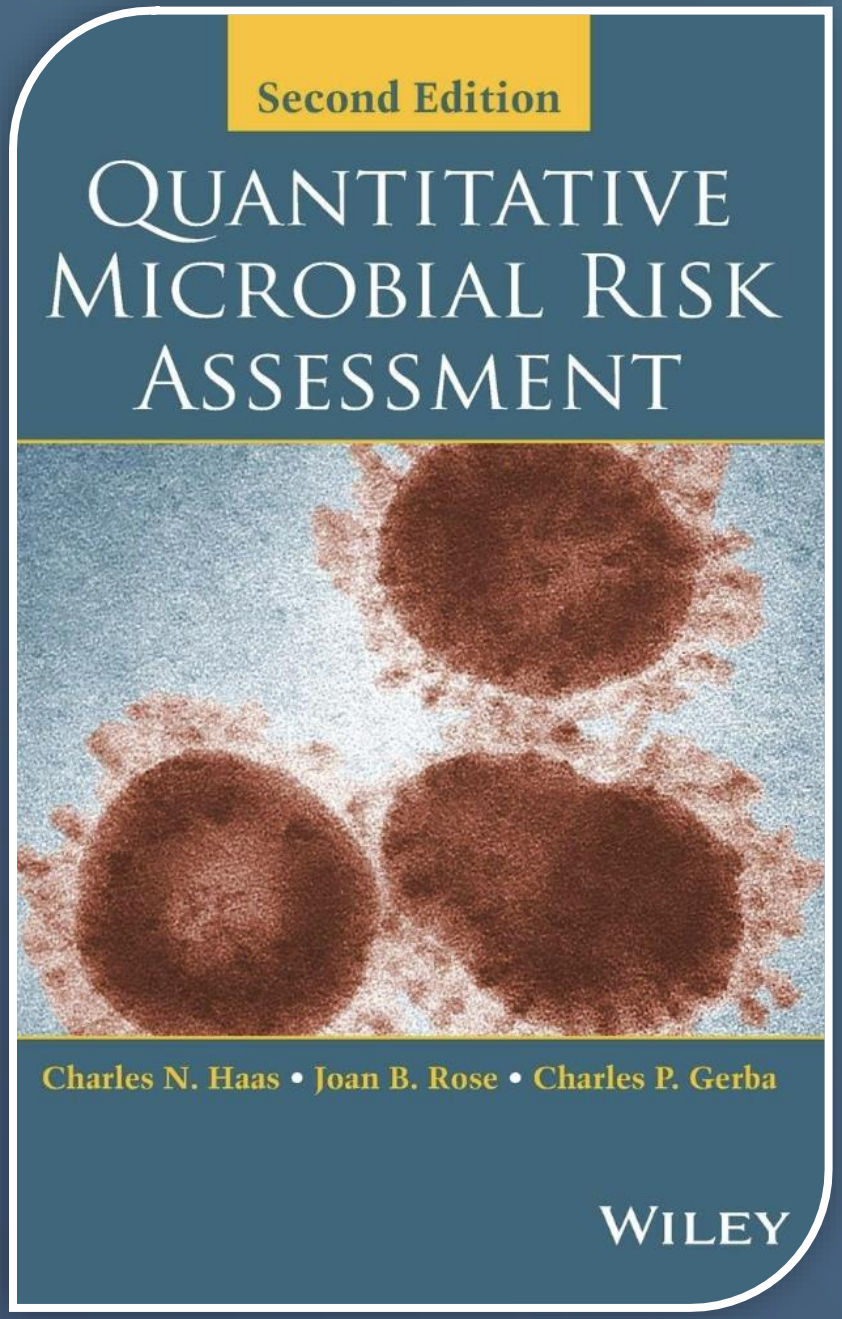
Slide adapted from Nicole Powers, PhD

Can we use this data to inform of site-specific health risks in Texas?

Human Health Risk Assessment

Quantitative Microbial Risk Assessment

- Follows the chemical risk assessment framework
- Accounts for the nature of biological contaminants and host-pathogen relationship
- Typically acute exposure
  - Infection/illness
- Validated by WHO, U.S. EPA, NHMRC (Australia)
- Can evaluate health risks from pathogens, fecal markers, and FIB

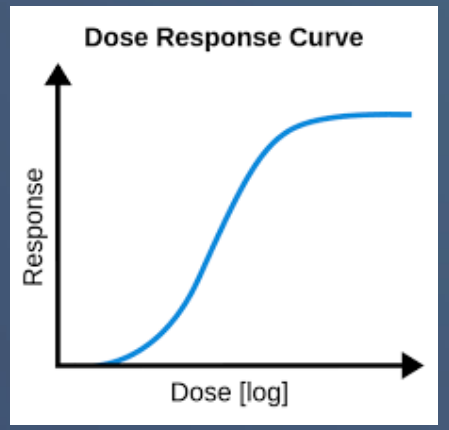


QMRA

Hazard Identification → Exposure Assessment → Dose-Response → Risk Characterization

Identify pathogens of greatest concern

Exposure pathway: ingestion of water



Probability of risk of infection
Probability of risk of illness

Estimate risks based on fecal markers or pathogens, compare to a risk threshold

Data we use…

Peer-reviewed literature

ELSEVIER

Water Research

Volume 111, 15 March 2017, Pages 366-374

Occurrence of norovirus in raw sewage – A systematic literature review and meta-analysis

Sorina E. Eftim [a], Tao Hong [a], Jeffrey Soller [b], Alexandria Boehm [c], Isaac Warren [a], Audrey Ichida [a], Sharon P. Nappier [d]

Original Article | Published: 08 November 2017

Child environmental exposures to water and sand at the beach: Findings from studies of over 68,000 subjects at 12 beaches

Stephanie DeFlorio-Barker, Benjamin F Arnold, Elizabeth A Sams, Alfred P Dufour, John M Colford Jr, Steven B Weisberg, Kenneth C Schiff & Timothy J Wade

Journal of Exposure Science & Environmental Epidemiology **28**, 93–100 (2018) | Cite this article

1652 Accesses | **25** Citations | **4** Altmetric | Metrics

Field Data

COASTAL BEND BAYS & ESTUARIES PROGRAM

A Bacterial Source Tracking Project to Identify Sources of Fecal Pollution at Little Bay: May 2018-January 2019

Publication – 127
Project Number – 1816
January 2019

Prepared by:
Jeffrey W. Turner, Principal Investigator
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Submitted to:

Coastal Bend Bays & Estuaries Program
615 N. Upper Broadway, Ste 1200
Corpus Christi, Texas 78401

Texas Bacterial Source Tracking Program (FY20-FY21)

Texas Water Resources Institute TR-542
May 2022

Texas Water Resources Institute

Lucas Gregory, Brian Hux, Terry J. Gentry, Anna Gitter, Carlos Monserrat, Kristina D. Mena
Texas Water Resources Institute

Published Handbook/ Reports

EPA United States Environmental Protection Agency

EPA/600/R-090/052F | September 2011 | www.epa.gov

Exposure Factors Handbook: 2011 Edition

Office of Research and Development, Washington, DC 20460
National Center for Environmental Assessment

Human Health Risk Assessment

can be used to help answer questions regarding safety and exposure risks:

What can we do to reduce our risk of infection?

Is it safe for me to swim?

Will this new strategy reduce health risks?

U.S. EPA Risk Threshold (2012 RWQC)

Contact Recreation (swimming, per recreator): 32 or 36 illnesses per 1,000 individuals (0.032 or 0.036)

Water Quality Standards (& Suggestions)

FIB levels	**Geometric mean:** < 35 CFU (Marine-Enterococci) <126 CFU (FW-*E. coli*) **Statistical threshold value:** < 10% of samples above Marine: <130 FW: <410
USEPA risk threshold	36 illnesses per 1,000 primary contact recreators
Host-associated marker levels	**Human*:** 525 gene copies / 100mL water **Gull*:** 200,000 gene copies / 100mL water **Canine*:** No risk-based threshold proposed yet

*Each proposed risk-based threshold is based on the assumption that no other sources of fecal pollution are present (Boehm and Soller, 2020)

Slide Adapted from: Nicole Powers, PhD

U.S. EPA Risk Thresholds

2012 RWQC

U.S. EPA Risk Thresholds (2012 RWQC)

Primary Contact Recreation (swimming, per recreator)

Table 1. Recommended 2012 RWQC.

Criteria Elements	Estimated Illness Rate (NGI): 36 per 1,000 primary contact recreators			Estimated Illness Rate (NGI): 32 per 1,000 primary contact recreators	
	Magnitude			Magnitude	
Indicator	GM (cfu/100 mL)[a]	STV (cfu/100 mL)[a]	OR	GM (cfu/100 mL)[a]	STV (cfu/100 mL)[a]
Enterococci – marine and fresh	35	130		30	110
OR					
E. coli – fresh	126	410		100	320
Duration and Frequency: The waterbody GM should not be greater than the selected GM magnitude in any 30-day interval. There should not be greater than a ten percent excursion frequency of the selected STV magnitude in the same 30-day interval.					

[a] EPA recommends using EPA Method 1600 (U.S. EPA, 2002a) to measure culturable enterococci, or another equivalent method that measures culturable enterococci and using EPA Method 1603 (U.S. EPA, 2002b) to measure culturable *E. coli*, or any other equivalent method that measures culturable *E. coli*.

United States Environmental Protection Agency. "Recreational Water Quality Criteria." Federal Register, vol. 77, no. 206, 2012, pp. 71191-71192, https://www.federalregister.gov/documents/2012/11/29/2012-28909/2012-recreational-water-quality-criteria.

Exposure Scenarios

- Primary Contact Recreation
  - Swimming, wading, water skiing (any activity with risk of head submersion)
- Secondary Contact Recreation
  - Kayaking, canoeing, fishing, boating

SCCWRP #0994

ACS ES&T Water > Vol 4/Issue 7 > Article

Open Access

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ARTICLE | June 27, 2024

Quantitative Microbial Risk Assessment with Microbial Source Tracking for Mixed Fecal Sources Contaminating Recreational River Waters, Iowa, USA

Tucker R. Burch*, Joel P. Stokdyk, Aaron D. Firnstahl, Sarah A. Opelt, Rachel M. Cook, Joseph A. Heffron, Amanda Brown, Claire Hruby, and Mark A. Borchardt

Water Research 121 (2017) 280–289

Contents lists available at ScienceDirect

Water Research

journal homepage: www.elsevier.com/locate/watres

Incidence of gastrointestinal illness following wet weather recreational exposures: Harmonization of quantitative microbial risk assessment with an epidemiologic investigation of surfers

Steele [b], John F. Griffith [b], Kenneth C. Schiff [b]

, Costa Mesa, CA 92626, USA

Volume 964, 10 February 2025, 178552

Integrating microbial source tracking with quantitative microbial risk assessment to evaluate site specific risk based thresholds at two South Florida beaches

Anna Gitter[1]*, Maribeth Gidley[2,3], Kristina D. Mena[1], Alesia Ferguson[4], Christopher Sinigalliano[3], Anthony and Helena Solo-Gabriele[7]

Water Research

Volume 158, 1 July 2019, Pages 34-45

ARTICLE | August 9, 2024

Assessing the Impact of Pathogen Decay on Quantitative Microbial Risk Assessment Infection Estimates

Katherine C. Crank, Lucas Rocha-Melogno, Emily Clements, and Kyle Bibby*

Microbial Risk Analysis

Volume 9, August 2018, Pages 22-32

Salmonella risks due to consumption of aquaculture-produced shrimp

Kerry A. Hamilton [a], Arlene Chen [b], Emmanuel de-Graft Johnson [c], Anna Gitter [d], Sonya Kozak [e], Celma Niquice [f], Amity G. Zimmer-Faust [g], Mark H. Weir [h], Jade Mitchell [i], Patrick L. Gurian [a]

Towards stormwater reuse risk management plans: Methodology and catchment scale evaluation of QMRA

Bartosz Szelag [a c], Lucia De Simoni [a], Adam Kiczko [b], Massimiliano Sgroi [a], Anna Laura Eusebi [a], Francesco Fatone [a]

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Research Article

Applying epidemiology and quantitative microbial risk assessment to ambient water quality evaluation: case study of fecal contaminated water in a US inland lake

John Ravenscroft, Sorina Eftim, Jeffrey Soller, Kaedra Jones, Audrey Ichida, Jason Marion & ...show all

Pages 459-488 | Received 08 Aug 2024, Accepted 11 Jan 2025, Published online: 17 Feb 2025

Cite this article https://doi.org/10.1080/10807039.2025.2464110 Check for updates

QMRA of adenovirus in drinking water drinking water treatment plant using U and chlorine dioxide disinfection

Jack Schijven [a b], Peter Teunis [c], Trudy Suylen [d], Henk Ketelaars [d], Luc Hornstra Saskia Rutjes [a]

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Environmental Science & Technology > Vol 58/Issue 29 > Article

Open Access

ECOTOXICOLOGY AND PUBLIC HEALTH | July 14, 2024

Quantitative Microbial Risk Assessment of Antibiotic-Resistant *E. coli*, *Legionella pneumophila*, and Mycobacteria in Nonpotable Wastewater Reuse Applications

Hunter Quon*, and Sunny Jiang

Remember:

We are not detecting pathogens but rather estimating potential pathogen concentrations and therefore doses when using MST data.

$$dose^{s}_{RP} = \frac{C_{MST}}{F^{S}_{MST} \times 100} \times R^{s}_{RP} \times P_{s} \times V$$

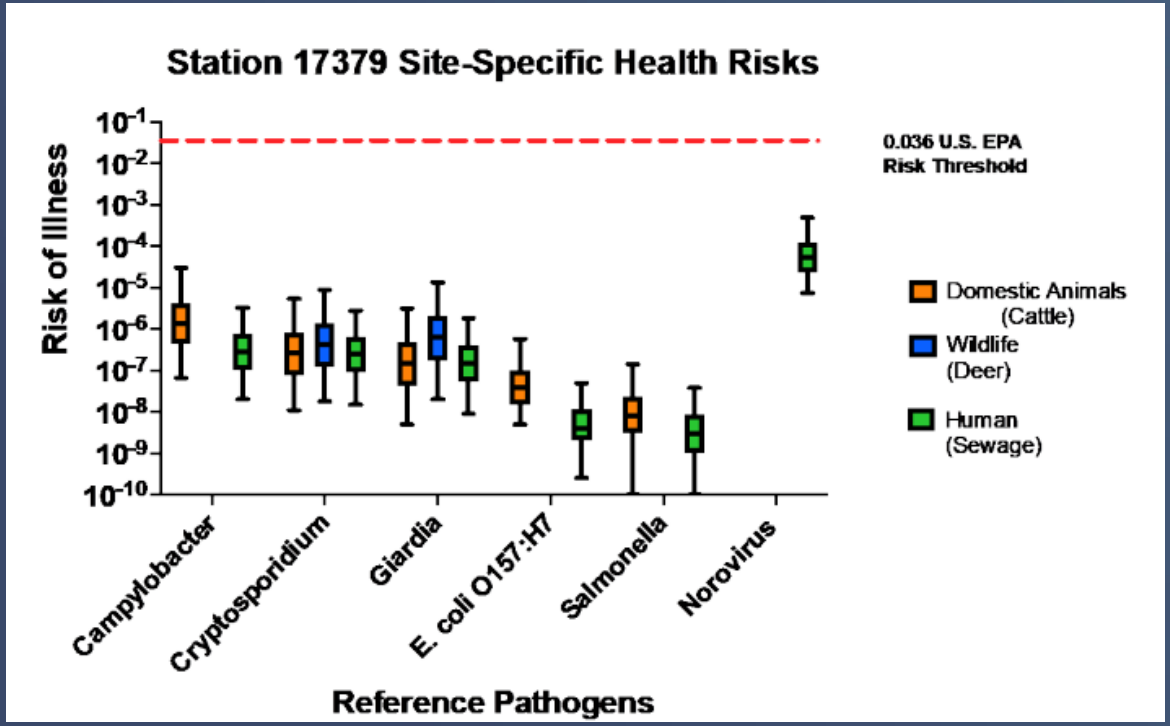
$$P^{s}_{ill} = 1 - \prod_{RP} (1 - P_{ill,RP})$$

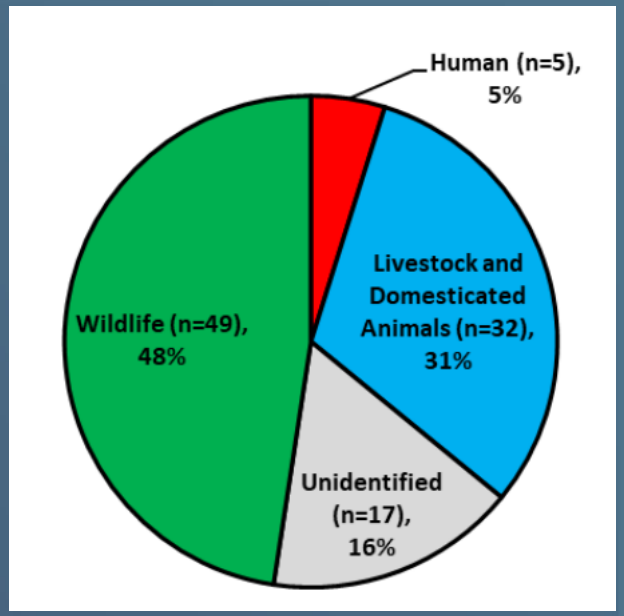
Parameter	Units	Concentration	Source
HF183 in the environment	copies/100mL	Interval Censored: Haulover (4.38822, 2.02544)[a]; Crandon (3.78605, 1.54293)[a]	Environmental data
		Substitution: Haulover (4.50538, 1.91507[a]; Crandon (3.88925, 1.46944)[a]	
Gull2 in the environment	copies/100mL	Interval Censored: Haulover (3.26340, 1.39613)[a]; Crandon (679.841, 0.388813)[b]	Environmental data
		Substitution: Haulover (67.31681, 0.93997)[b]; Crandon (835.67521, 0.44577)[b]	
DogBact in the environment	copies/100mL	Interval Censored: Haulover (21.1045, 0.423840)[b]; Crandon 0 or 25[c]	Environmental data
		Substitution Haulover (63.18327, 0.90705)[b]; Crandon 0 or 25[c]	
HF183 in human sewage	copies/mL	(5.212, 0.566)[d]	(Shanks et al., 2010)
Gull2 in gull waste	copies/g	(8.7,8.3)[e]	(Brown et al., 2017a)[i]
DogBact marker in dog waste	copies/g	(5,9)[f]	(Ervin et al., 2014)
***Campylobacter* in Dog Feces**	organisms/g	(3, 8)[f]	(Chaban et al., 2010)
***Campylobacter* in Gull Feces**	CFU/g	(3.3, 6)[f]	(Lévesque et al., 2000)
***Salmonella* in Gull Feces**	CFU/g	(2.3, 9.0)[f]	(Lévesque et al., 2000)
***Salmonella* in Sewage**	CFU/L	(0.5,5)[f]	(Koivunen et al., 2003; Lemarchand and Lebaron, 2003)
***Campylobacter* in Sewage**	MPN/L	(2.9,4.6)[f]	(Stampi et al., 1993)
***E. coli* O157:H7 in sewage**	CFU/L	(-1,3.3)[f,j]	(Garcia-Aljaro et al., 2005)
***Cryptosporidium* in sewage**	oocysts/L	(-0.52, 3.7)[f]	(Harwood et al., 2005; Crockett, 2007; Yang et al., 2015; Nasser, 2016; Schoen et al., 2017)
***Giardia* in sewage**	cysts/L	(0.51, 4.2)[f]	(Harwood et al., 2005; Kitajima et al., 2014)
Norovirus in sewage	copy/L	(4.7, 1.5)[d]	(Eftim et al., 2017
Adenovirus in sewage	IU/L	(1.75, 3.84)[f]	(Hurst et al., 1988; Hew 2011; Soller et al., 2017)

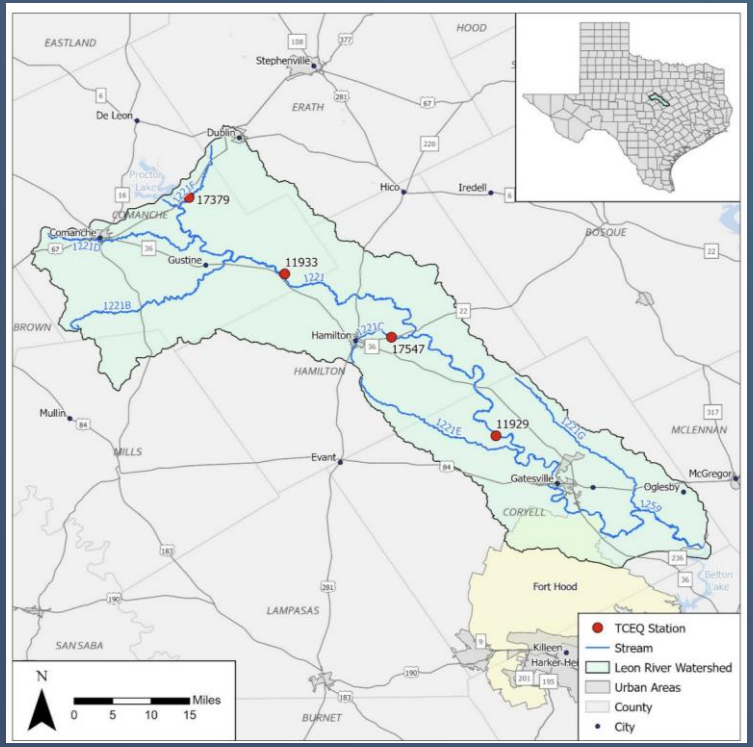
Examples of MST & QMRA in Texas

- Leon River (Central Texas)
- Lavaca River (Southeast Texas)
- Little Bay (Rockport, TX)
- City-by-the-Sea (Canal Community on TX Coast)
- Ongoing: Baffin Bay & Medina River

Leon River (Central Texas)







State of Texas BST Grant FY20-21

TEXAS STATE Soil & Water CONSERVATION BOARD

TEXAS A&M AGRILIFE

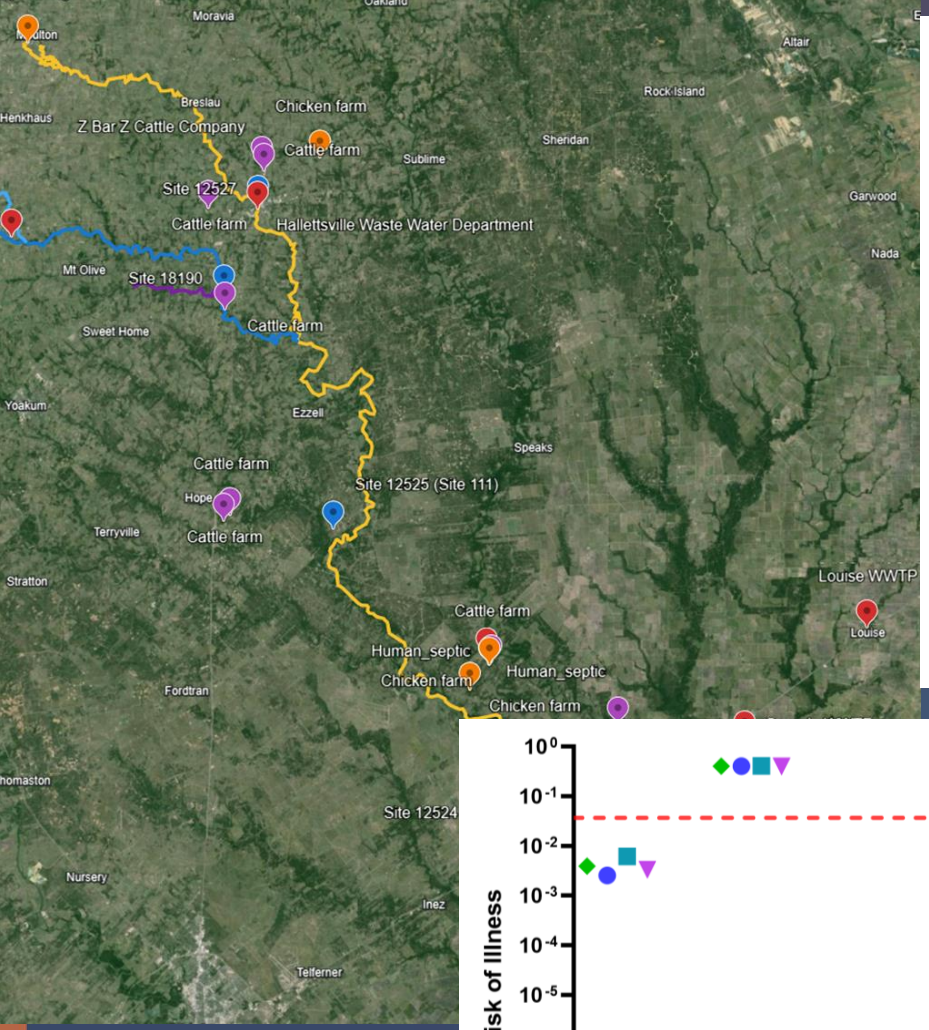
UTHealth Houston | School of Public Health

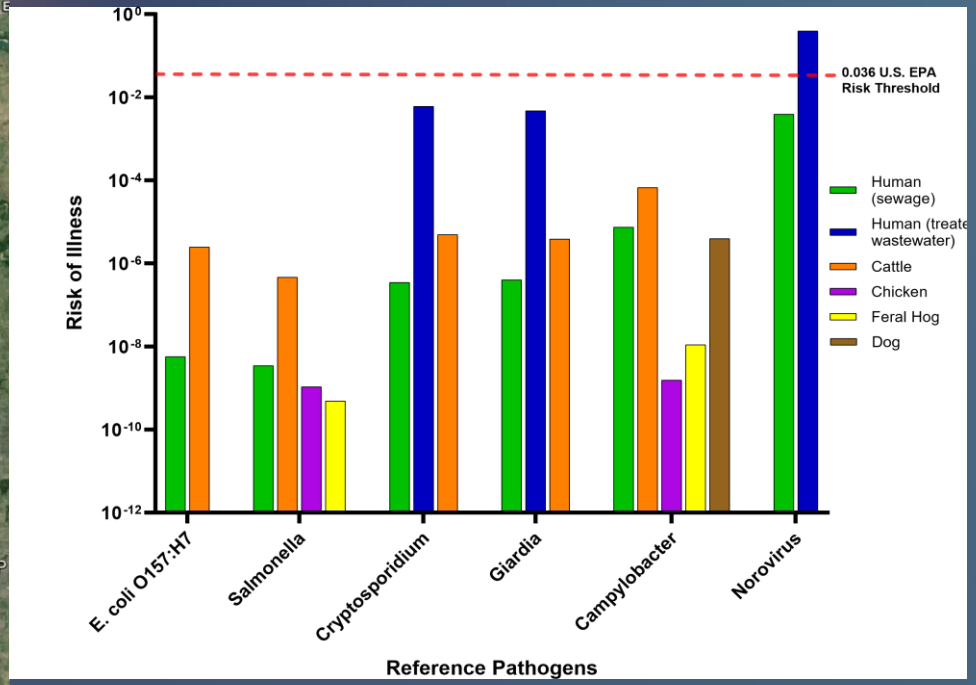
Examples of MST & QMRA in Texas

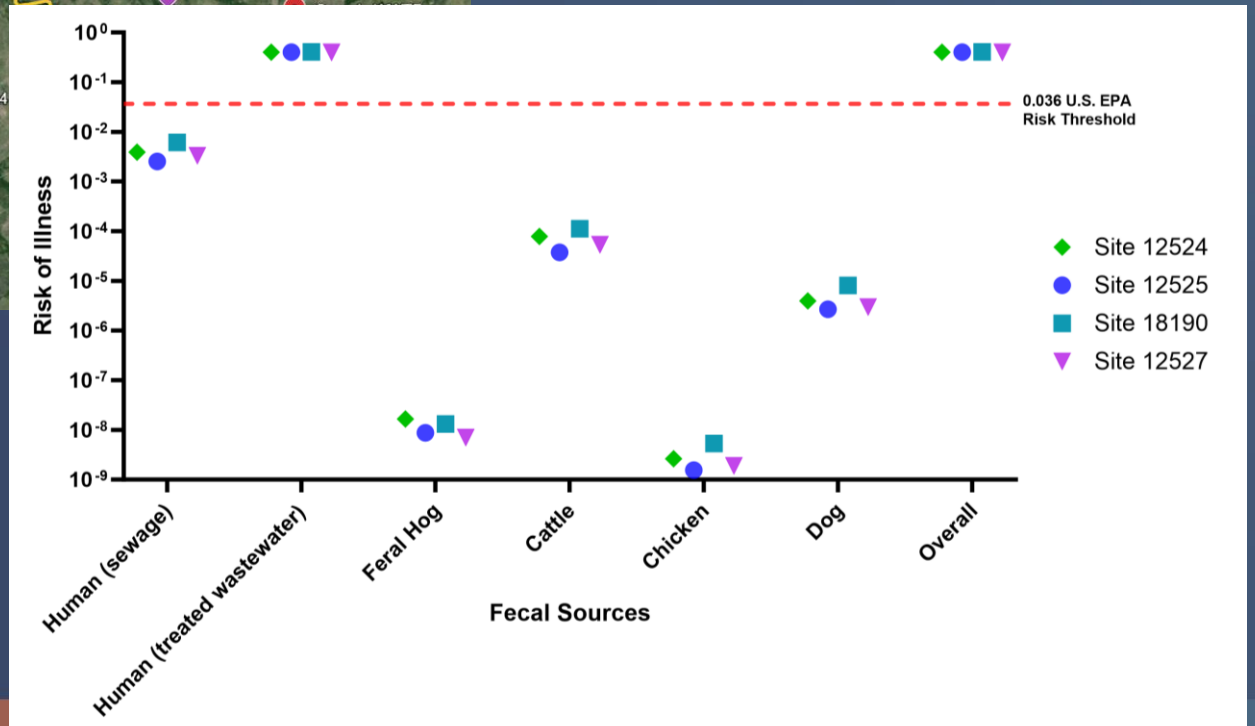
- Leon River (Central Texas)
- Lavaca River (Southeast Texas)
- Little Bay (Rockport, TX)
- City-by-the-Sea (Canal Community on TX Coast)
- Ongoing: Baffin Bay & Medina River

Lavaca River

State of Texas BST Grant FY22-23





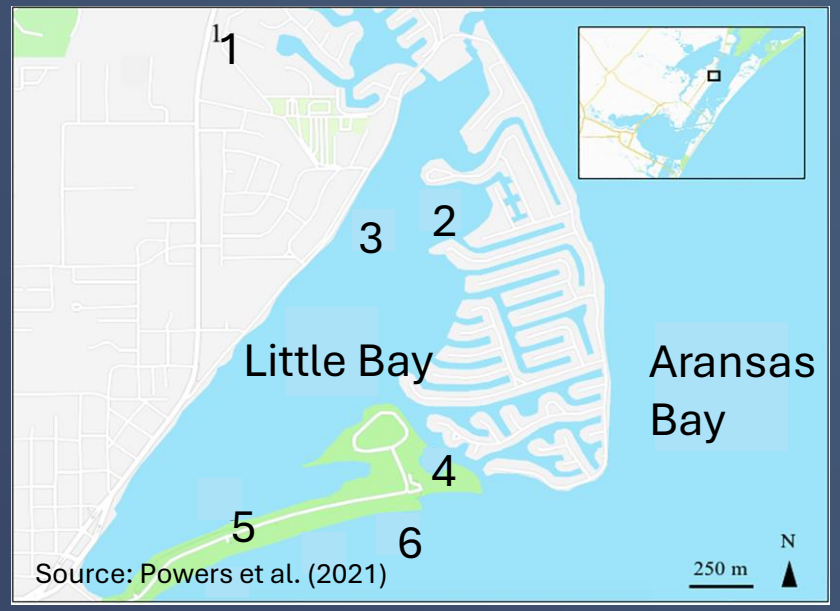


- Utilized NGS techniques to identify fecal sources (an advancement in traditional approaches)
- Treated wastewater found to be a consistent and significant fecal contributor
- Evaluating this molecular approach for assessing water quality and utility for QMRA
- HF183 marker detection to inform QMRA paper

Examples of MST & QMRA in Texas

- Leon River (Central Texas)
- Lavaca River (Southeast Texas)
- Little Bay (Rockport, TX)
- City-by-the-Sea (Canal Community on TX Coast)
- Ongoing: Baffin Bay & Medina River

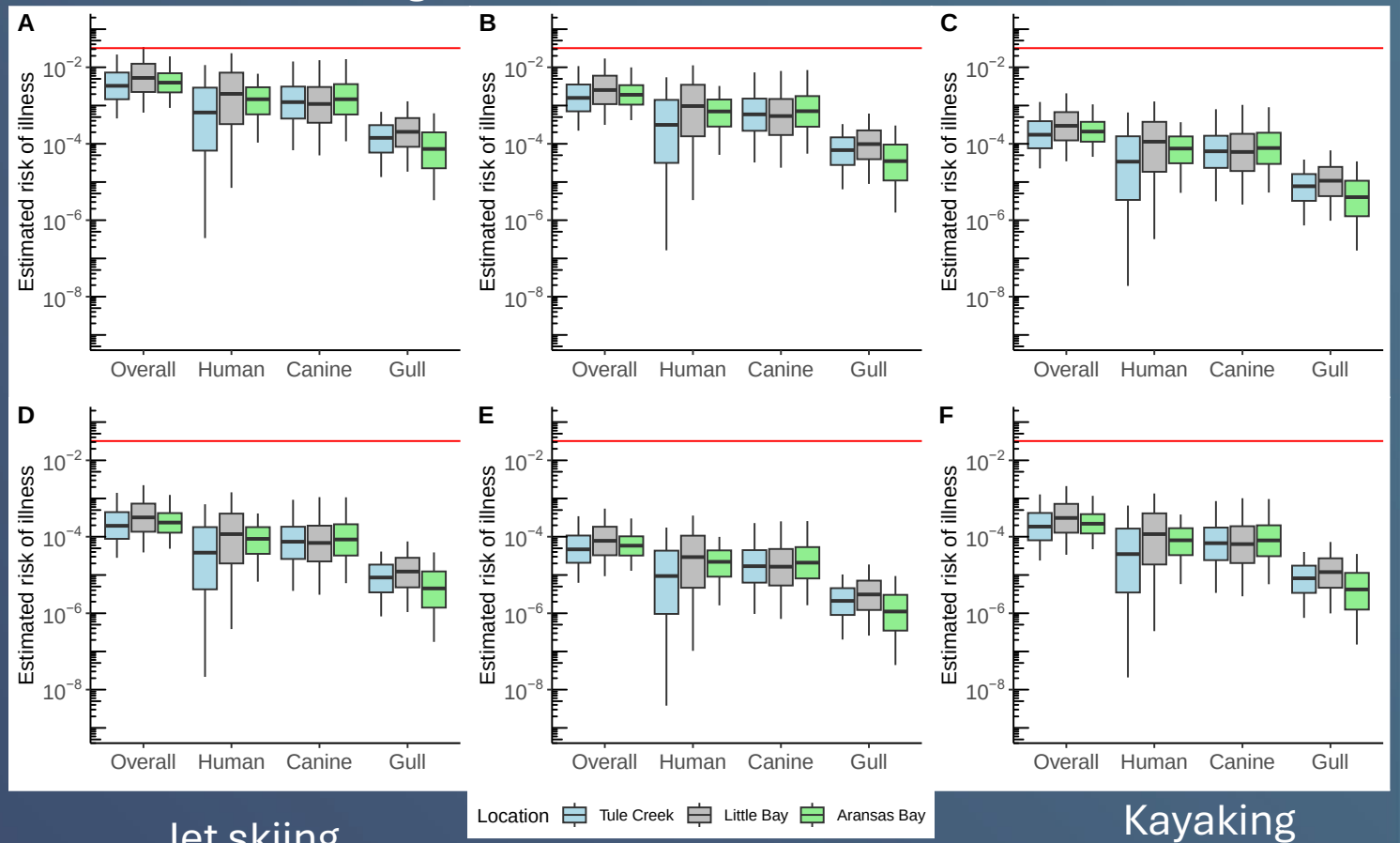
Little Bay (Rockport, Texas)



Source: Powers et al. (2021)

Credit: RockportFulton.com

Child Swimming | Adult Swimming | Fishing



Jet skiing | Boating | Kayaking

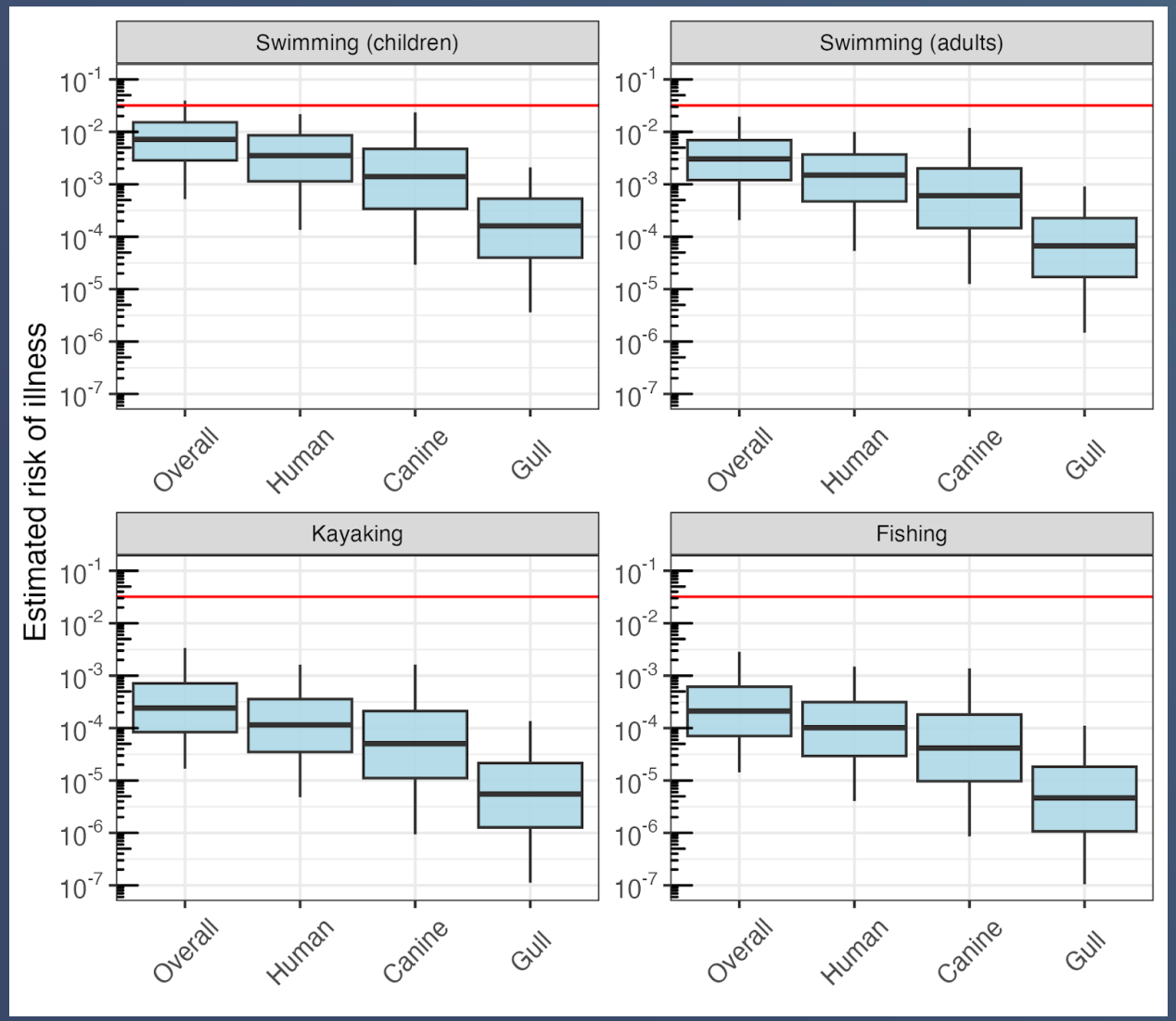
Red line = 32 illnesses per 1,000 people

UTHealth Houston School of Public Health | Texas A&M University Corpus Christi | Texas A&M AgriLife

Examples of MST & QMRA in Texas

- Leon River (Central Texas)
- Lavaca River (Southeast Texas)
- Little Bay (Rockport, TX)
- City-by-the-Sea (Canal Community on TX Coast)
- Ongoing: Baffin Bay & Medina River

City-by-the-Sea (Canal Community on TX Coast)



Red line = 32 illnesses per 1,000 people

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Examples of MST & QMRA in Texas

- Leon River (Central Texas)
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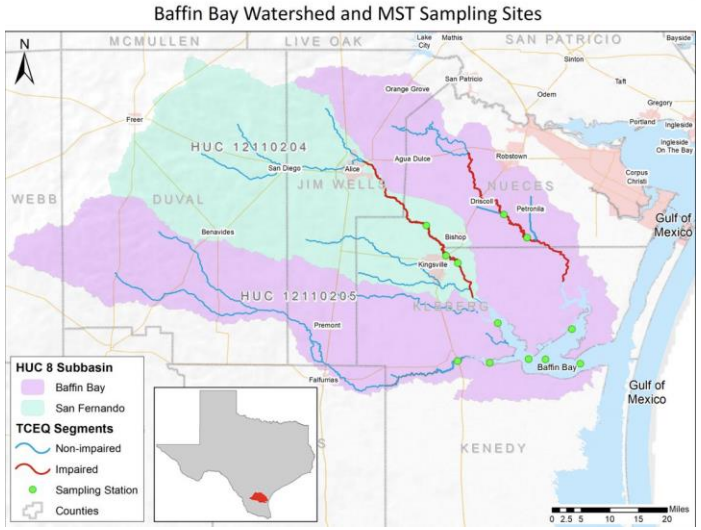
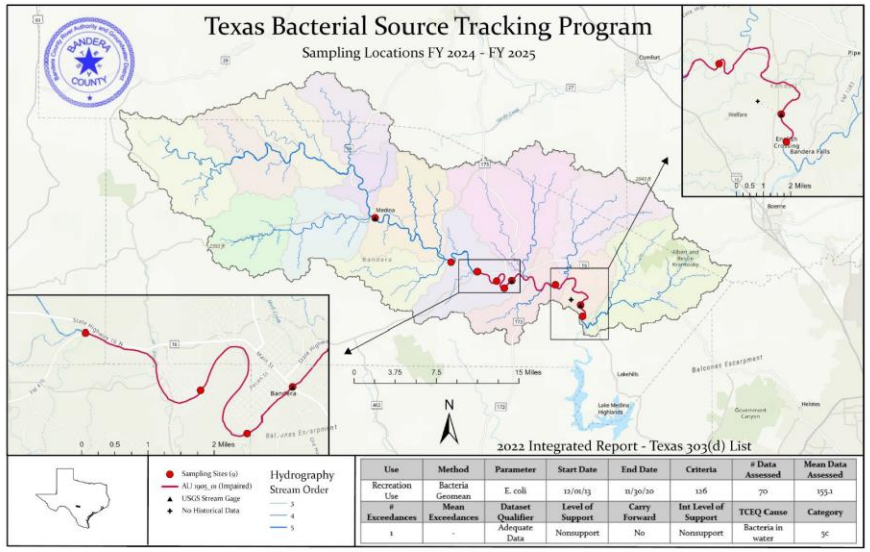
Ongoing Projects

Baffin Bay



- Human, pig, cow, and gull markers
- Across four sites: San Fernando, Petronila, and Los Olmos Creeks and Baffin Bay
- Evaluating health risks for both primary and secondary contact activities
- USEPA GOM/GOA, TAMUCC, TWRI, UTHealth

Medina River



Use	Method	Parameter	Start Date	End Date	Criteria	# Data Assessed	Mean Data Assessed
Recreation Use	Bacteria Geomean	E. coli	12/01/13	11/30/20	126	70	135.1
# Exceedances	Mean Exceedances	Dataset Qualifier	Level of Support	Carry Forward	Int Level of Support	TCEQ Cause	Category
1	-	Adequate Data	Nonsupport	No	Nonsupport	Bacteria in water	5c

- FIB and NGS analyses across nine sites
- Evaluating health risks for both primary and secondary contact activities
- TSSWCB, TWRI, UTHealth, BCRA

Key findings so far…

- Not all fecal sources created equal…
  - Human fecal source often drives risk (but not always the case)
  - Cattle fecal source can contribute a significant health risk (as supported by U.S. EPA guidance)
  - What about dogs?
  - Greatest risk stems from multiple fecal sources co-occurring
- Current approaches addressing water quality through bacteria loading may not capture the health risks associated with pathogens

It takes a village (of water quality experts)

Texas Water Resources Institute
make every drop count

TEXAS A&M UNIVERSITY CORPUS CHRISTI | HARTE RESEARCH INSTITUTE FOR GULF OF MEXICO STUDIES

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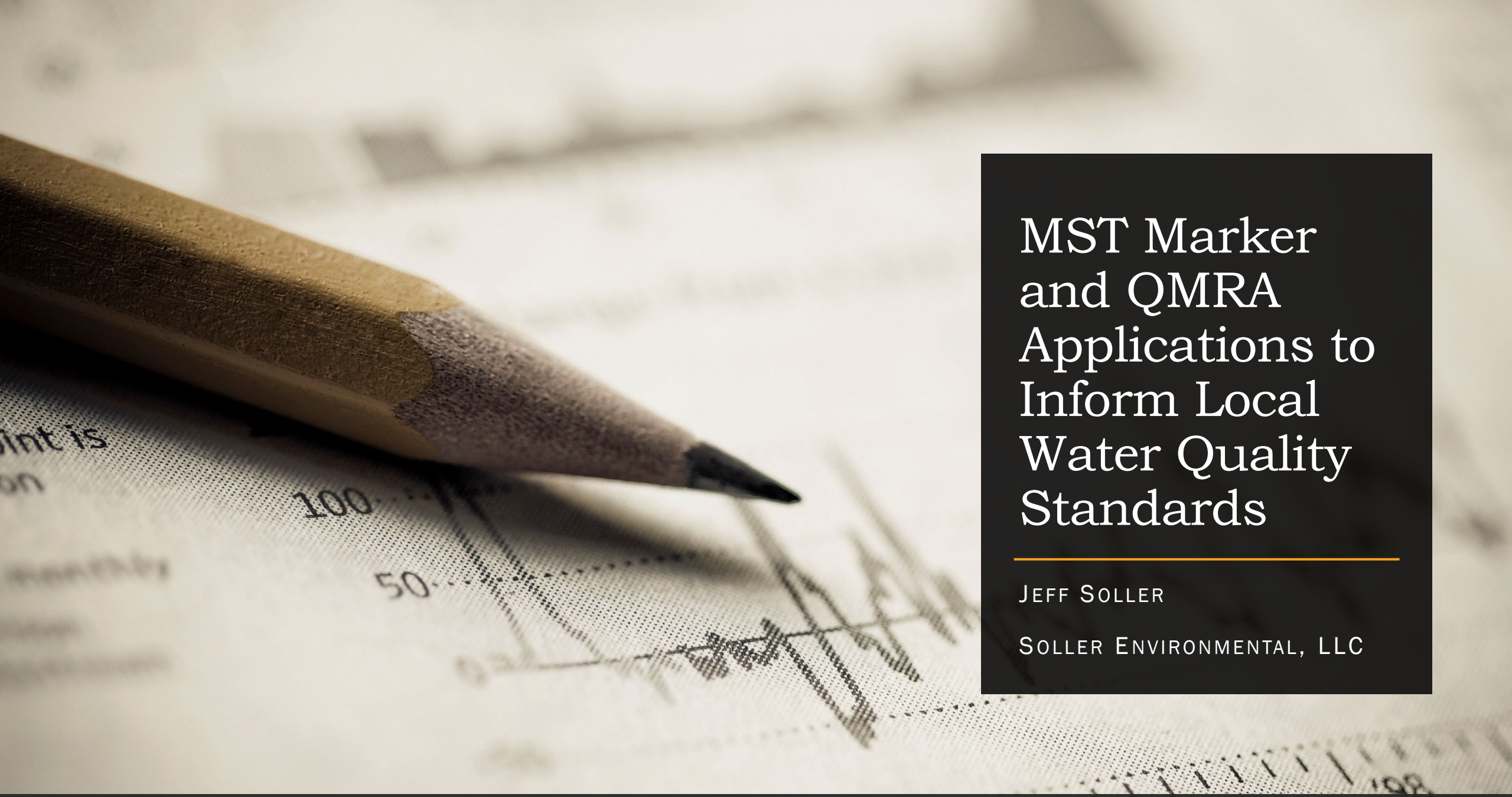
TEXAS STATE Soil & Water CONSERVATION BOARD

Thank you for your time!

Anna Gitter, PhD
anna.gitter@uth.tmc.edu



MST Marker and QMRA Applications to Inform Local Water Quality Standards

Jeff Soller

Soller Environmental, LLC

Outline

- Context for considering local / state water quality standards
  - Basis for national recommendations for recreational waters
  - Characteristics of foundational epidemiological studies
  - What is the same as / different than 1986
  - Magnitude, duration, frequency
  - How changes can influence WQS
- Relative risks from disparate sources of fecal contamination
  - Human
  - Non-human
- MST / QMRA example applications
  - HF183 for freshwater
  - Marker panel for estuarine waters
- Considerations
  - When to consider alternatives to RWQC
  - Use attainment vs notification management
  - Potential approaches for using markers and QMRA to inform WQS / beach management

Context

2012 Recreational Water Quality Criteria (RWQC)

Table 1. Recommended 2012 RWQC.

Criteria Elements	Estimated Illness Rate (NGI): 36 per 1,000 primary contact recreators			Estimated Illness Rate (NGI): 32 per 1,000 primary contact recreators	
	Magnitude			Magnitude	
Indicator	GM (cfu/100 mL)[a]	STV (cfu/100 mL)[a]	OR	GM (cfu/100 mL)[a]	STV (cfu/100 mL)[a]
Enterococci – marine and fresh	35	130		30	110
OR					
E. coli – fresh	126	410		100	320
Duration and Frequency: The waterbody GM should not be greater than the selected GM magnitude in any 30-day interval. There should not be greater than a ten percent excursion frequency of the selected STV magnitude in the same 30-day interval.					

[a] EPA recommends using EPA Method 1600 (U.S. EPA, 2002a) to measure culturable enterococci, or another equivalent method that measures culturable enterococci and using EPA Method 1603 (U.S. EPA, 2002b) to measure culturable *E. coli*, or any other equivalent method that measures culturable *E. coli*.

EPA is also providing information for developing site-specific criteria that measure enterococci using EPA's *Enterococcus* spp. qPCR Method 1611 (U.S. EPA, 2012b). For the purposes of beach notification, EPA encourages the use of a BAV, which approximates the 75th percentile of a water-quality distribution based on the desired GM. See section 5.1 and 5.2 for 'Supplemental Elements.'

Context - Foundational epidemiology studies used to inform 2012 RWQC

- Temperate freshwater (Great Lakes)
  - West beach, Huntington beach, Silver beach, Washington Park beach
- Temperate marine
  - Edgewater beach (MS), Fairhope beach (AL), Goddard beach (RI)
- Tropical marine
  - Boquerón beach (Puerto Rico)
- Urban runoff impacted marine
  - Surfside beach (SC)

Context - Common characteristics of 2012 RWQC epidemiology studies

- Officially designated recreational area near a large population center
- Large enough attendance to support epi study (min 300-400 attendees / day)
- Generally met state /local WQS with a range of indicator densities
- Range of indicator density was related to contamination from identified point source (WWTP effluent)
- Swimming season was at least 90 days long

Context - 2012 RWQC vs. 1986 AWQC

- Similar FIB criteria values
- Different Illness endpoint
  - Prior – HCGI
  - Current - NGI
- Similar level of protection
  - Prior – level varied
  - Current – level is consistent
- Similar use of two WQ characteristics
  - Prior - GM / SSM
  - Current – GM / STV
- Different recreational water use intensity
  - Prior – multiple levels
  - Current – single level
- Different technical basis for criteria derivation
  - Prior – Water quality-based derivation
  - Current – Risk basis is embedded
    - Culturable E. coli
    - Enterococcus spp. via qPCR
    - Alternative sources of contamination
  - Magnitude, duration, and frequency are explicit components of criteria

1986 Ambient Water Quality Criteria

TABLE 4. CRITERIA FOR INDICATOR FOR BACTERIOLOGICAL DENSITIES

	Acceptable Swimming Associated Gastro-enteritis Rate per 1000 swimmers	Steady State Geometric Mean Indicator Density	Single Sample Maximum Allowable Density: Designated Beach Area (upper 75% C.L.)	Moderate Full Body Contact Recreation upper 82% C.L.)	Lightly Used Full Body Contact Recreation upper 90% C.L.)	Infrequently Used Full Body Contact Recreation (upper 95% C.L.)
Freshwater						
enterococci	8	33(1)	61	78	107	151
E. coli	8	126(2)	235	298	409	575
Marine Water						
enterococci	19	35(3)	104	158	276	501

Context – How do / can 2012 RWQC influence local / state WQS?

- State Water Quality Standards (WQS) including alternative criteria need to be scientifically defensible and protective of the use
- Tools are now available and approved
  - Evaluate and manage their waterbodies
  - Develop alternative WQC that differ from EPA's recommended criteria
    - QMRA
    - Alternative fecal indicators / methods

WQS that differ from 2012 RWQC

- Alternative WQS may involve adoption of different numerical values that are based on
  - An alternative health relationship derived using epidemiology with or without QMRA
  - QMRA results to determine water quality values associated with a specific illness rate
  - A different indicator/method combination

WQS that differ from 2012 RWQC

- KEY POINT: Alternative criteria may be adopted into a state WQS provided that the resulting site-specific WQS are scientifically defensible, protective of the use, and reviewed and approved by EPA under CWA §303(c).
  - There is much more flexibility embedded than most people realize
  - Careful consideration of magnitude, duration, frequency is merited
    - Example – duration evaluation!

Relative Risks from Various Sources of Contamination

WATER RESEARCH 44 (2010) 4674–4691

Available at www.sciencedirect.com

ScienceDirect

journal homepage: www.elsevier.com/locate/watres

Estimated human health risks from exposure to recreational waters impacted by human and non-human sources of faecal contamination☆

Jeffrey A. Soller [a,*], *Mary E. Schoen* [b], *Timothy Bartrand* [c], *John E. Ravenscroft* [d], *Nicholas J. Ashbolt* [b]

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[b] US Environmental Protection Agency, Office of Research and Development, 26 West Martin Luther King Drive, Cincinnati, OH 45268, USA
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[d] US Environmental Protection Agency, 1200 Pennsylvania Avenue, N. W, 4304T, Washington DC 20460, USA

Relative Risks from Various Sources of Contamination

Reference pathogens – account for most illnesses of all non-foodborne illness in the US

- Norovirus
- *Cryptosporidium* spp.
- *Giardia lamblia*
- *Campylobacter jejuni*
- *Salmonella enterica*
- *E. coli* O157:H7

Relative Risks from Various Sources of Contamination

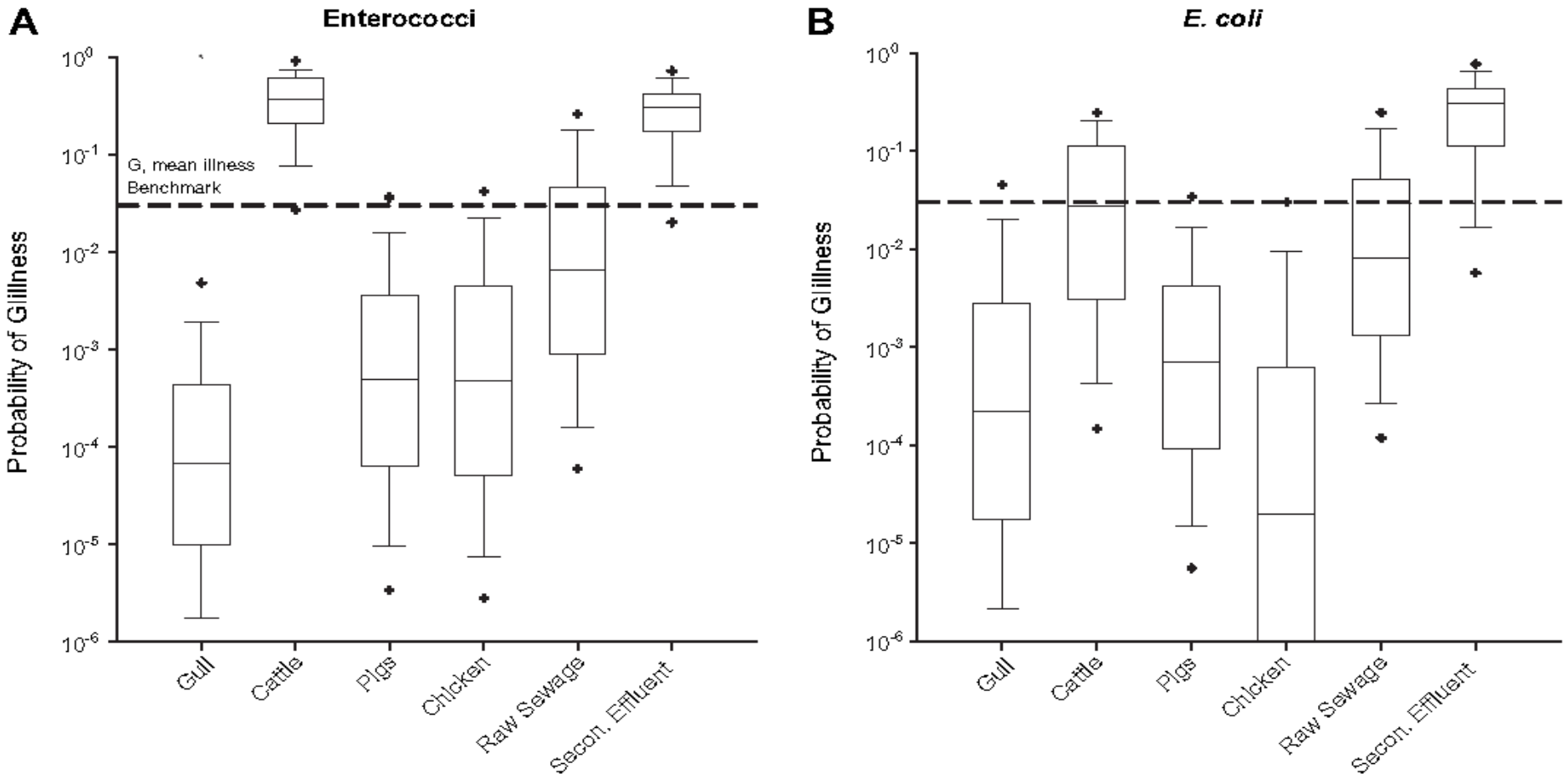

Fig. 5 – Run 3 probability of GI illness. Run 3 probability of GI illness from ingestion of water containing fresh faecal pollution at densities of 35 cfu 100 mL^{-1} ENT (5A) and 126 cfu 100 mL^{-1} *E. coli* (5B). Predicted risk (median, interquartile range, 10th and 90th percentiles, and 5th and 95th percentiles) for fresh gull, cattle and pig faeces, and chicken litter. Human impacts are presented for primary sewage (Human 1) and secondary disinfected effluent (Human 2). The Illness Benchmark represents a geometric mean probability of illness of 0.03.

Relative Risks from Various Sources of Contamination

WATER RESEARCH 44 (2010) 4674–4691

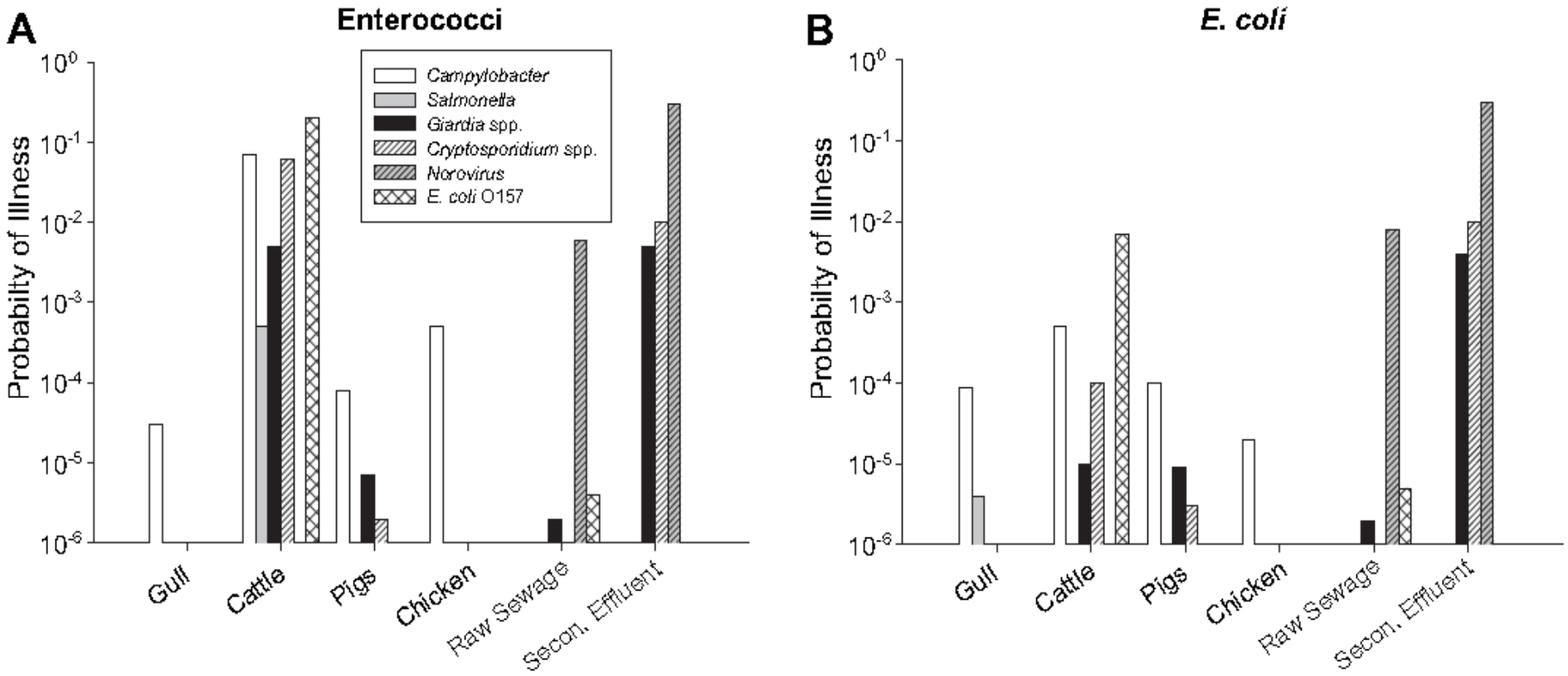

Fig. 6 – Run 3 contribution of each pathogen. Run 3 contribution of each reference pathogen to the probability of GI illness from ingestion of water containing fresh faecal pollution from animals or sewage at faecal indicator densities of 35 cfu 100 mL^{-1} ENT (6A) and 126 cfu 100 mL^{-1} *E. coli* (6B).

When to consider alternatives to RWQC

- Consider the conditions that the RWQC are based on
- Is the waterbody under consideration fundamentally different than the RWQC conditions in some important way (*e.g.*, different source of contamination)?
- Is there a sound reason to believe that the recommended FIB are not functioning well?
- We use "Risk Based Threshold" (RBT) for MST markers
  - RBT = median marker concentration that corresponds to an average GI illness risk value (*e.g.* 0.032)
  - This value aligns with the "Magnitude" in RWQC

MST / QMRA example applications

Microbial Risk Analysis 16 (2020) 100139

Contents lists available at ScienceDirect

Microbial Risk Analysis

journal homepage: www.elsevier.com/locate/mran

Refined ambient water quality thresholds for human-associated fecal indicator HF183 for recreational waters with and without co-occurring gull fecal contamination

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[b] Soller Environmental, Berkeley, California, United States

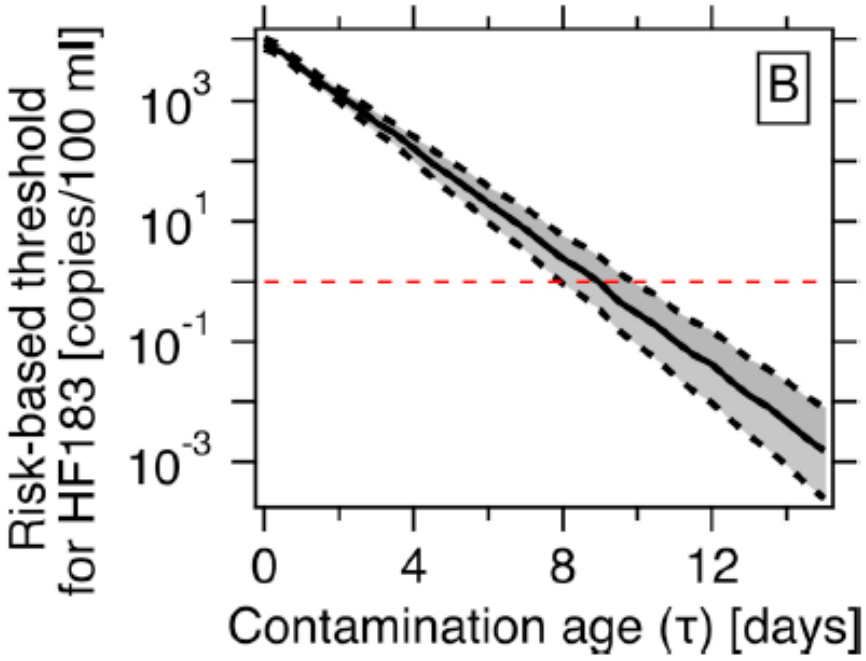
QMRA parameter information

Table 1
Untreated sewage concentrations for reference enteric pathogens and indicators, and dose-response relations, and $P_{ill|inf}$ for reference enteric pathogens. Unit (refs) is the concentration in sewage, μ is the dose, P_{inf} is probability of infection, $P_{ill|inf}$ is probability of becoming ill after infection. Note that units of pathogens are per liter and for indicators is per ml to reflect the units used in the literature for these parameters. CFU is colony forming unit, MPN is most probable number, copy refers to gene copy number, IU is infectious unit, and PFU is plaque forming unit. ${}_1F_1$ is the hypergeometric function. When specified, $P_{ill|inf}$ are represented by a range of parameters, as indicated, drawn from a uniform distribution. $P_{ill|inf}$ for *Campylobacter* is dose-dependent with $r = 2.44 \times 10^8$ and $n = 3.63 \times 10^{-9}$. References (Refs) for P_{inf} and $P_{ill|inf}$ are provided in the last column. References for sewage concentration range are provided adjacent to the unit.

Organism/Target	Ci_sewage	Unit (refs)	Pinf	Pill|inf (distribution)	Refs
Salmonella spp.	[0.5,5]#	CFU/L (Koivunen et al., 2003; Lemarchand and Lebaron, 2003)	$1-(1+\mu/2884)^{-0.3126}$	0.17–0.4 (uniform)	Haas et al., 1999; Fazil, 1996; Teunis et al., 1999
Campylobacter	[2.9,4.6] #	MPN/L (Stampi et al., 1993)	$1-{}_1F_1(0.024,0.024+0.011,-\mu)$	$1-(1+n\mu)^{-r}$	Teunis et al., 2005
E. coli O157:H7	[−1,3.3] #,*	CFU/L (García-Aljaro et al., 2004)	$1-(1+\mu/48.8)^{-0.248}$	0.2–0.6 (uniform)	Teunis et al., 2008; Ludwig et al., 2002; Werber et al., 2008; Bielaszewska et al., 1997
Cryptosporidium	[−0.52, 3.7] #	oocysts/L (Jian et al., 2015; Crockett, 2007; Harwood et al., 2005; Nasser, 2016; Schoen et al., 2017)	$1-\exp(-0.09\,\mu)$	0.3–0.7(uniform)	US EPA 2006
Giardia	[0.51,4.2] #	cysts/L (Harwood et al., 2005; Kitajima et al., 2014)	$1-\exp(-0.0199\,\mu)$	0.2–0.7 (uniform)	Rose and Gerba, 1991; Eisenberg et al., 1996
norovirus	[4.0,1.1] ^	copy/L (Eftim et al., 2017)	$1-{}_1F_1(0.04, 0.04+0.055, -\mu)$	0.3–0.8 (uniform)	Teunis et al., 2008
adenovirus	[1.75,3.84] #	IU/L Soller et al., 2017b; Hurst et al., 1988; Hewitt et al., 2011	$1-{}_1F_1(5.11, 5.11+2.8, -\mu)$	0.5 (uniform)	Teunis et al., 2016
HF183	[5.212, 0.566] ^	copies/ml (Shanks et al., 2010)	NA	NA	
enterococci	[2.8, 5]#	CFU/ml (Soller et al., 2010a)	NA	NA	

The two values separated by a comma are the minimum and maximum of the $\log_{10}$-uniform distribution.
^ The two values separated by a comma are the mean and standard deviation of a $\log_{10}$-normal distribution.
* Lower range is not detected and −1 is used as a lower bound. NA means not applicable.

Risk based thresholds for Hf183 of known and unknown contamination age



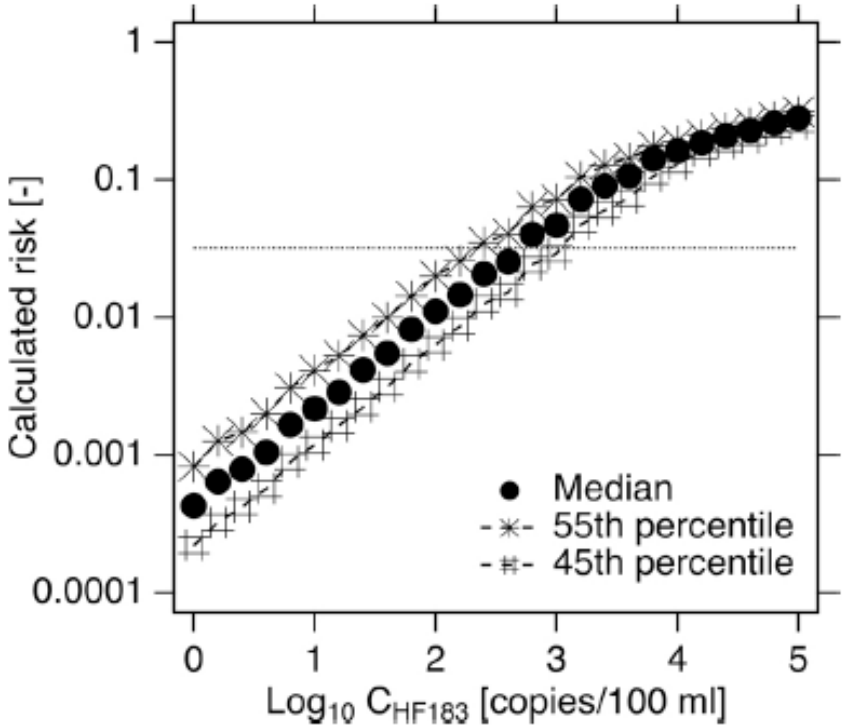


Fig. 2. The median, 45th, and 55th percentiles of calculated risk for a measured concentration of HF183 in surface waters when the age of contamination is unknown, and thus assumed to be any possible age in the Monte Carlo simulations. The median risk in the figure is the median of 50,000 Monte Carlo simulations for each C_{HF183}. Reference line corresponds to 32/1000 illness level.

RBTs for gull marker of unknown age and gull marker / Hf183 mixtures

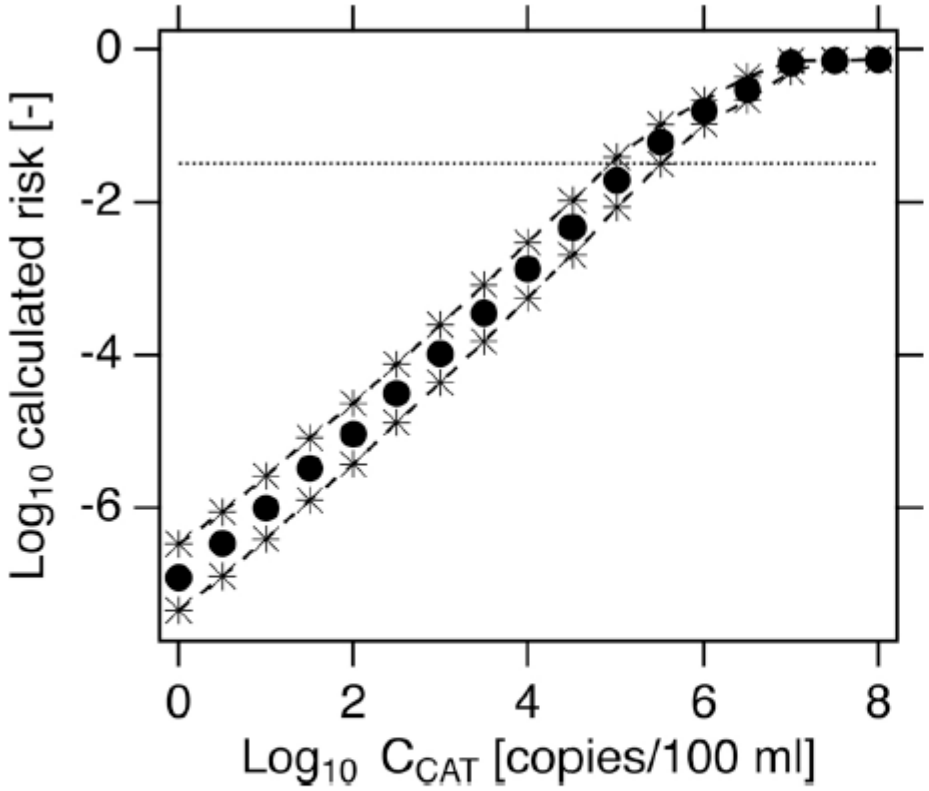


Fig. 5. The median, 45th, and 55th percentiles of calculated risk for a measured concentration of CAT in surface waters when the age of contamination is unknown, and thus assumed to be any possible age in the Monte Carlo simulations. The median risk in the figure is the median of 50,000 Monte Carlo simulations for each C_{CAT}.

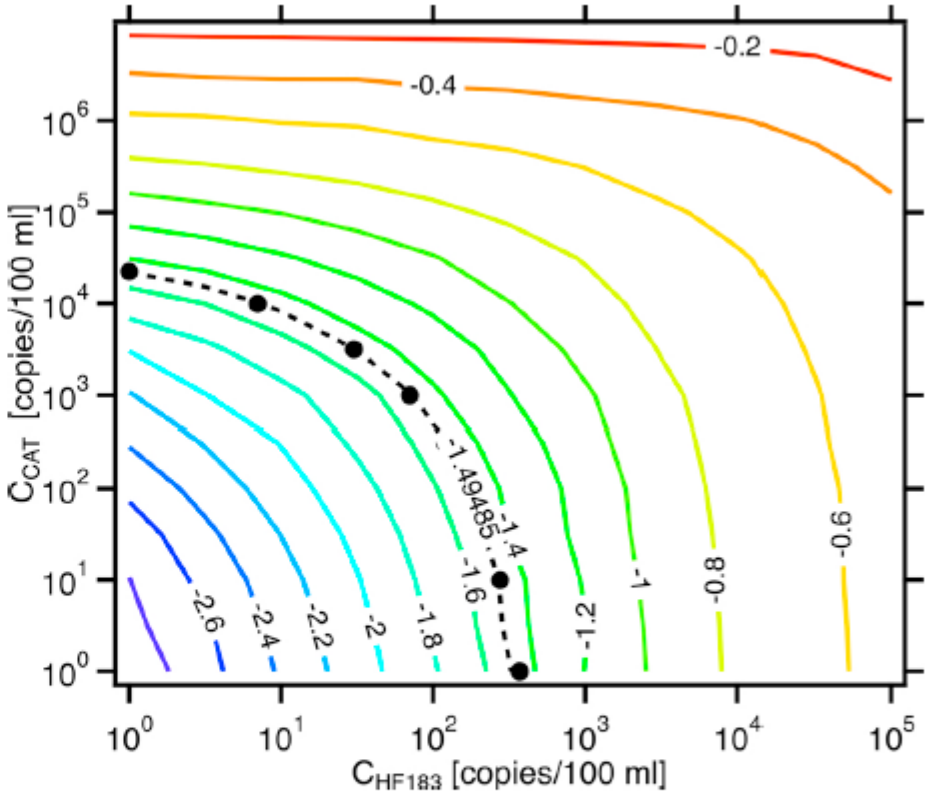


Fig. 6. Median calculated risk as a function of C_{HF183} and C_{CAT}. The lines represent lines of constant median risk and are labeled with the $\log_{10}$-transform of the risk value. The line of constant risk = 32/1000 is shown in black and is labeled with the $\log_{10}(32/1000) = -1.49485$. The symbols represent the values used to create Table 5. Similar contours for the 45th and 55th percentiles of risk can be found in the supporting material (Figures S3 and S4).

MST / QMRA example applications

Science of the Total Environment 929 (2024) 172448

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Site-specific risk-based threshold (RBT) concentrations for sewage-associated markers in estuarine swimming waters

Warish Ahmed [a,*], Mary E. Schoen [b], Jeffrey Soller [b], Joanna Ciol Harrison [c], Kerry A. Hamilton [c,d], Metasebia Gebrwold [a], Stuart L. Simpson [a], Sudhi Payyappat [e], Michele Cassidy [e], Nathan Harrison [e], Colin Besley [e]

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QMRA parameter information

- Similar technical methodology for QMRA as presented in previous slides
- Panel of markers included to evaluate the benefits and drawbacks of each

Table 2
Mean decay rates (k/day) and of sewage-associated marker and human norovirus (HNoV) in Davidson Park (DP) and Hen and Chicken Bay (HCB) mesocosms under ambient sunlight conditions (Ahmed et al., 2024).

Markers and HNoV	Mean k/day	
	DP	HCB
HF183	0.414	0.328
Lachno3	0.272	0.201
CrAssphage	0.259	0.289
PMMoV	0.162	0.064
HNoV GII	0.181	0.114

Table 1
Concentration, distribution and parameters of sewage-associated markers and human norovirus (HNoV) in untreated sewage.

Markers and HNoV	Concentration (range $\log_{10}$ GC/L of untreated sewage)	Distribution	Distribution parameters of concentration ($\log_{10}$ GC/L of untreated sewage)
HF183	8.31–9.93	Weibull	Scale – 31.8 Shape – 9.50
Lachno3	8.13–9.88	Log-normal	Mean – 9.20 SD – 0.40
CrAssphage	8.27–9.88	Weibull	Scale – 31.6 Shape – 9.40
PMMoV	7.94–9.37	Weibull	Scale – 23.3 Shape – 8.70
HNoV GI + GII	3.00–6.35	Log-normal	Mean – 5.00 SD – 0.90

SD: standard deviation.

Risk based thresholds for Hf183 for known contamination age

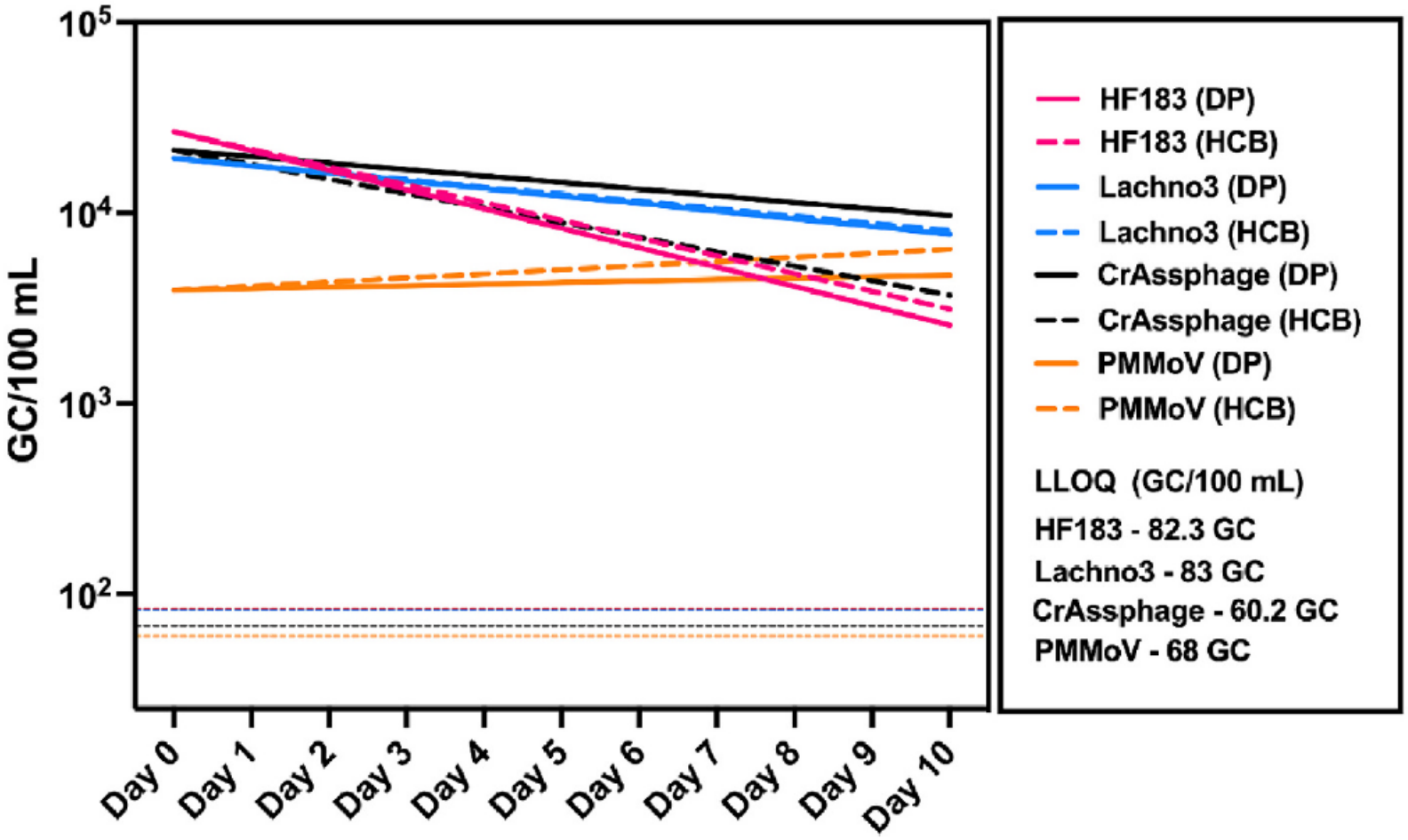

Fig. 2. HF183, Lachno3, CrAssphage and PMMoV RBT median concentrations (GC/100 mL) in Davidson Park (DP) and Hen and Chicken Bay (HCB) estuarine waters corresponding to the illness benchmark of 0.032 for fresh (day 0) and aged (day 1 to day 10) sewage contamination. Dotted lines represent LLOQ values.

Take home messages from RBT derivations

- Using MST marker RBTs may facilitate the interpretation of quantitative data and enable better understanding of risks from exposure recreational waters
- Each MST may have desirable attributes and drawbacks (*i.e.*, differential decay with pathogens of primary concern, specificity, etc.)
- Age of contamination may be critical factor, depending on the differential decay between marker used and pathogen(s) of concern

Considerations - Interpreting marker-based evaluation results

- Determine a priori how the results are to be used
  - Use attainment vs notification management
- For attainment - Understand the implications of duration and/or frequency when evaluating marker-based results (up to 50% of the results could be >RBT and use could be attained)

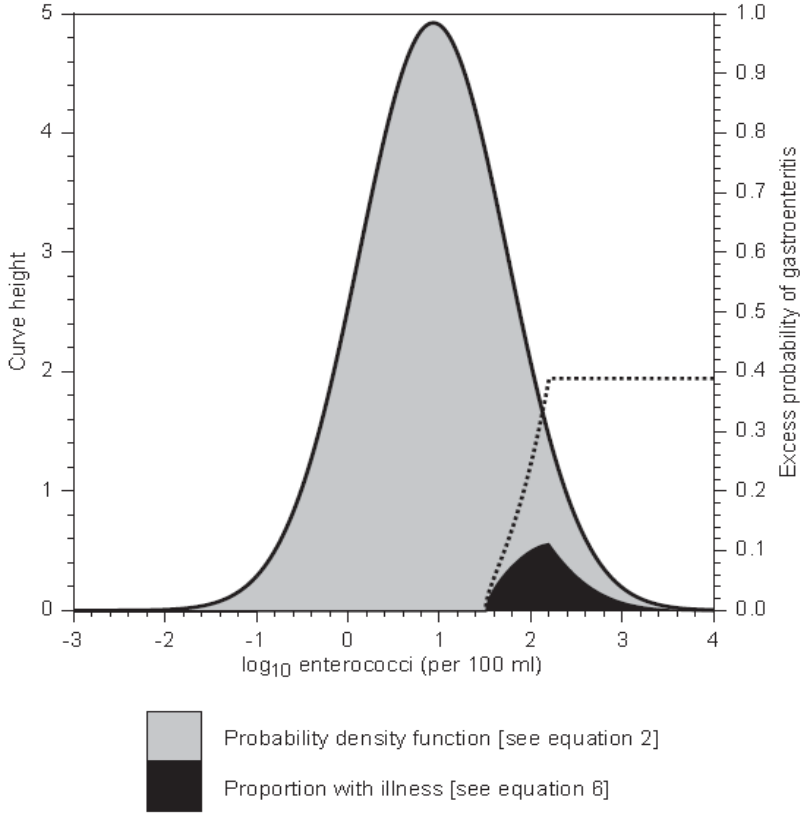

Fig. 2. Probability density function for intestinal enterococci derived from 11,000 EU bathing waters superimposed studies by Kay et al. [40], with the dose response relationship derived from Fig. 1 dotted line.

D. Kay et al. / Water Research 38 (2004) 1296–1304

Considerations - Interpreting marker-based evaluation results

- For use attainment: use of multiple, short duration periods and rolling GM evaluations require careful consideration in interpretation
  - Potential unintended consequence – more stringent WQS than intended potentially leading to allocation of resources to waterbodies that do not require additional work
- I am not aware of any marker-based WQS yet (attainment evaluation of beneficial use)

Considerations - Potential approach for using markers and QMRA to inform WQS / beach management

- Use longest reasonable duration (increases data availability)
- Improve health protection by focusing on and managing days of highest risk
- Use multiple markers simultaneously to provide useful insight regarding days of relatively higher risk (Ahmed, et al, 2024)
  - Useful for management action decision-making
  - Could minimize the drawbacks of individual markers
  - Days in which multiple markers exceed predetermined thresholds could be candidates to inform management action
  - Note that the RBTs may or may not be the threshold values for comparison
- Interpretation of results must be consistent with derivation of RWQC (or WQS) – (must account for magnitude, duration, and frequency considerations)

Questions / Comments

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https://urbanriparian.twri.tamu.edu

UPCOMING TEXAS WATERSHED PLANNING PROGRAM TRAININGS

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Ag BMPs Course

- September 2025
- Thrall – Stiles Farm
- $50 registration fee
- Topics:
  - Ag BMPs to protect water quality
  - Ag Conservation Programs
  - Farm Demonstration Tour
  - Landowner Process for Technical Assistance

Urban BMPs Course

- November 2025
- Dallas
- $50 registration fee
- Topics:
  - Value of urban stormwater BMPs
  - Coordinating with cities/developers
  - Challenges faced in urban settings
  - Low Impact Development

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Stakeholder Facilitation

- December 2025
- Online Only
- Charlie McPherson, Tetra Tech
- $50 registration fee
- Topics:
  - Understanding your audience
  - Engaging stakeholders
  - Facilitating meetings
  - Sustaining stakeholder groups

ROUNDTABLE WRAP UP

- Feedback form → Scan the QR Code →
  - Topics of interest for next time
  - Programs that you would like to learn more about

- Next Roundtable: October 2025 – Austin Area
  - Registration info will be in a future Trainings Newsletter

Questions or Comments:

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