

# Improving Community Health through Microbial Source Tracking

Brandi Kiel Reese, Ruth H. Carmichael,  
Sinéad Ní Chadhain,  
with Ania Brown, Penny Demetriades, Bree Janssen

Stakeholder Meeting 6

November 1, 2024



# Stakeholders & Community Partners

- ▶ Alabama Association of Conservation Districts
- ▶ Alabama Department of Conservation & Natural Resources
- ▶ Alabama Department of Environmental Management
- ▶ Alabama Marine Mammal Stranding Network
- ▶ Auburn University Shellfish Laboratory
- ▶ City of Mobile
- ▶ Dog River Clearwater Revival
- ▶ FDA Gulf Coast Seafood Laboratory
- ▶ Grand Bay National Estuarine Research Reserve
- ▶ Mississippi-Alabama Sea Grant Consortium
- ▶ Mobile Bay National Estuary Program
- ▶ Mobile Baykeeper
- ▶ Navy Cove Oyster Company
- ▶ The Nature Conservancy
- ▶ The Water Institute of the Gulf
- ▶ Weeks Bay National Estuarine Research Reserve



## Objectives

1. To **define microbial sources** to Alabama waters, with the goal to distinguish at least wastewater treatment plant, septic, wildlife (boar/hog), livestock (chicken, cow), and other non-human (dog) inputs.
2. To **define the conditions, location and timing of indicator microbe influences**, specifically including factors used in determining shellfish area closures.
3. To **facilitate data sharing** using an existing online platform, “Our Wastewater Footprint”  
<https://www.disl.org/wastewaterfootprint>
4. To **enhance local capacity** for enduring advanced microbial source tracking.

# Project updates: Objectives 1 & 2

Ania Brown  
Penny Demetriades

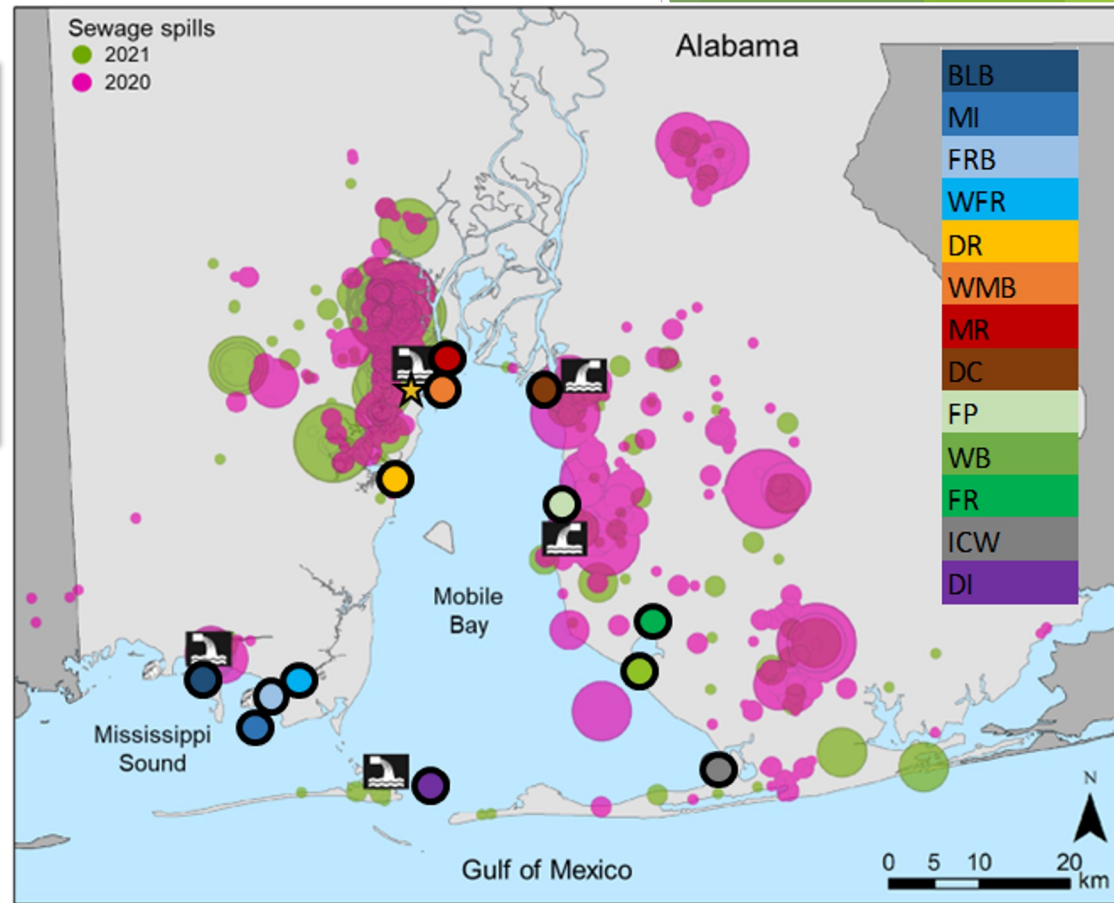


# Project Overview



## Water Sampling

- ▶ 1 year (2022-2023), 4 seasons
- ▶ Monthly (4-week intervals); 14 sampling events
- ▶ 13 sites (Mobile Bay, EMSS)





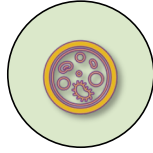
# Project Overview



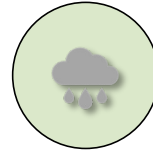
DISCHARGE/  
SALINITY



NUTRIENTS/  
STABLE  
ISOTOPES



INDICATOR  
MICROORGANISMS



SEASONAL  
VARIATION

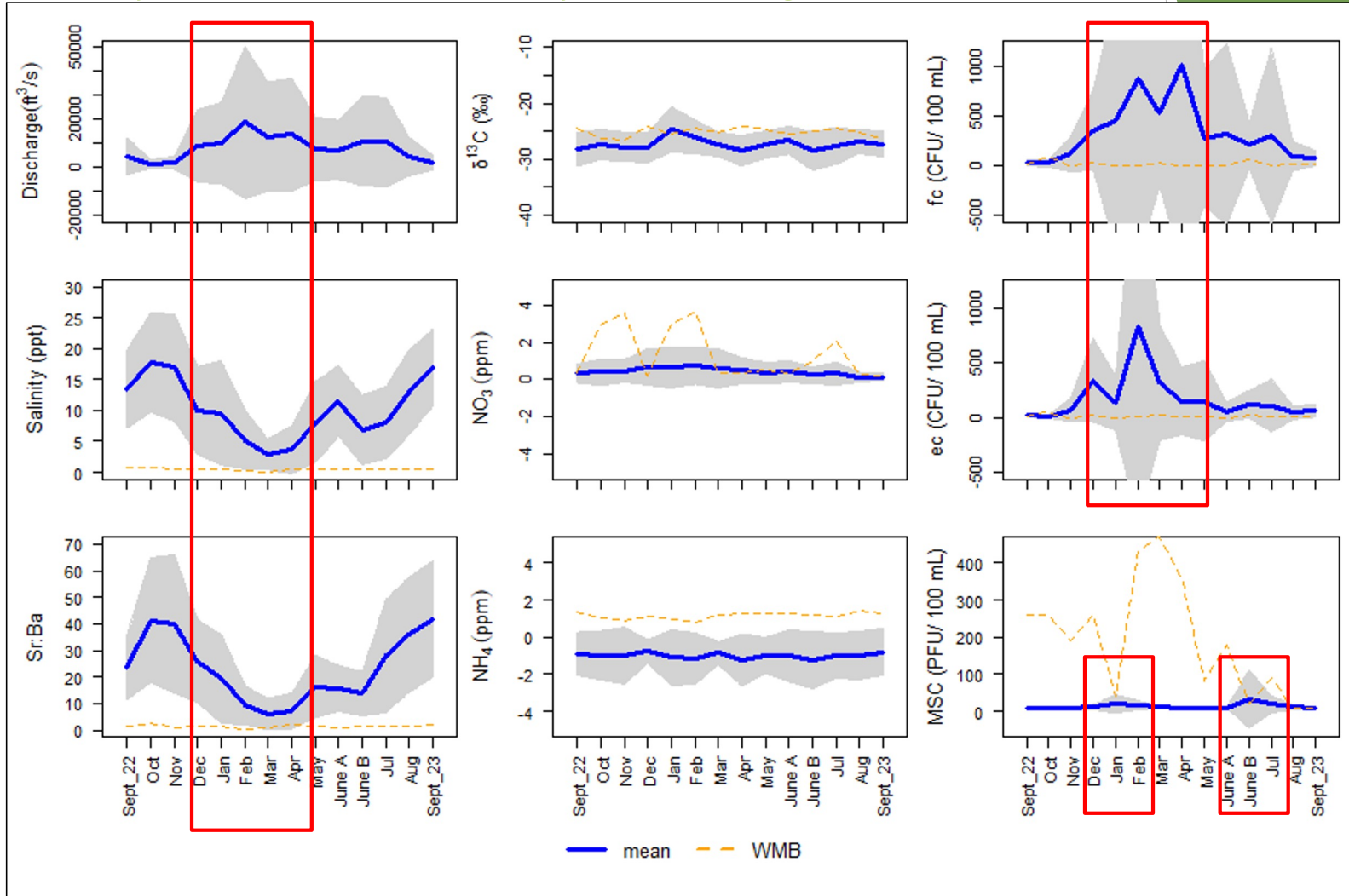


SPATIAL  
VARIATION

## Water Sampling

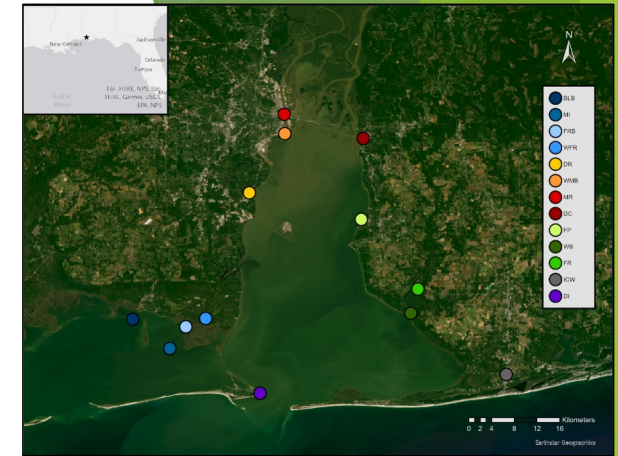
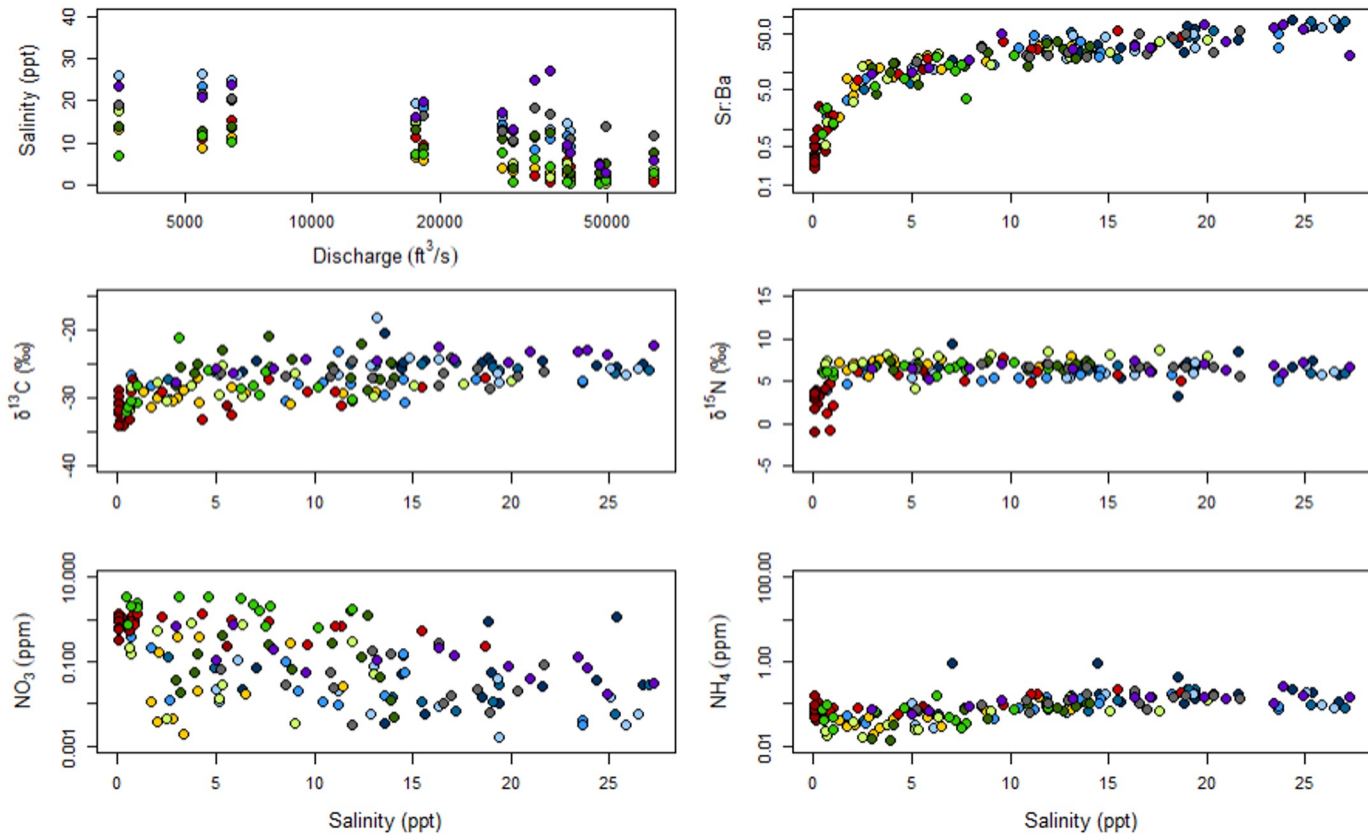
- ▶ 180 distinct sampling events
- ▶ 7 sites with local discharge data
- ▶ 180 samples fc, ec, MSC
- ▶ 360 samples nutrients (pseudo-replicates, averaged)
- ▶ 360 samples stable isotopes (only 180 analyzed)

# Preliminary data: Monthly averages

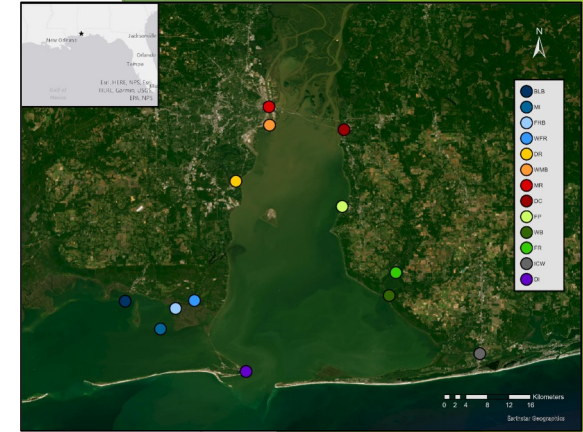
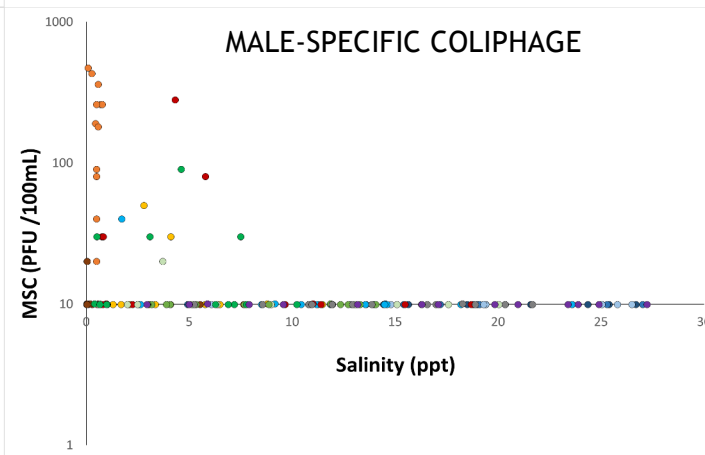
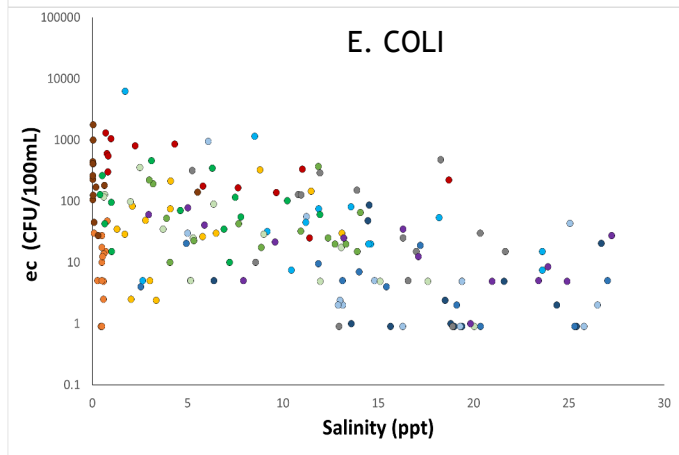
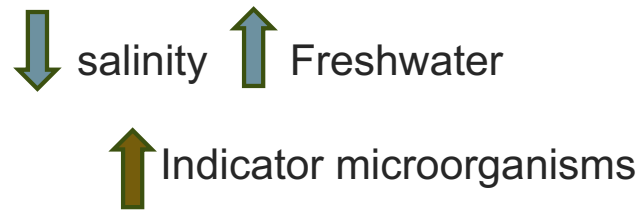
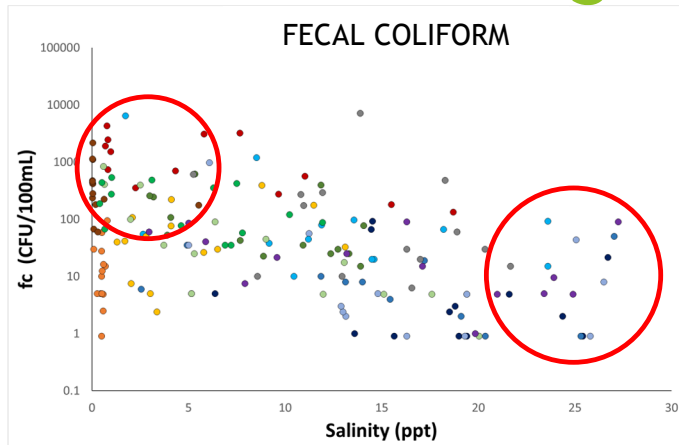




# By site: Salinity, SI, and nutrients







# Indicator microorganisms

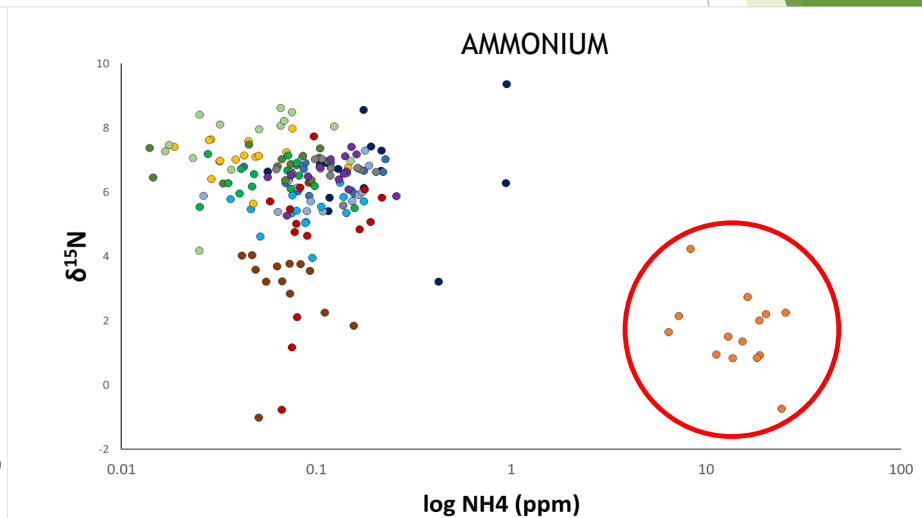
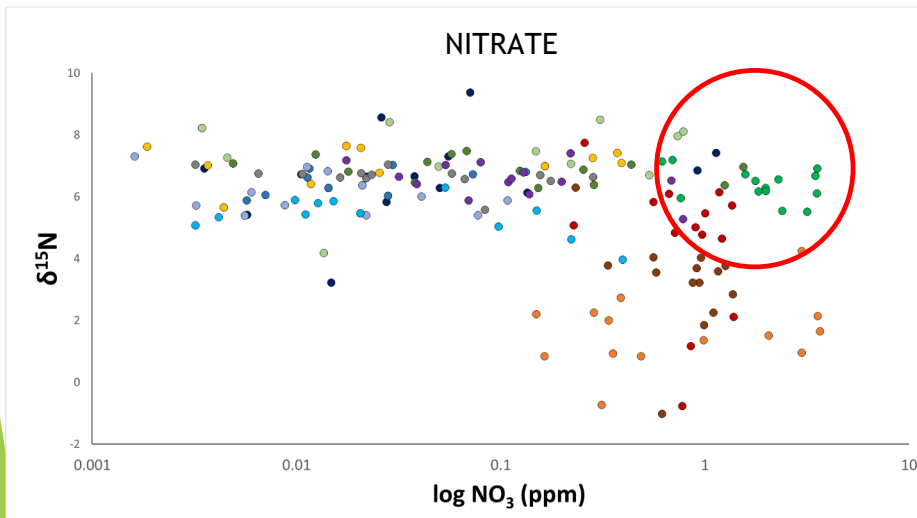
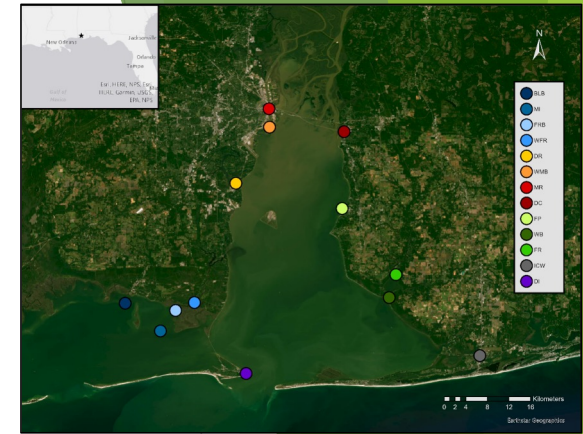


- BLB
- MI
- FRB
- WFR
- DR
- WMB
- MR
- DC
- FP
- WB
- FR
- ICW
- DI

# Multiple Indicators: SI, Nutrients

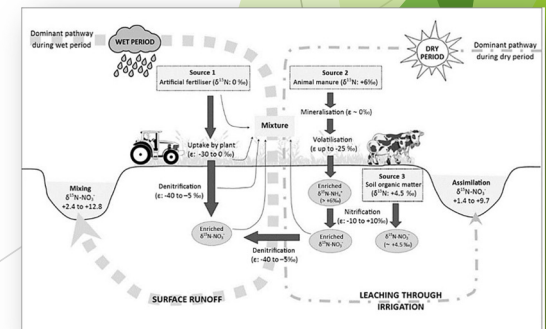
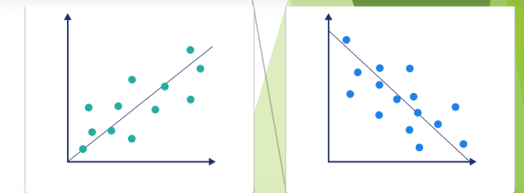
  $\text{NO}_3$    $\delta^{15}\text{N}$   
 processed waste

  $\text{NH}_4$    $\delta^{15}\text{N}$   
 raw waste



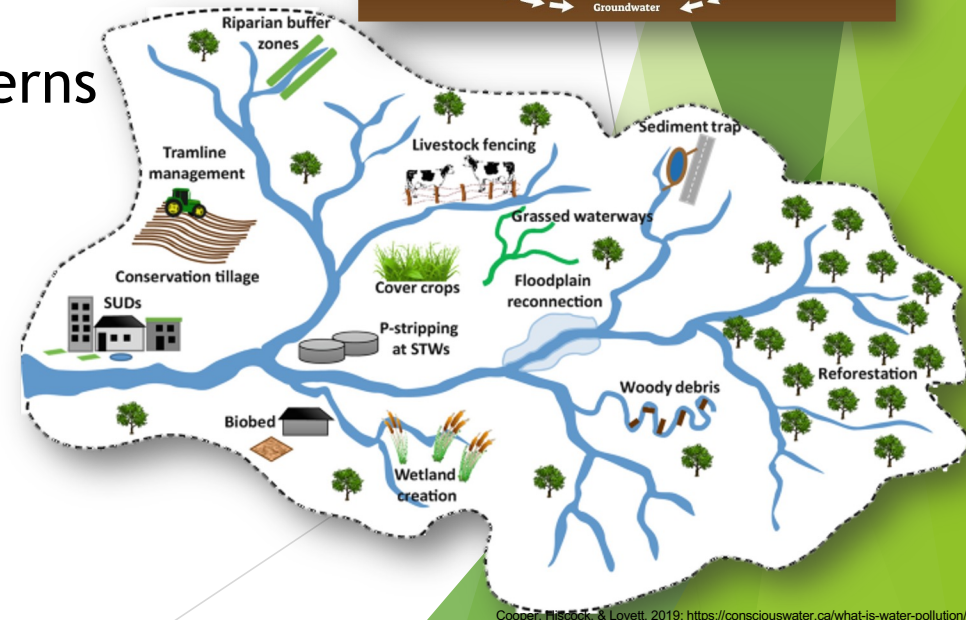
# Preliminary conclusions

- ▶ Salinity correlated with discharge
  - ▶ Sr:Ba indicator of discharge-related salinity
  - ▶ **SI, nutrients, classical microbial indicators** correlated with discharge, salinity
- ▶ Distinct signatures of relationships **between indicators** (e.g.,  $\text{NO}_3^-$ ,  $\text{NH}_4^+$  vs  $\delta^{15}\text{N}$ )
- ▶ **Precipitation** not significant driver of overall discharge or salinity
- ▶ Site and month affected response variables, with **spatial** variation more important



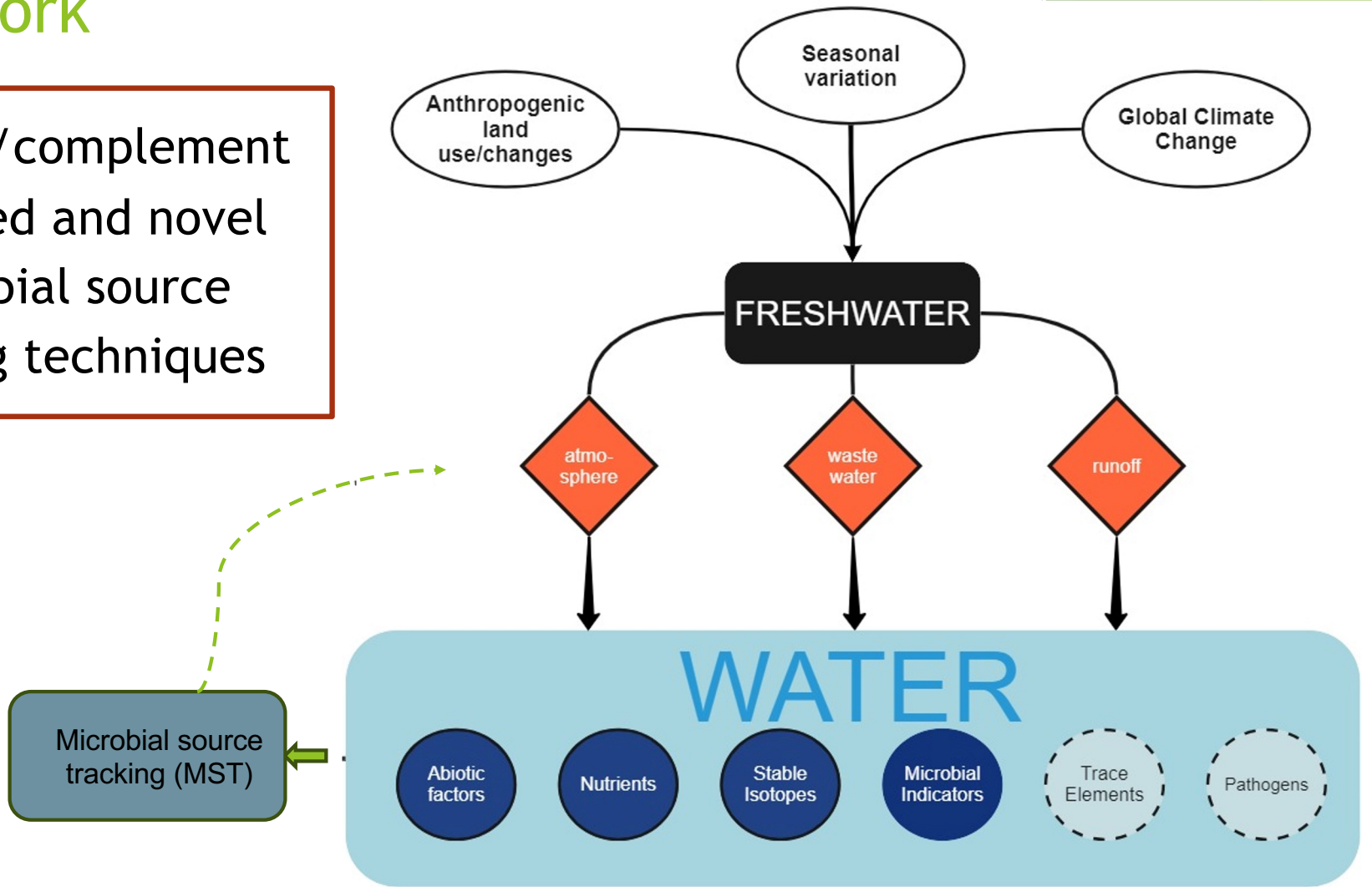
# Implications

- ▶ Use multiple indicators to understand:
  - ▶ potential contaminant sources
  - ▶ pathways
  - ▶ Influence of local climatic and land-use conditions
- ▶ Evaluate spatial and temporal patterns
- ▶ Applications for tailored monitoring/management strategies



## Future work

Validate/complement advanced and novel microbial source tracking techniques



# Molecular Source Tracking

- ▶ Species-specific contributions to microbial indicators in Alabama waters remain largely unknown
- ▶ 2 molecular source tracking techniques



# Molecular Source Tracking

Quantitative PCR (qPCR) will identify and quantify fecal-associated bacteria by targeting genetically distinct strains of *Bacteroides*



General (All) *Bacteroides*  
(total)



Human



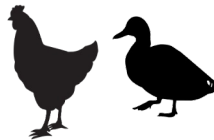
Pig (including feral hog)



Cow



Dog

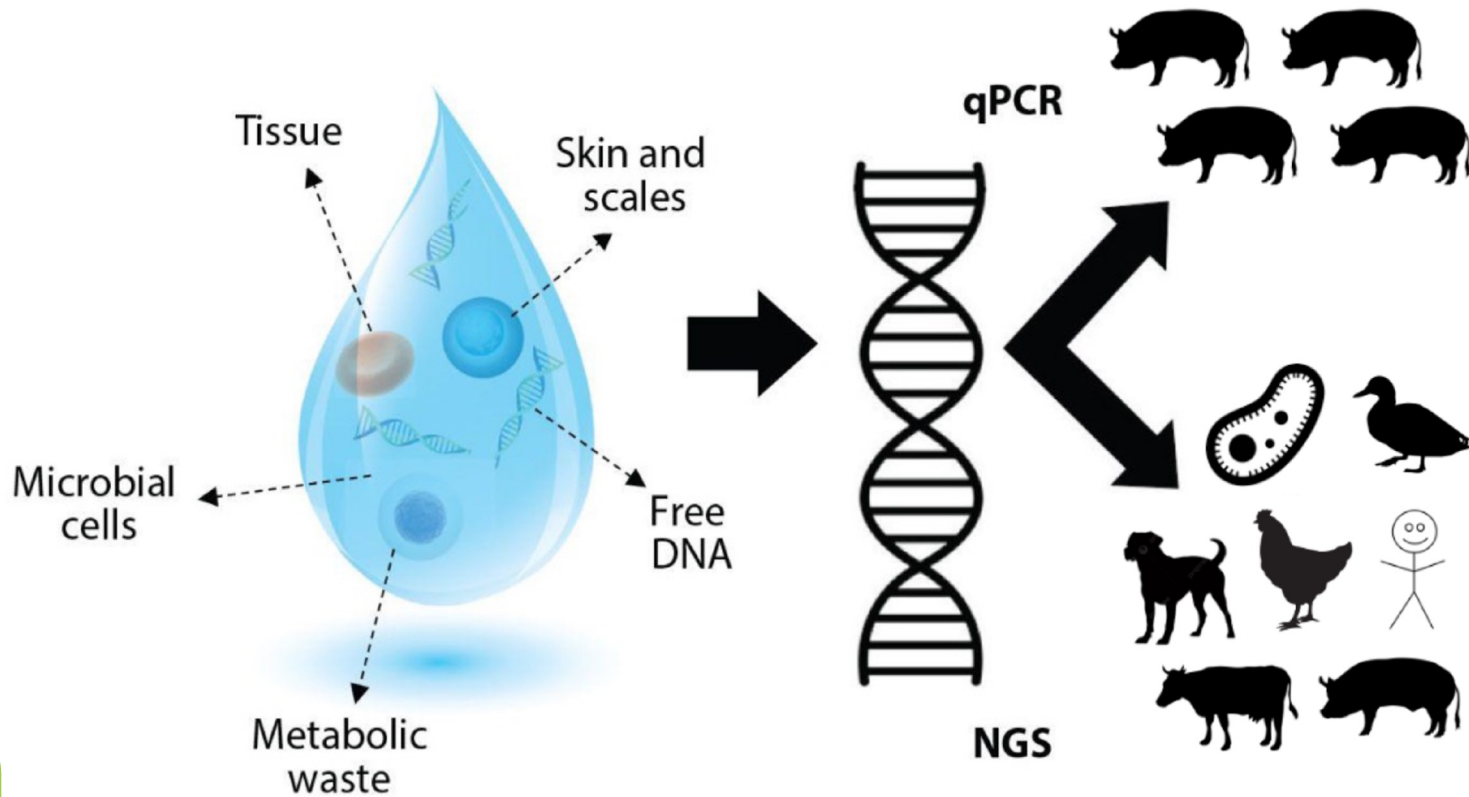


Fowl (Chicken/duck)



# Molecular Source Tracking

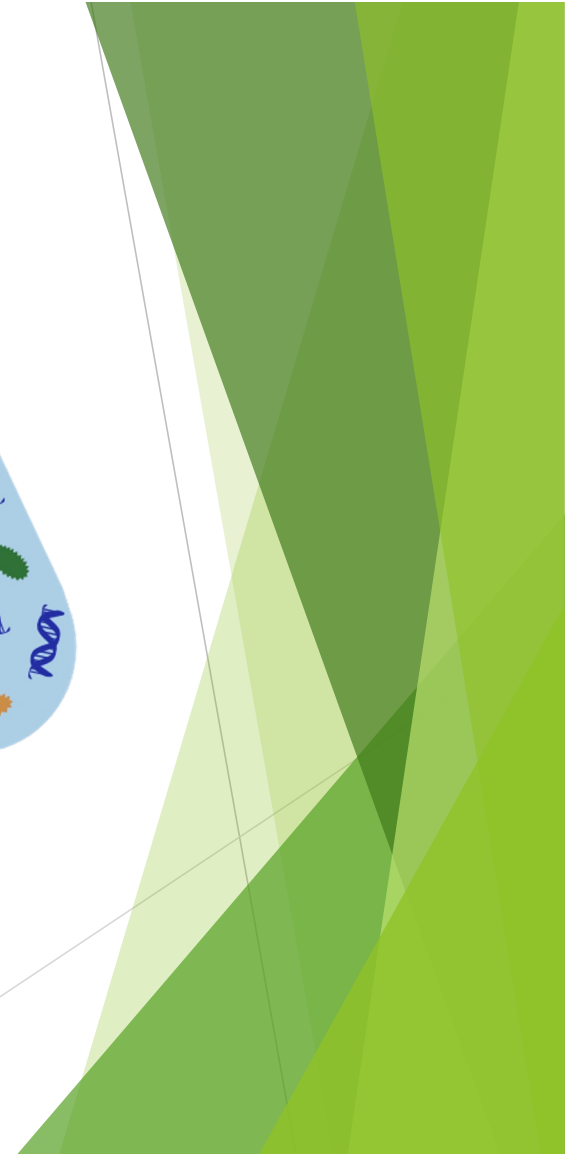
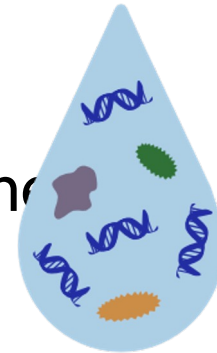
eDNA - all DNA present in the environment



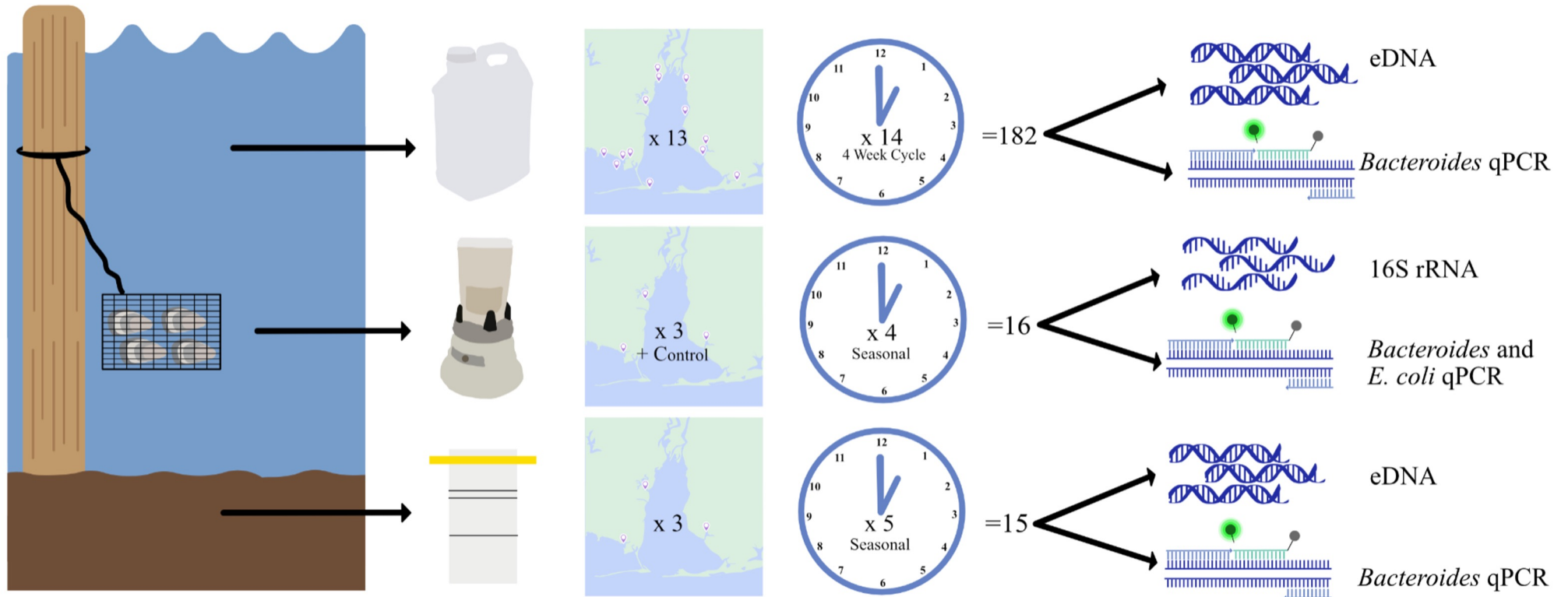
# Molecular Source Tracking

Environmental DNA (eDNA) metagenomics will identify all bacterial and DNA-based viral markers within a sample

- ▶ Does not depend on prior knowledge of the system
- ▶ Has not been implemented as an MST method



# Molecular Matrix

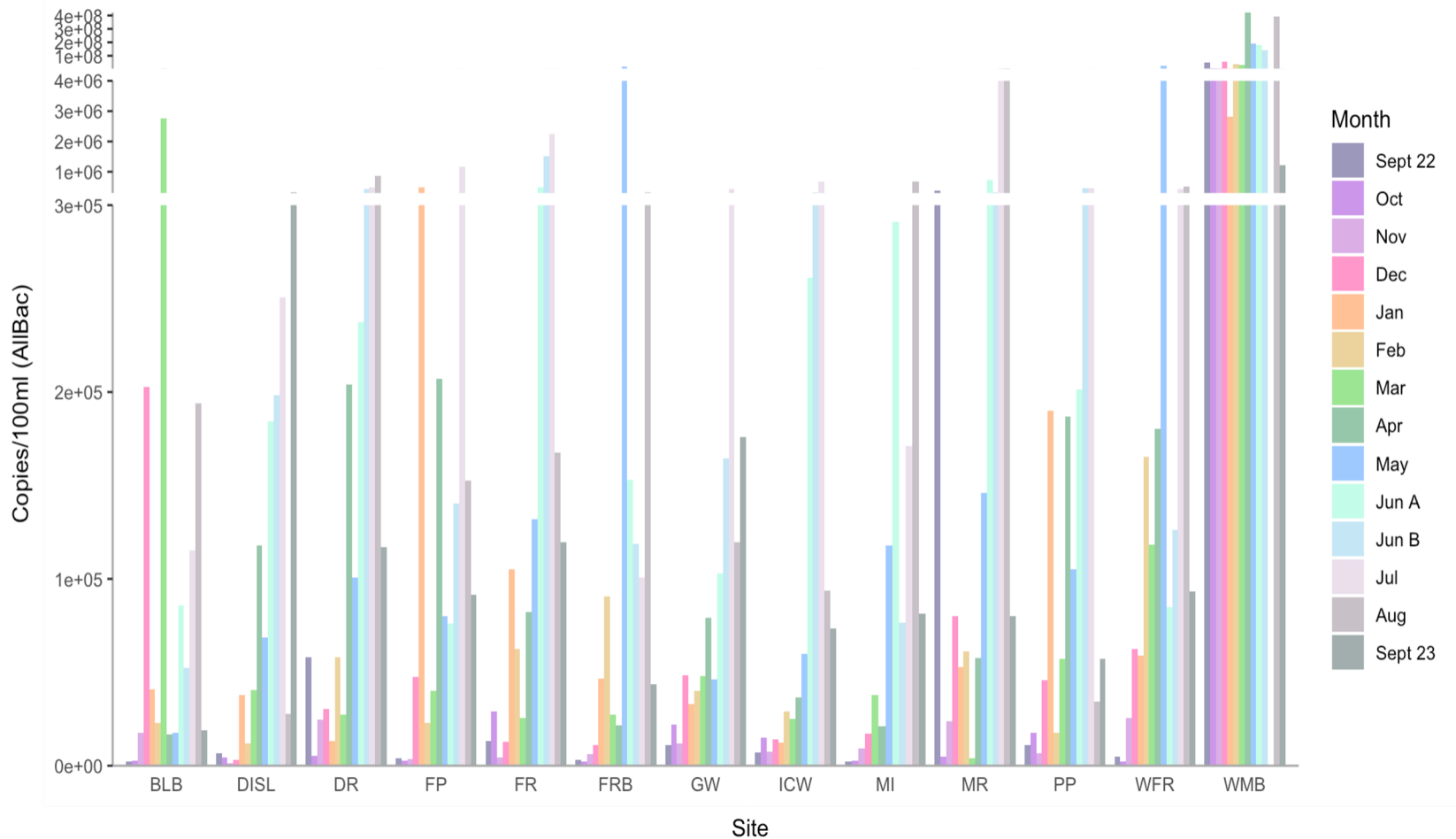


# Progress

- ▶ Bioinformatic analysis underway
- ▶ All source tracking qPCR completed
- ▶ Next steps: multivariate statistics to analyze trends and drivers

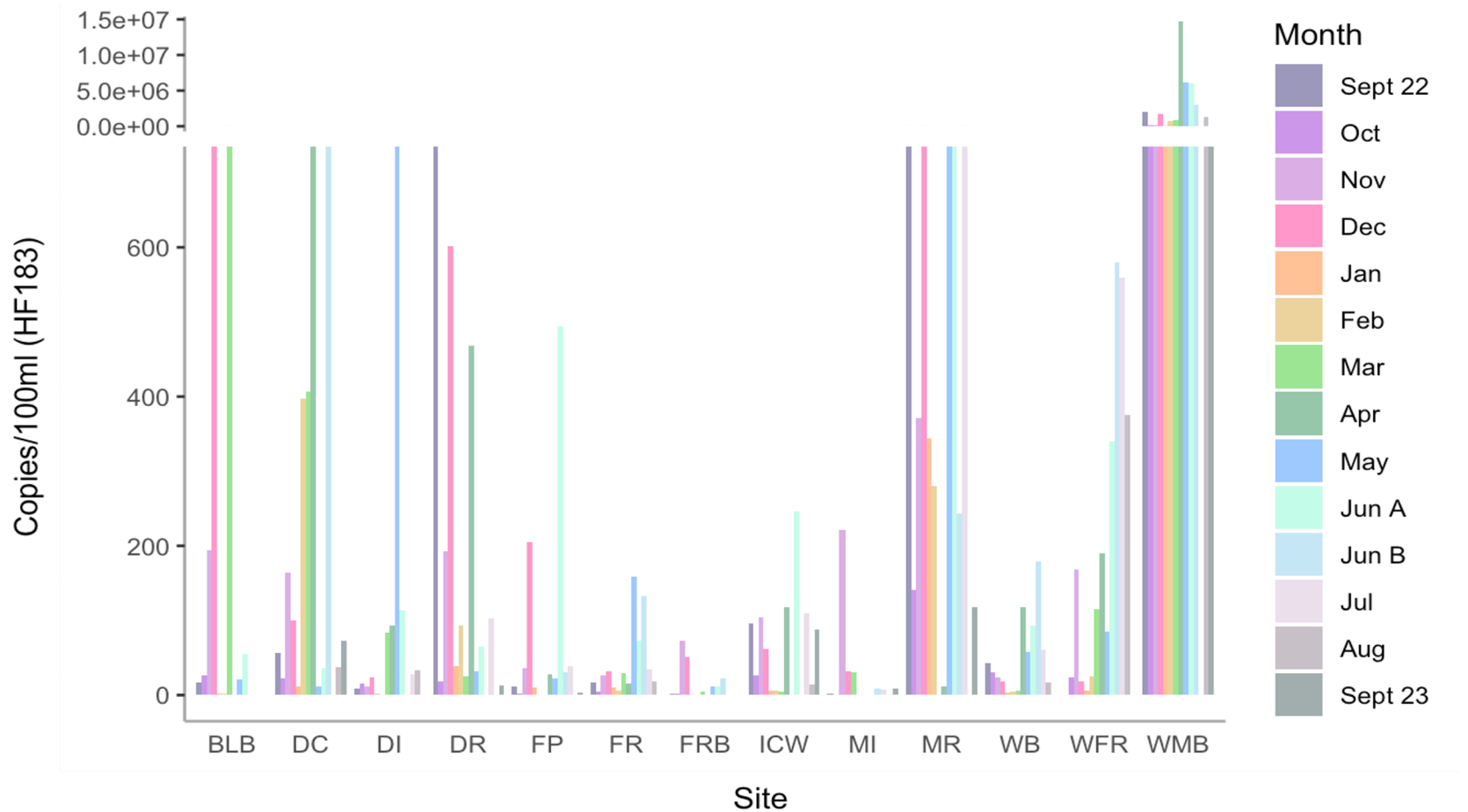
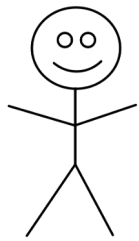


# qPCR data - All *Bacteroides*



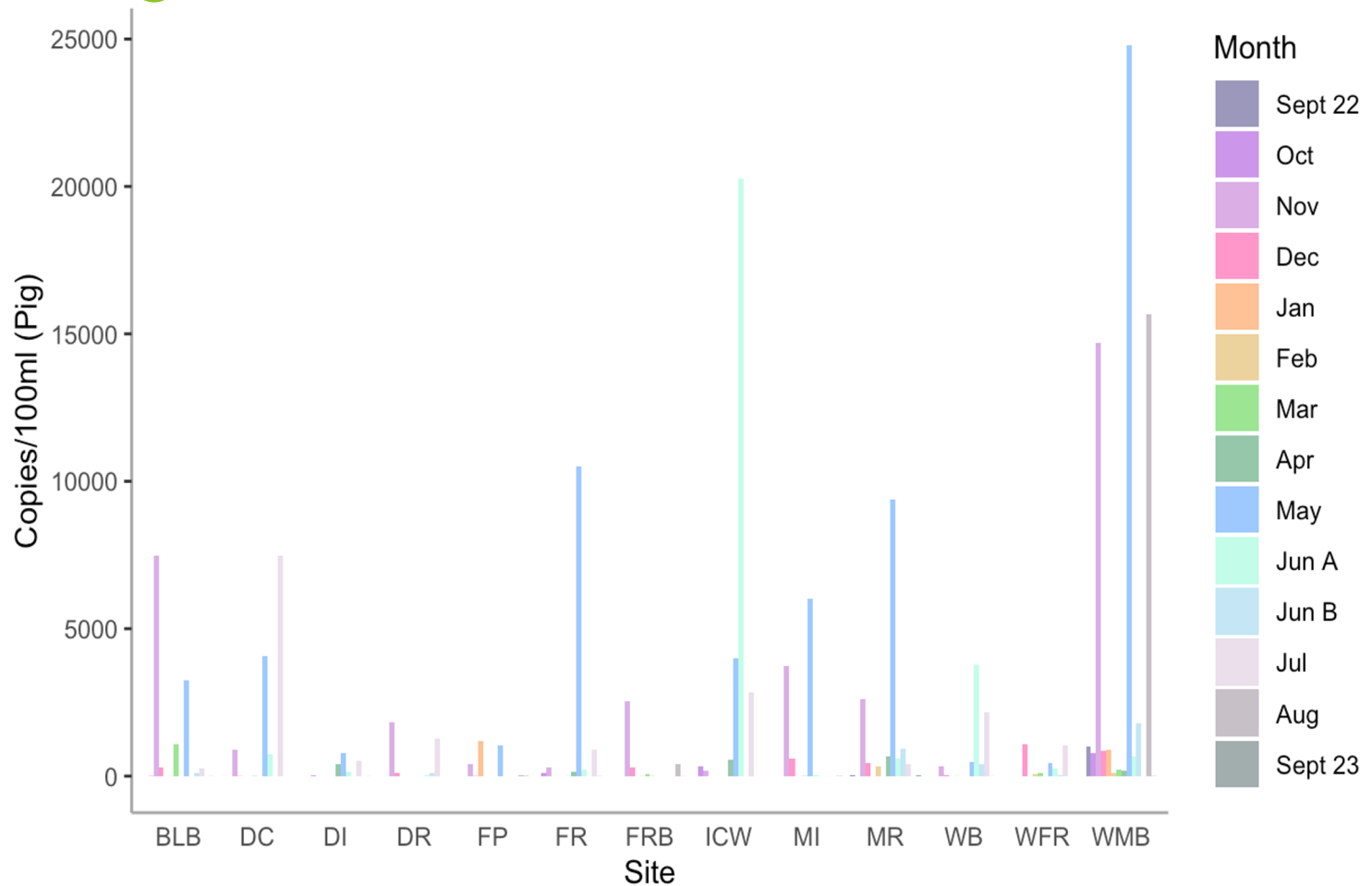
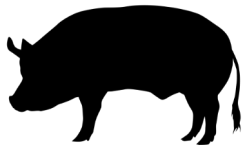
All *Bacteroides* marker was prevalent at all sites over all time points

# qPCR data - Human



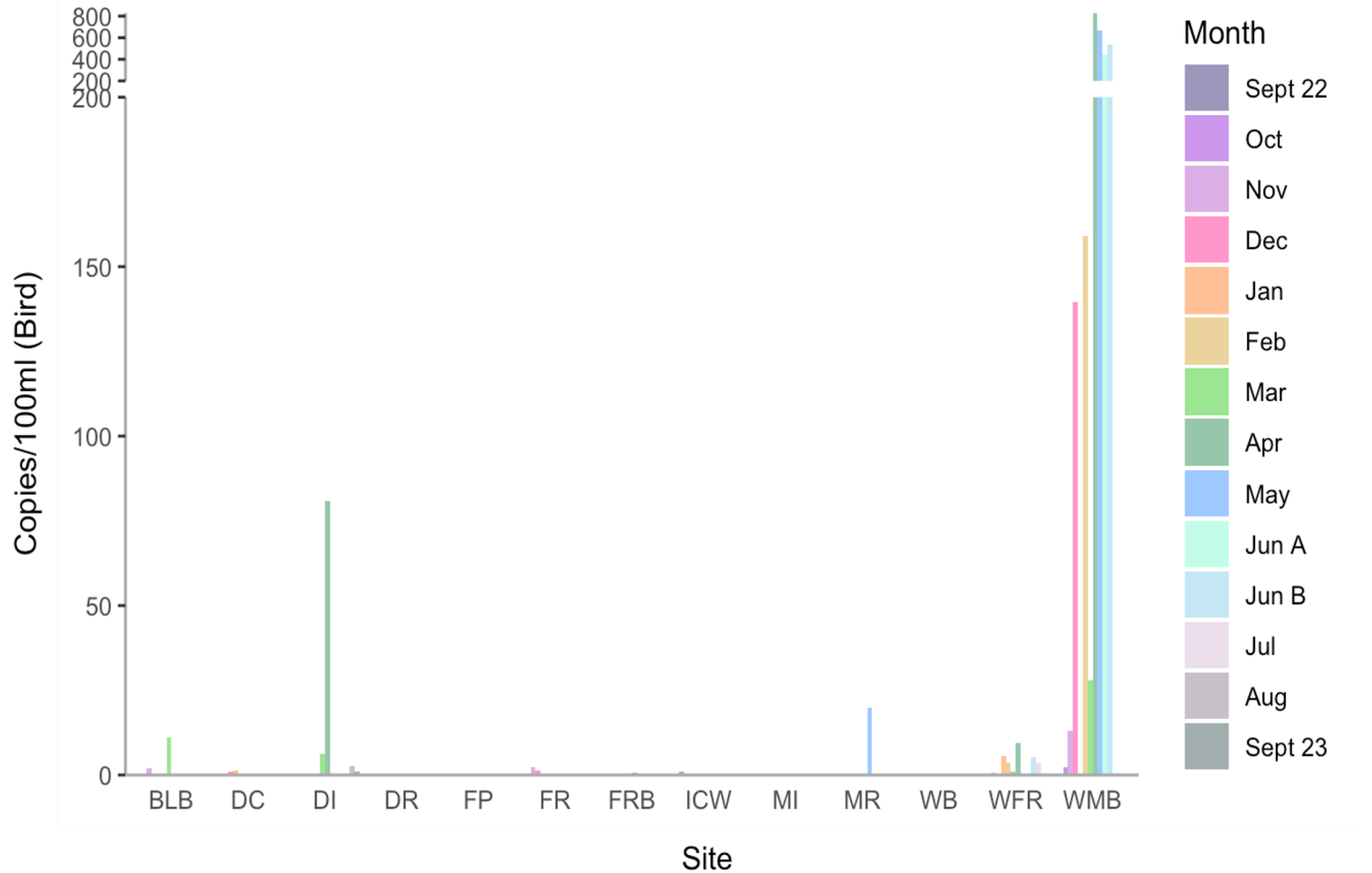
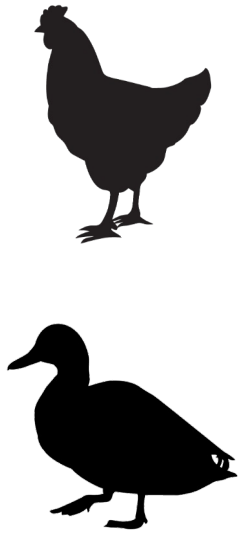
Human marker was found at all sites, and was the major contributor to AllBac

# qPCR data - Pig



Pig marker was found at all sites episodically

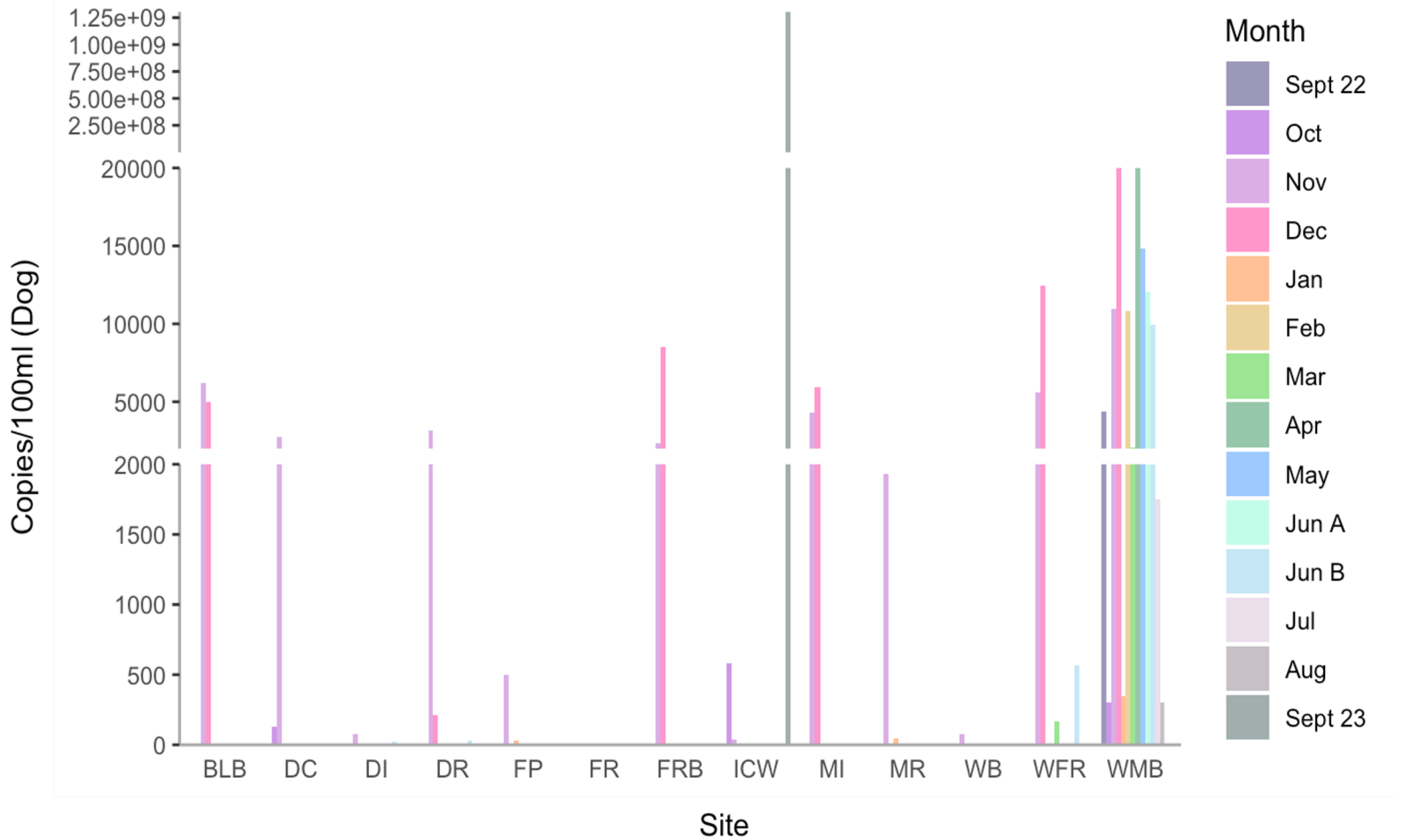
# qPCR data - Fowl



Fowl marker was found at a few sites

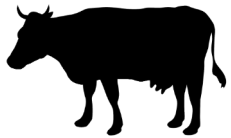


# qPCR data - Dog



Dog marker was found at most sites, but seems seasonally dependent

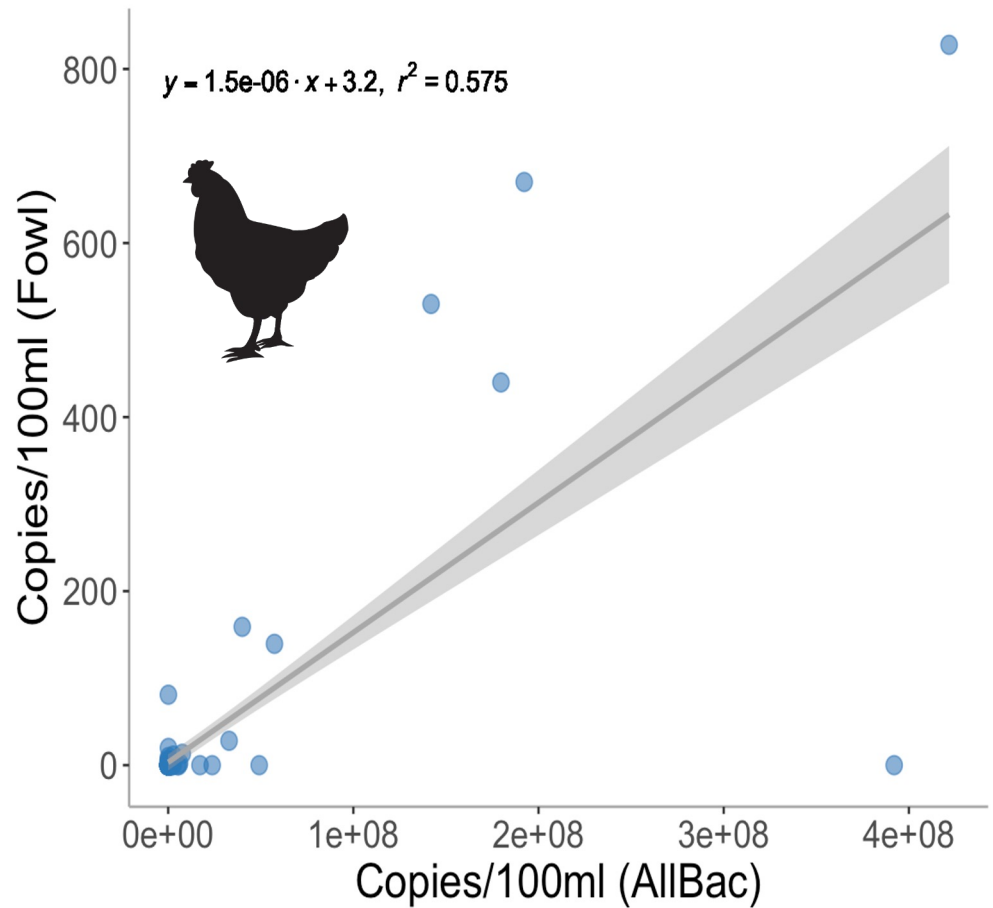
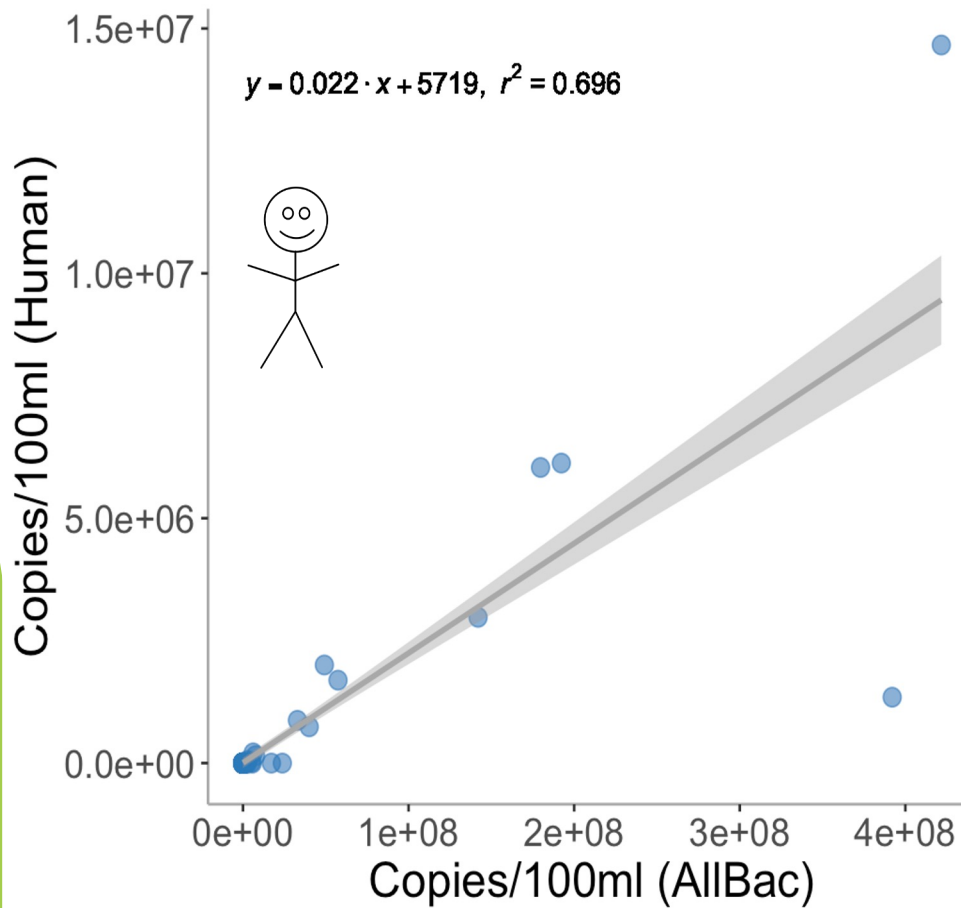
## qPCR data - Cow



The cow marker was found at 2 sampling events  
(site 10 in December and site 4 in March)

# qPCR data

Human and fowl were significantly correlated with the total (AllBac)



# Project Updates: Objective 3

Bree Janssen



# Metadata Clearinghouse

“Our Wastewater Footprint”

<https://www.disl.org/wastewaterfootprint>

- ▶ A living resource to provide up-to-date data on how human wastewater affects water quality on the northern Gulf of Mexico coast data reported for Baldwin County
- ▶ Continued support from Pat David (Data Architect-DISL)



Our Wastewater Footprint

[Home](#) » [Our Research](#) » [Our Wastewater Footprint](#)



## Our Wastewater Footprint

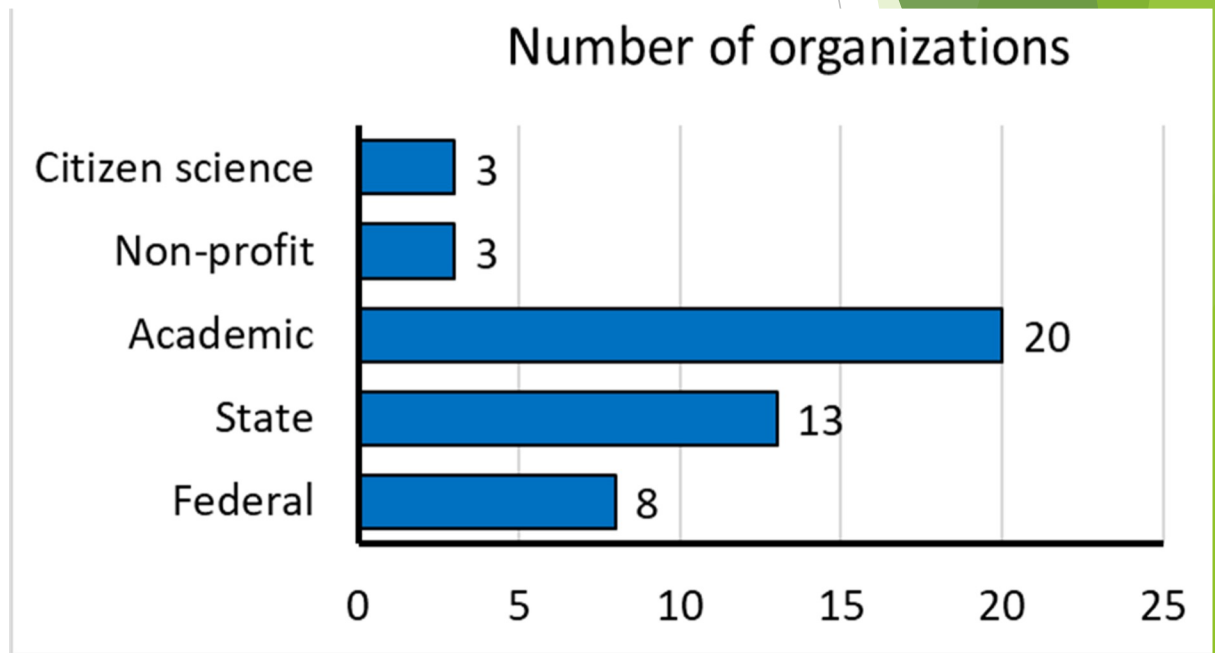
Water quality on the Gulf of Mexico coast



*A first step to water quality improvement*

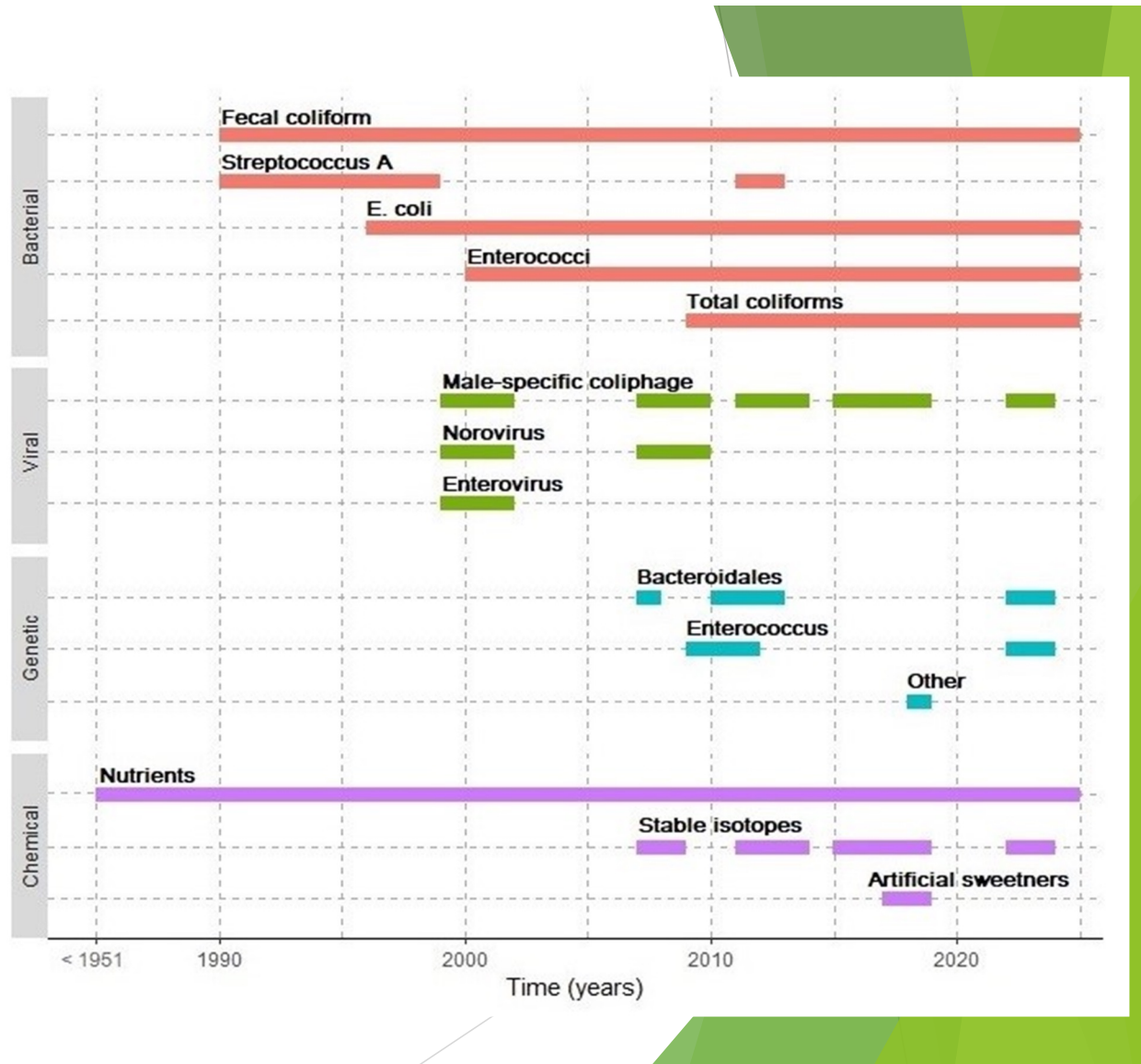
# Metadata Clearinghouse

- ▶ Compile existing microbial indicator and source tracking data and identify other ongoing projects.
- ▶ 30 metadata entries
- ▶ Encourage data sharing and use
- ▶ Invite contributions to Clearinghouse
  - Website & email
  - Questionnaire



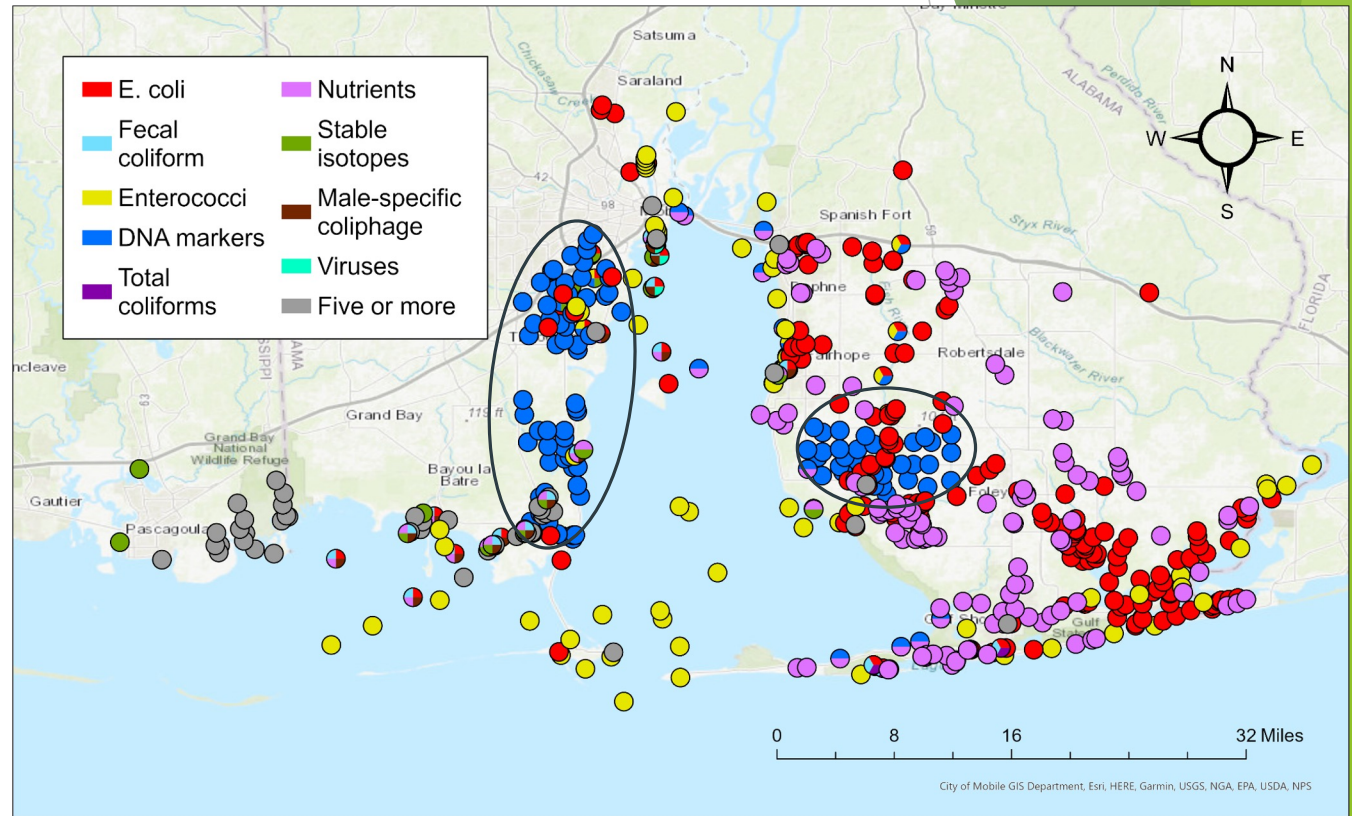
# Temporal Analysis

- ▶ Four major indicator categories: **bacterial**, **viral**, **genetic**, **chemical**
- ▶ Data date back to 1951
  - ▶ Nutrients are most consistently available
  - ▶ Classical indicators (fc, E. coli) prominent after 1990
  - ▶ Newer genetic indicators prominent in the mid-2000s



# Spatial Analysis

- ▶ More data reported for Baldwin County
- ▶ Nutrient, E. coli, & enterococci data are widely collected
- ▶ DNA markers from one comprehensive study in 2018

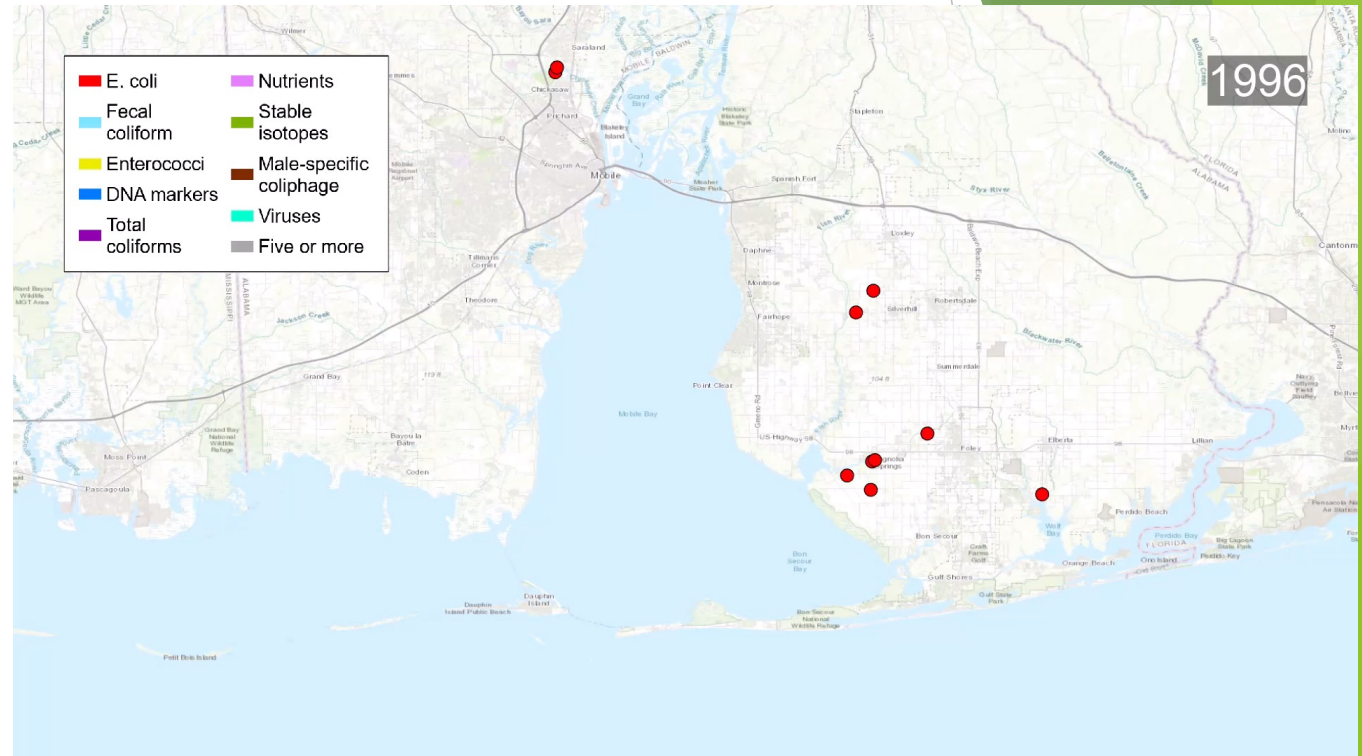




# Spatiotemporal Analysis



- ▶ Shift from “traditional” to “newer” indicators with inclusion of western Mobile Bay
- ▶ Lack of long-term monitoring for advanced indicators, but covers a wide range of locations
- ▶ Likely due to large, discrete studies



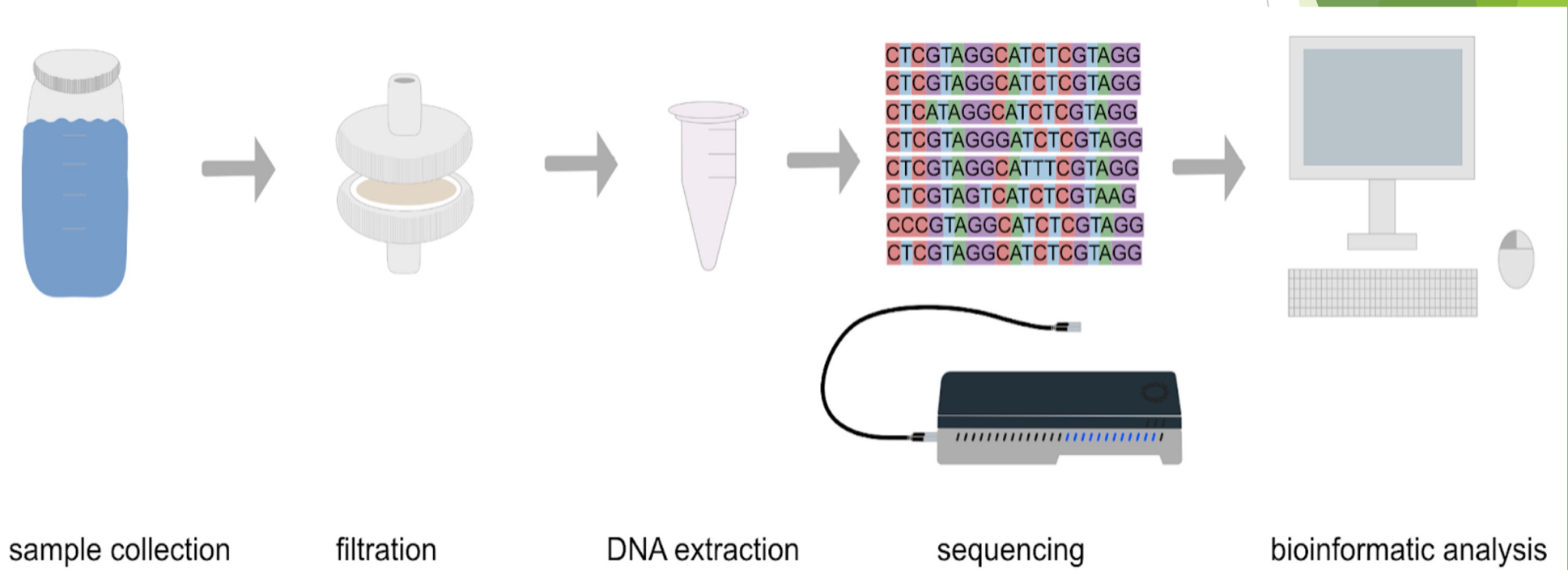
Project Updates: Objective 4  
eDNA Workshop

Penny Demetriades



# eDNA Source Tracking Toolkit

Implement eDNA as an accessible next generation source tracking tool with the creation of an eDNA toolkit and workshop

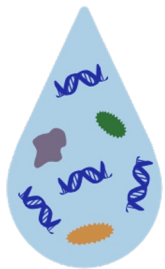


# eDNA Source Tracking Toolkit

The workshop will be hosted at the U South Alabama campus  
**April 25, 2025**

<https://sites.google.com/view/ednatoolkit/>

**Register by April 4**



eDNA  
Source Tracking  
Toolkit





The eDNA Source Tracking Toolkit is a resource for implementing eDNA metagenomics as a fecal source tracking tool.

Environmental DNA (eDNA) metagenomics techniques have the capacity to provide important biological context to source tracking identification and fill in data gaps left by source-specific microbial source tracking methods, such as qPCR.

Metagenomics data can show community composition and function to provide a comprehensive assessment of water quality in a system.

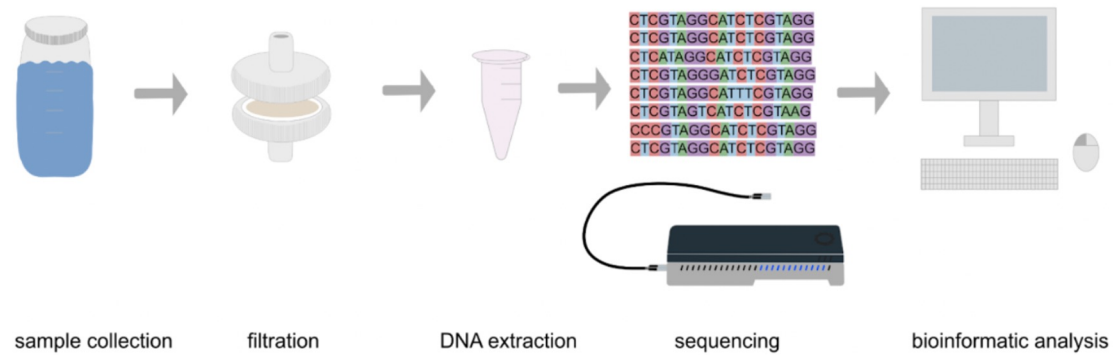
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This toolkit is hosted through the [Kiel Reese lab](#) at the University of South Alabama and the Dauphin Island Sea Lab with funding provided by Environmental Protection Agency Gulf of Mexico Division grant MX-02D17922. Please direct any questions to [pdemetriades@disl.org](mailto:pdemetriades@disl.org).

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# Workshop Information



Learn how to implement eDNA Source Tracking methods during our Toolkit Workshop on **April 25, 2025!**

Participants will learn best practices for eDNA sample collection, filtration, and DNA extraction. Participants will be able to engage in a hands-on sequencing run with a MinION sequencer and will be guided through subsequent bioinformatic analysis and key data visualization.

## eDNA Source Tracking Toolkit Workshop Registration

Learn how to implement eDNA Source Tracking methods to enhance fecal contamination monitoring efforts during our Toolkit Workshop. Participants will learn best practices for eDNA sample collection, filtration, and DNA extraction. Participants will be able to engage in a hands-on sequencing run with a MinION sequencer and will be guided through subsequent bioinformatic analysis and key data visualization.

Please use this form to register for the workshop on April 25, 2025 (9am-12pm) at the University of South Alabama.

Registration will close on April 4.



# eDNA Source Tracking Toolkit Workshop Registration

Learn how to implement eDNA Source Tracking methods to enhance fecal contamination monitoring efforts during our Toolkit Workshop. Participants will learn best practices for eDNA sample collection, filtration, and DNA extraction. Participants will be able to engage in a hands-on sequencing run with a MinION sequencer and will be guided through subsequent bioinformatic analysis and key data visualization.

Please use this form to register for the workshop on **April 25, 2025** from 9am-12pm. This workshop will be hosted in person on the University of South Alabama campus (EOB Room 101, Stokes School of Marine and Environmental Sciences). Participation will be capped at 12 individuals. **Registration will close on April 4.**

demetriadespenny@gmail.com [Switch account](#)

Not shared

Draft saved

\* Indicates required question

Email \*

Your answer

First and Last Name \*

Your answer

Please register by  
April 4!



# Tracking wastewater for health and resilience in Alabama (aka EPAII)

## PIs and Partners

- Brandi Kiel Reese, USA/DISL
- Ruth H. Carmichael, DISL/USA
- Sinéad Ní Chadhain, USA
- Brian Dzwonkowski, USA/DISL
- Zhilong Liu, USA/DISL
- Elica Moss, Alabama A&M University
- Kathleen Roberts, Bishop State
- Mobile BayKeeper
- Gulf States Health Policy Center





# Tracking wastewater for health and resilience in Alabama (aka EPAII)

1. Conduct community-driven, spatially explicit shoreline **water-quality surveys** in the 4 most disadvantaged and vulnerable coastal communities in Alabama

**intersectionality  
of multiple  
environmental &  
demographic  
stressors**

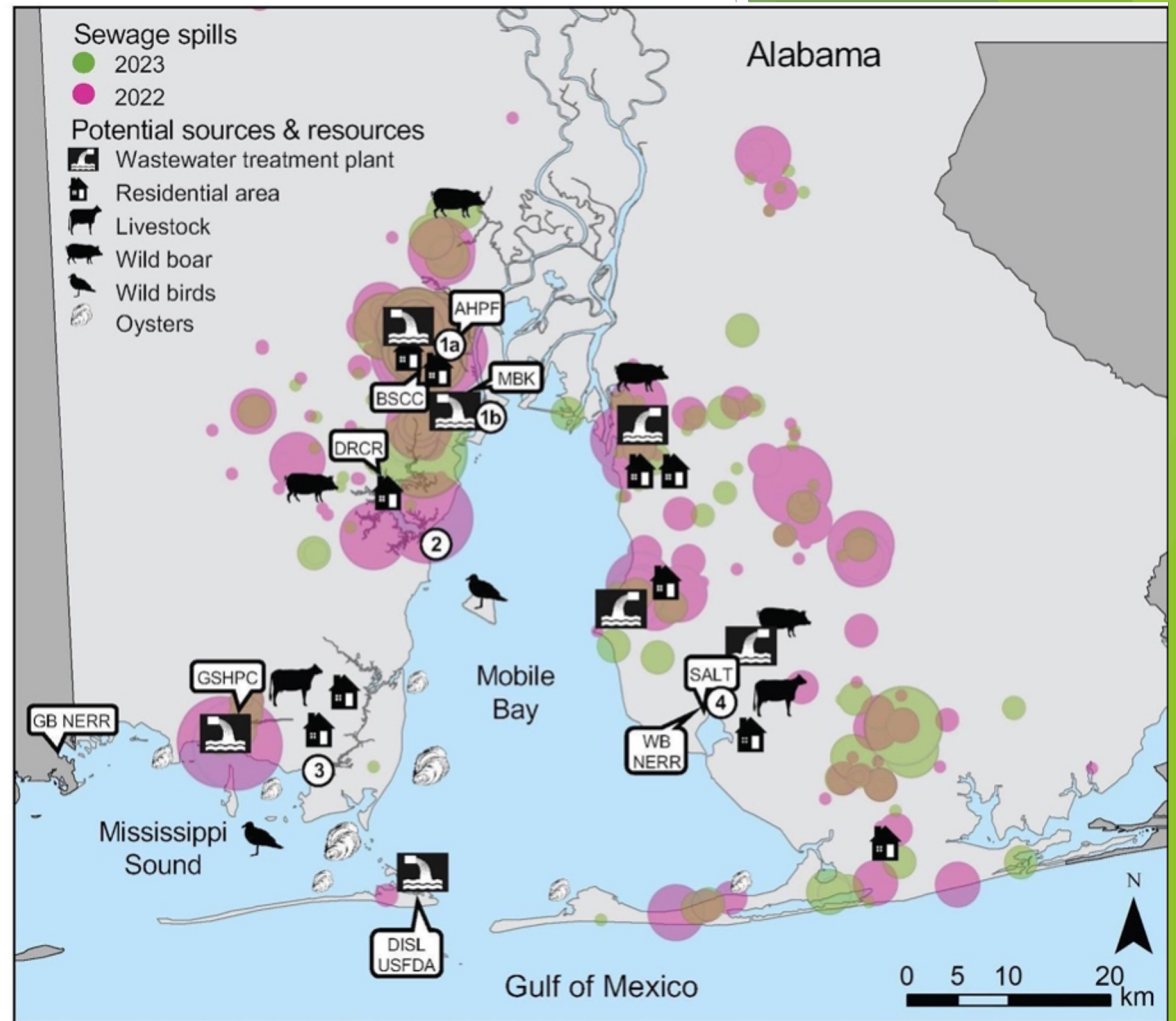
- ▶ Africatown/ Three-mile Creek
- ▶ Dog River
- ▶ Fish River
- ▶ Fowl River

# Tracking wastewater for health and resilience in Alabama (aka EPAII)

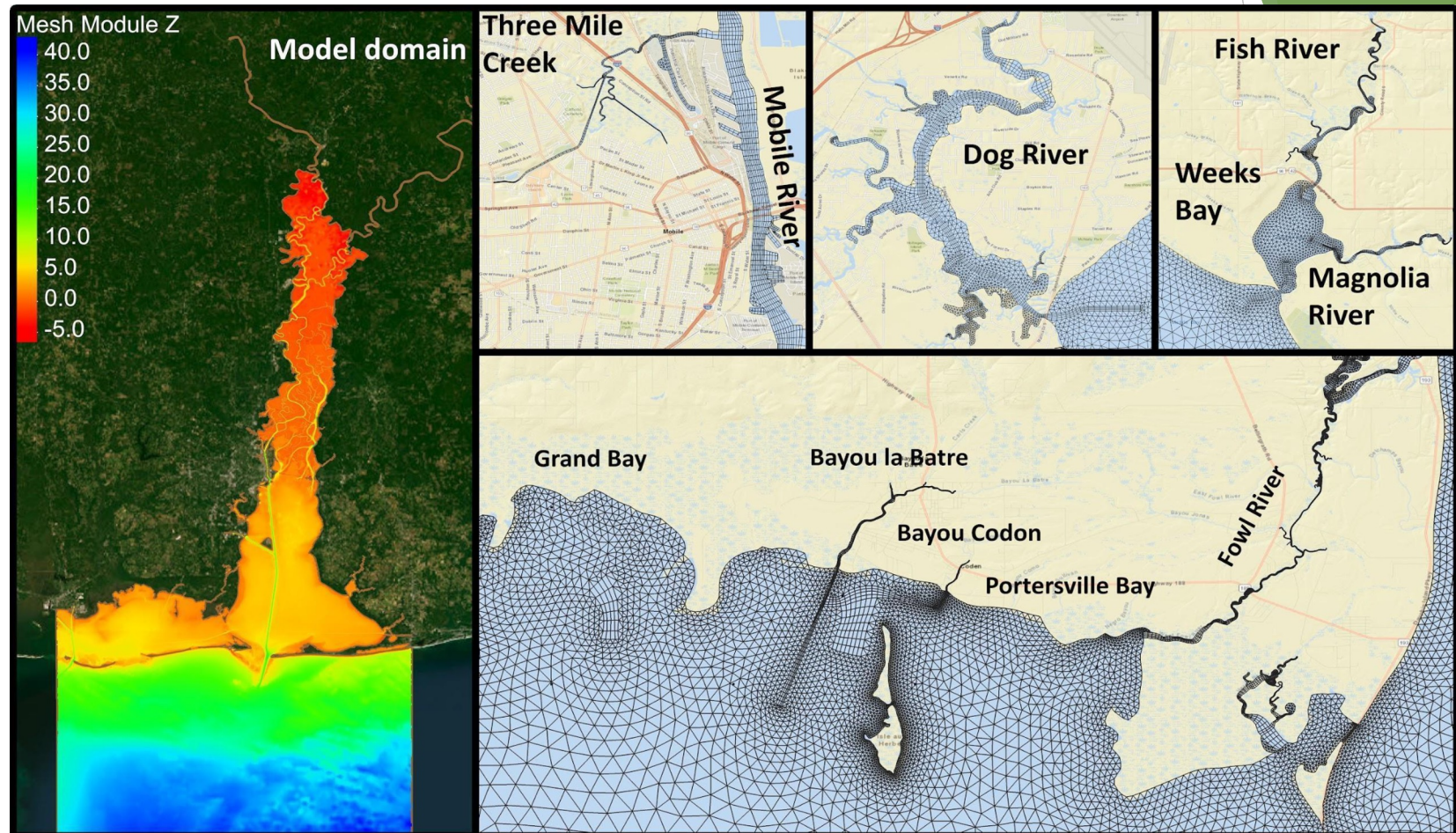
- 2. Assess potential health risks** from water use (e.g., fishing, swimming) by defining wastewater-derived microbial sources to the waterways using traditional, biogeochemical, and advanced (genomics) microbial source-tracking approaches
- 3. Determine if water quality in these areas affects adjacent communities** by modeling flow to downstream sentinel sites
- 4. Meaningfully involve community members** in the project from planning to outreach through partnerships with a Community Engagement Facilitator and stakeholder groups

# Sampling Approach

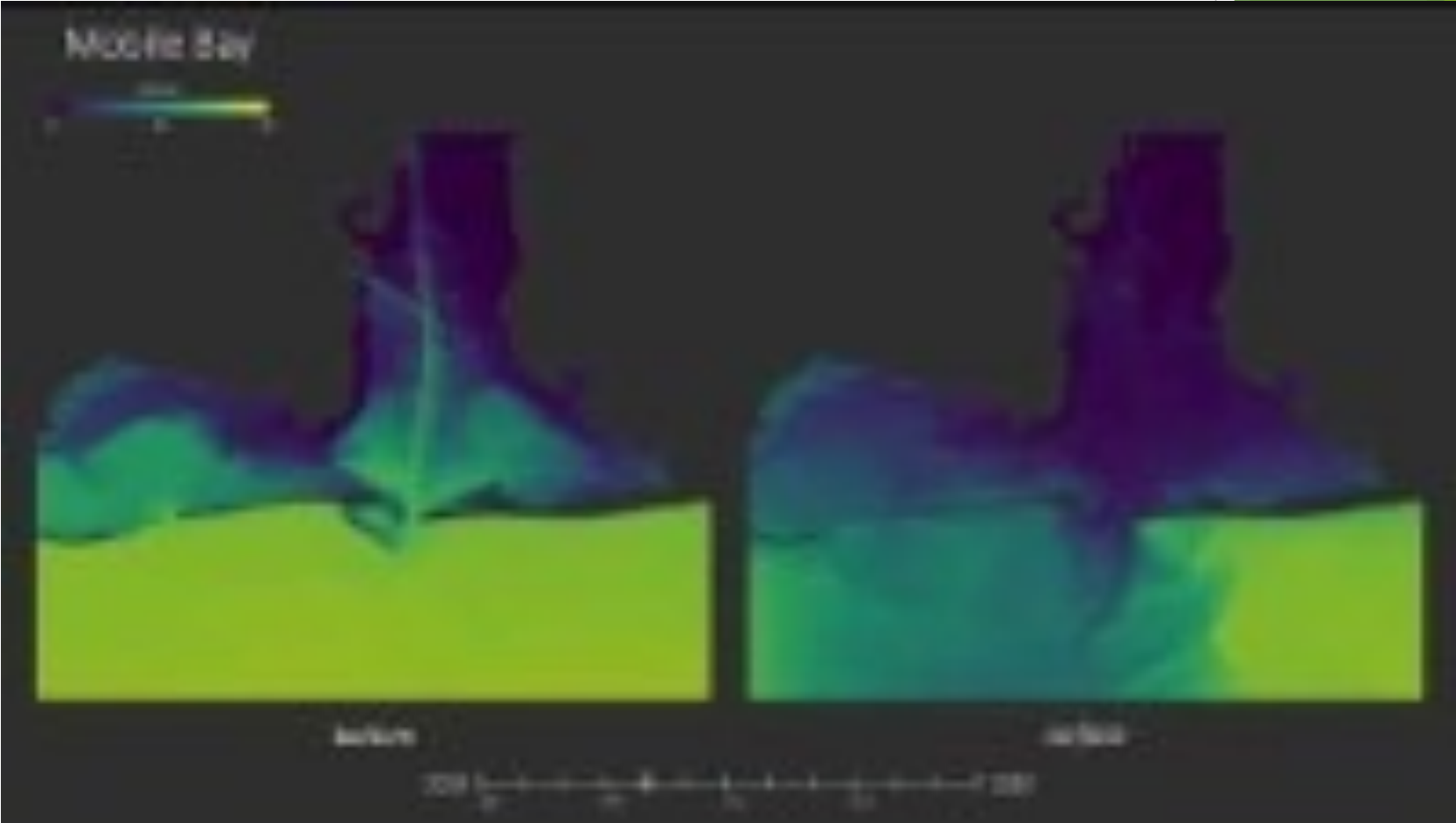
- ▶ Shoreline surveys in four local communities (tributaries 1-4)
  - ▶ 10 sites along each tributary
  - ▶ 2 sentinel sites downstream
- ▶ Sampling quarterly
- ▶ Tributaries 1 & 2 in Y1-Y2
- ▶ Tributaries 3 & 4 in Y3-Y4
- ▶ Event sampling



# Modeling Approach: Transport & dispersion



# Mobile Bay Salt Dynamics -- ROMS



[https://www.youtube.com/watch?v=\\_JKu-bH9K\\_Y](https://www.youtube.com/watch?v=_JKu-bH9K_Y)

# Community engagement

Align project goals with community interests and values (JFF) through a **Community Engagement Facilitator** (GSHPC)

- ▶ Define baseline concerns & conditions
- ▶ Refine sampling locations in each community
- ▶ Incentivized community meetings
- ▶ Community-based sampling (test kits & validation)
- ▶ Curriculum workshops & internships for partner HBCU/ MSIs
- ▶ Seek new perspectives & stakeholders
- ▶ Co-produce outputs of interest and use to improve water quality, community health and resilience



# Timeline

Aim	Task	2025				2026				2027				2028				2029			
		1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4	1	2	3	4
<b>All</b>	Project planning	■																			
<b>Aim 1</b>	Shoreline surveys		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Sentinel site & oyster sampling		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Nutrients & Stable isotopes (Carmichael)		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Microbial indicators (Carmichael)		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Environmental DNA (Kiel Reese)		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Sequencing									■	■	■	■	■	■	■	■	■	■	■	■
	Bioinformatics									■	■	■	■	■	■	■	■	■	■	■	■
	qPCR source specific (Ní Chadhain)			■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	qPCR pathogens (Carmichael)			■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	<b>Aim 2</b>	Collect hydrologic data (Dzwonkowski, Liu)		■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
Modeling & Data Integration			■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
<b>Aim 3</b>	Citizen Science training & validation	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Outreach materials development	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Data sharing and Website updates	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
<b>All</b>	Annual reporting & manuscripts									■	■	■	■	■	■	■	■	■	■	■	■
	Team meetings	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■	■
	Community meetings									■	■	■	■	■	■	■	■	■	■	■	■

## How to get involved...

- Attend stakeholder meetings
- Provide feedback
- Provide data: CLEARINGHOUSE
- Tell colleagues
- How will you use these data?
- What would you or your colleagues like to gain from the eDNA toolkit workshop?



Questions or Comments?

