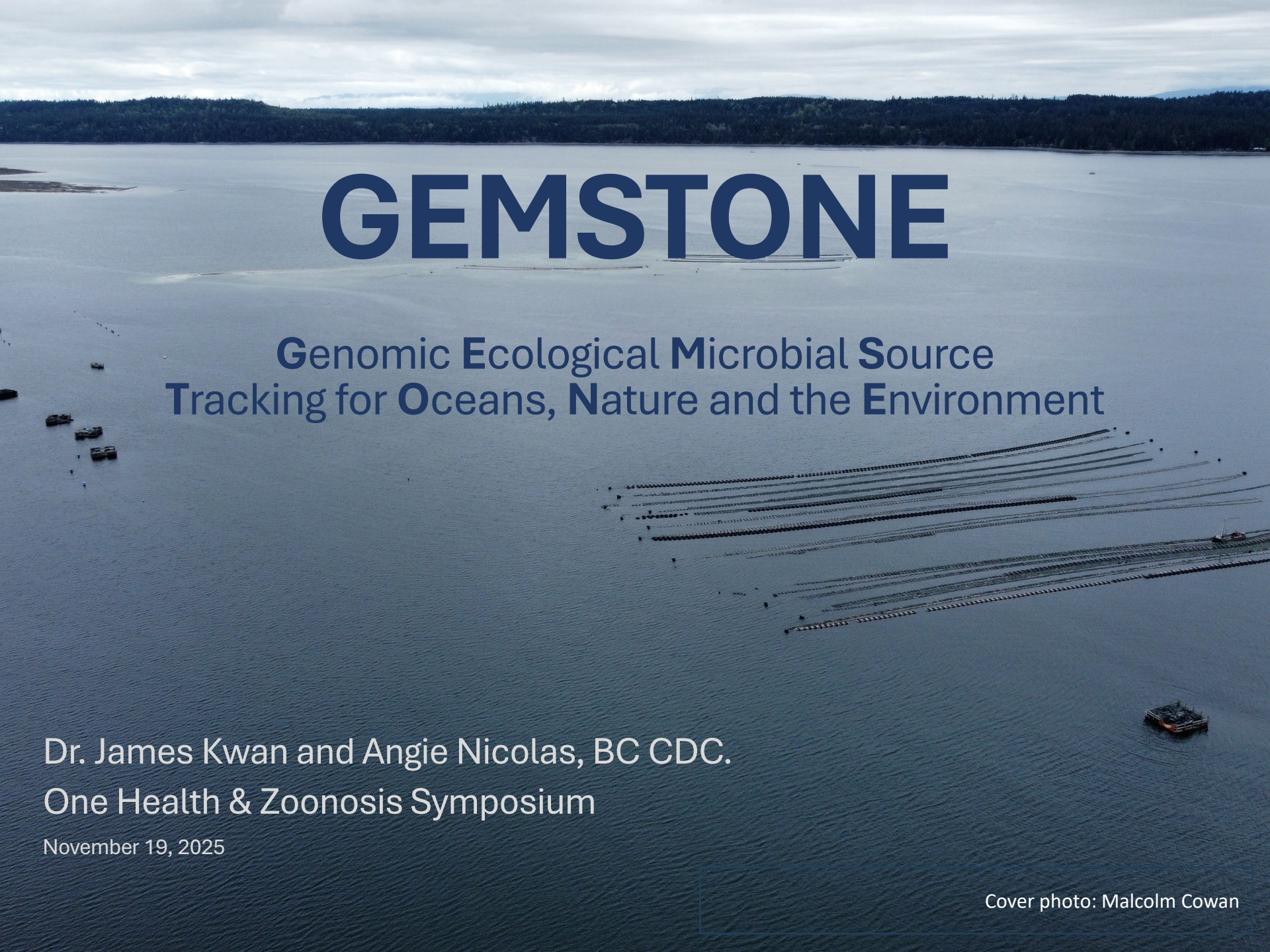


GEMSTONE

Genomic **E**cological **M**icrobial **S**ource Tracking for **O**ceans, **N**ature and the **E**nvironment

Dr. James Kwan and Angie Nicolas, BC CDC.

One Health & Zoonosis Symposium

November 19, 2025

Cover photo: Malcolm Cowan

BC Centre for Disease Control

Provincial Health Services Authority
Province-wide solutions. Better health.

UBC

We gratefully acknowledge that we live and work on the traditional, ancestral, and unceded territories of the Coast Salish Peoples, including the Squamish, Musqueam, Tsleil-Waututh and Stó:lō First Nations.

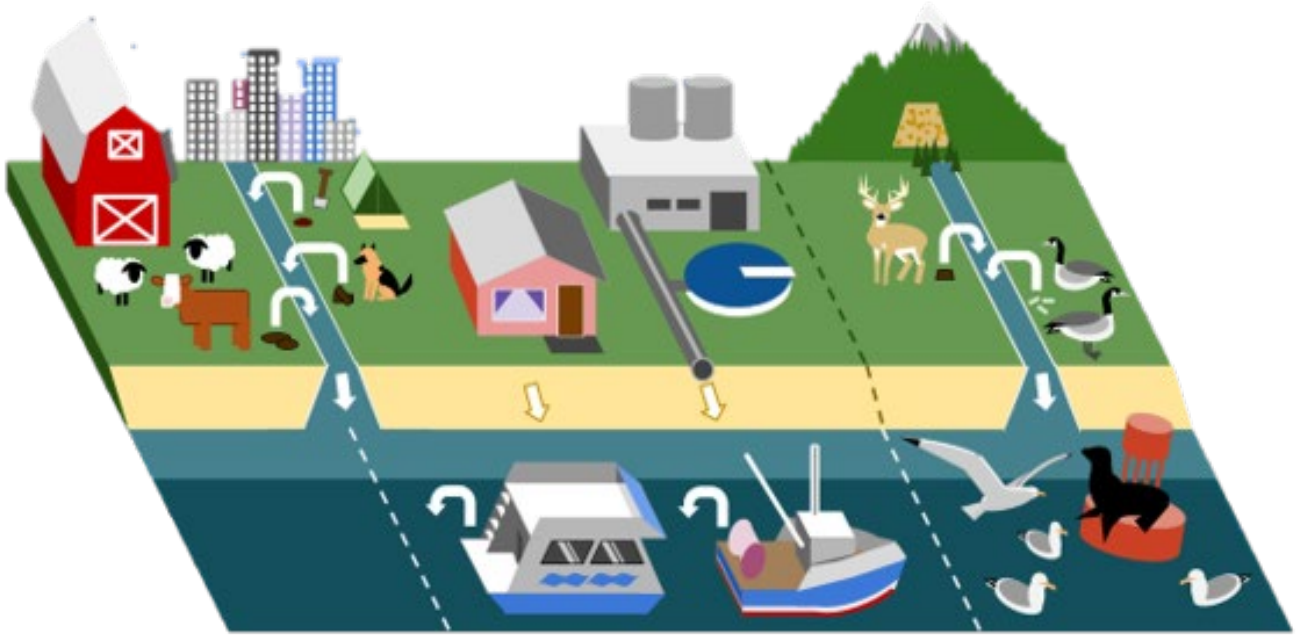


Marine fecal contamination

- **Recurrent and ongoing issue**
- **One Health impacts**
  - Shellfish contamination
  - Human illness
  - Harvest site closures
    - Reduced access to traditional and healthy foods for sustenance and spiritual purposes
    - Economic losses
    - Damaged reputations
  - Ecosystem harms and water quality degradation

Fecal sources are everywhere

- Closures informed by fecal coliforms
- Indicator of presence/absence only
- Does not inform source management
- Need tools to identify fecal source



Microbial Source Tracking can support targeted interventions

Photo: Malcolm Cowan, BCSGA

Objectives

1. Develop and validate microbial source tracking (MST) tools to identify fecal sources at BC marine shellfish harvest sites
2. Investigate spatial and temporal trends in fecal contamination
3. Transfer knowledge and technology to sector partners

Study design

Longitudinal sampling

- Biweekly water samples from 3 historically contaminated sites

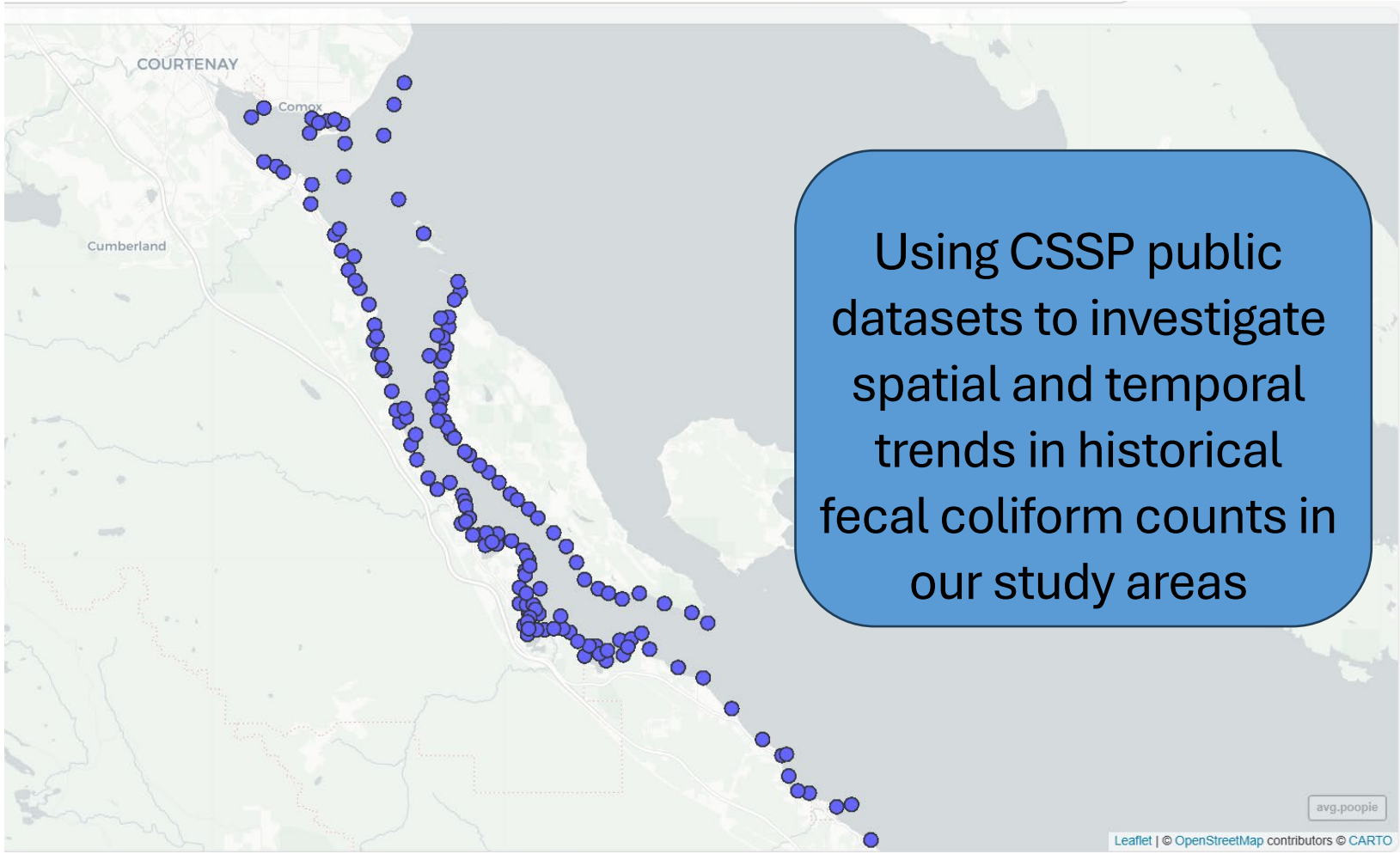
Surge sampling

- During high rainfall periods when conditions allow

Complementary target sampling

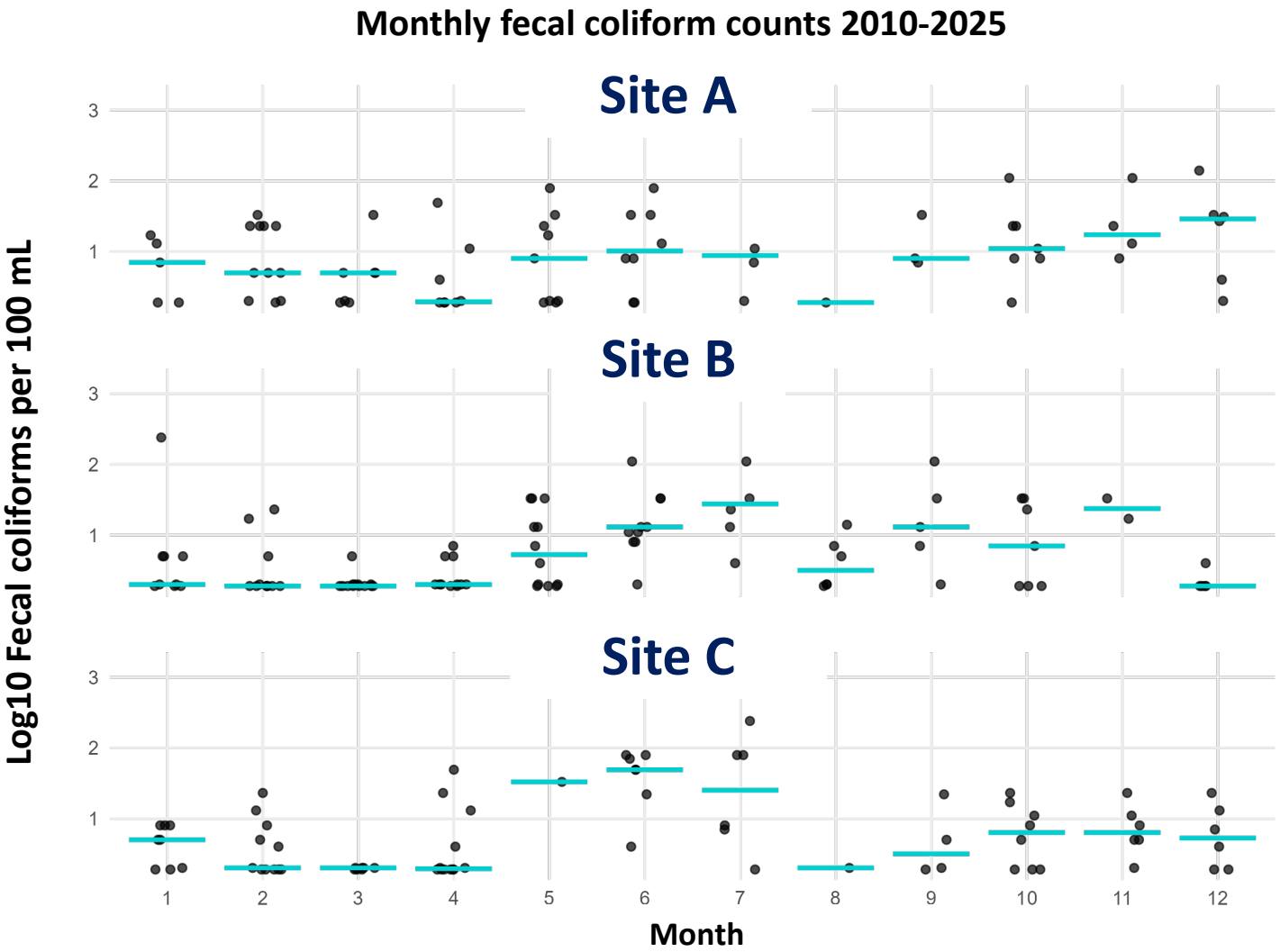
- 2-3 locations within the vicinity of longitudinal sites

Analyzing historic CSSP Data

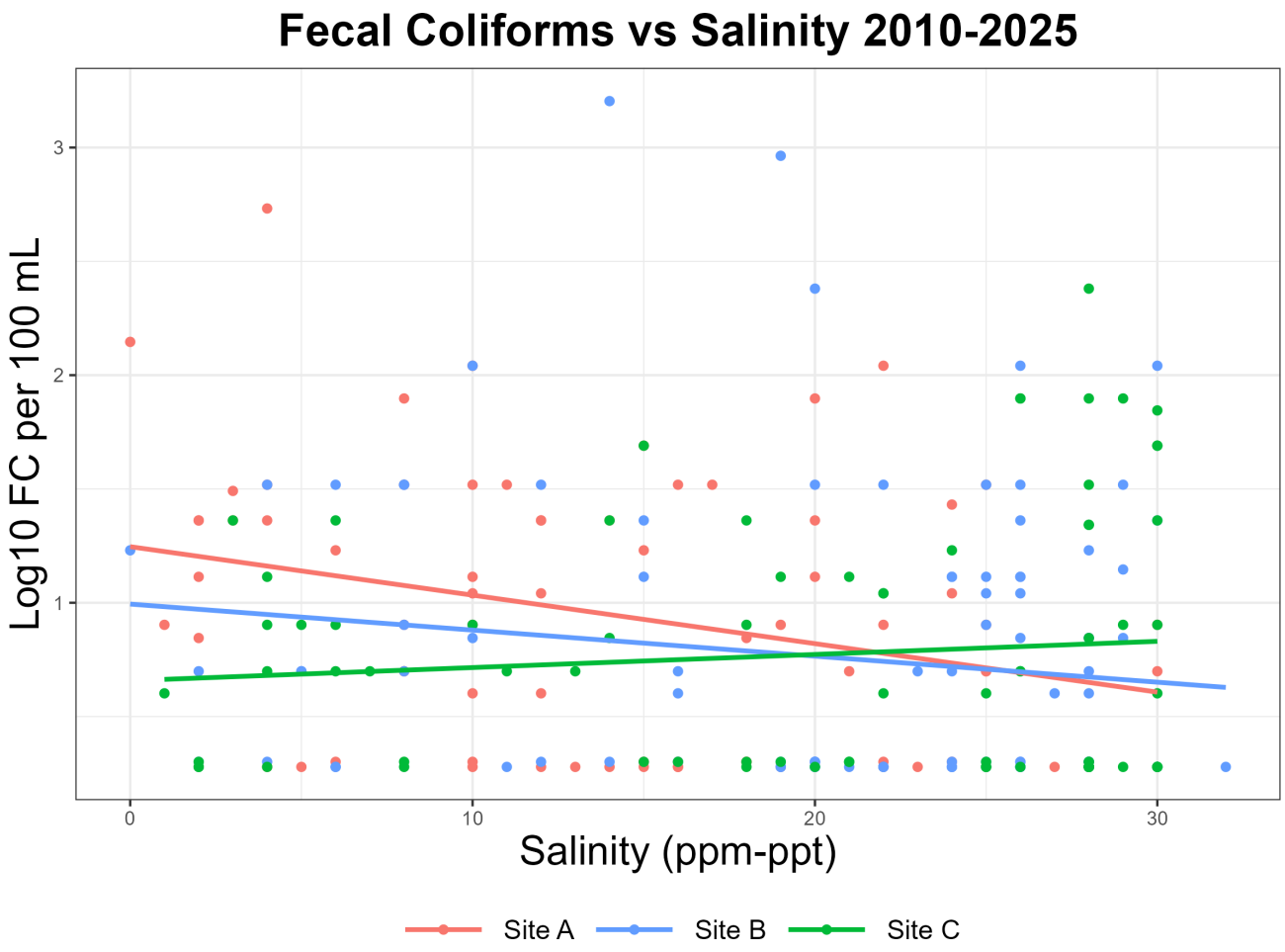


Using CSSP public datasets to investigate spatial and temporal trends in historical fecal coliform counts in our study areas

FC temporal variability

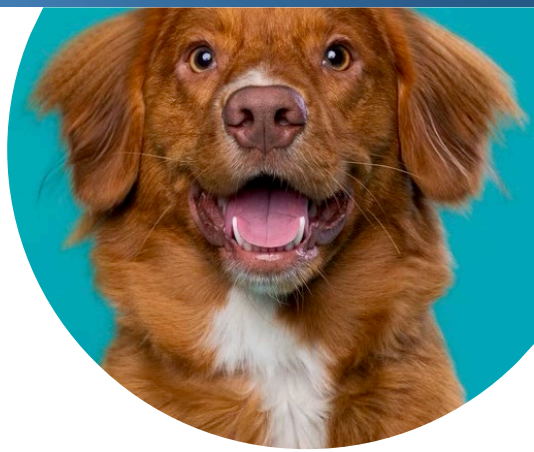


Environmental factors can affect FC



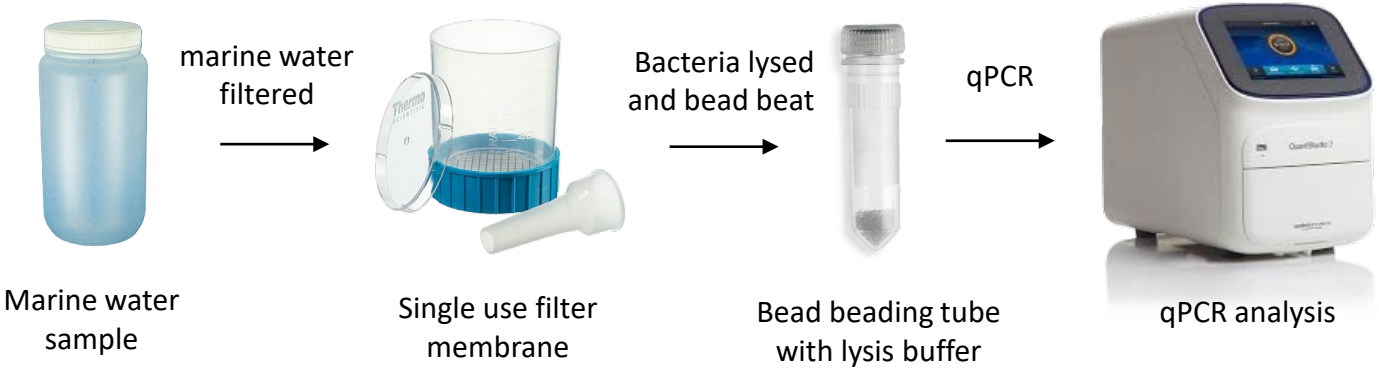
MST Methodology

1. General Bacteroides
   - Human and Animal
2. Human Bacteroides
3. Ruminant Bacteroides
   - Cattle, sheep, deer
4. Canine Bacteroides
5. Gull Fecal Marker

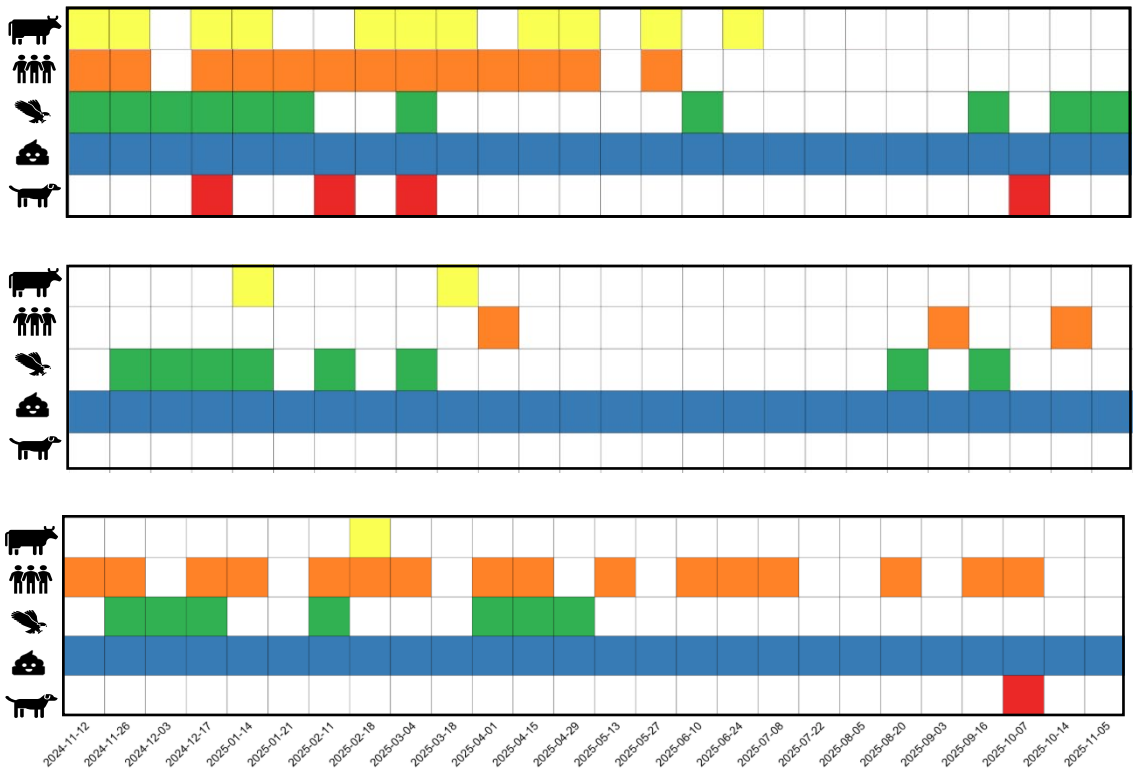


Bacterial MST Target workflow

- Collect marine water samples from partners
- Filter the marine water sample through a membrane to capture bacteria and DNA
- Bacteria is lysed and bead beat to break up bacteria and release DNA into the solution
- Perform qPCR, a laboratory technique that allows you to determine measure the amount of DNA in a solution



Preliminary results



General Bacteroides were detected in all collections at all sites

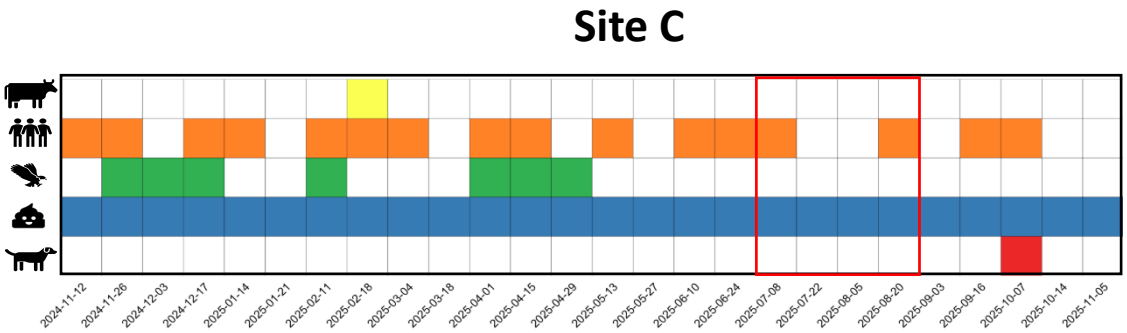
Site C had the highest abundance of Human Bacteroides

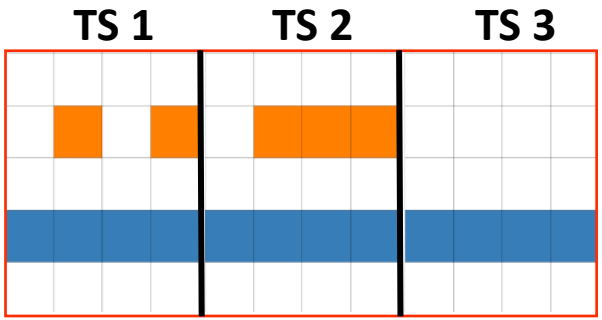
Gull feces was detected periodically at all sites

Ruminant fecal pollution was more prevalent at Site A

Canine fecal pollution was sporadically detected

Longitudinal and target sites



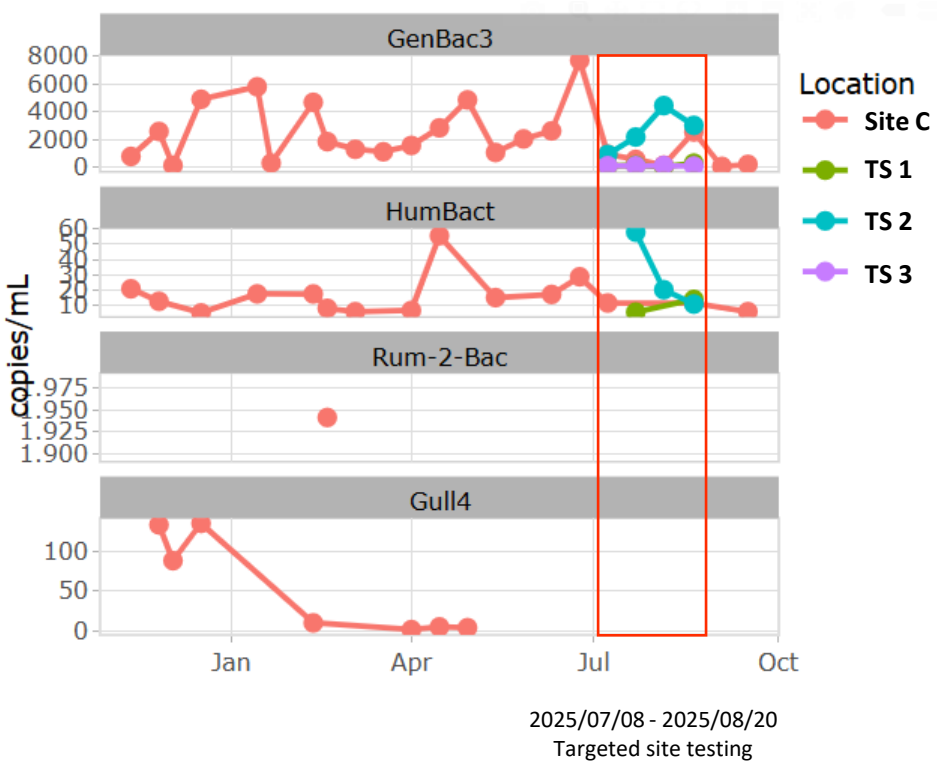


2025/07/08 - 2025/08/20
Targeted site testing

- General Bacteroides was still detected at all 3 targeted sites
- Human detection at TS 1 and 2, but not TS 3
- Gull detection earlier in the regular site, but no Gull detections at targeted sites

Longitudinal and target site trends

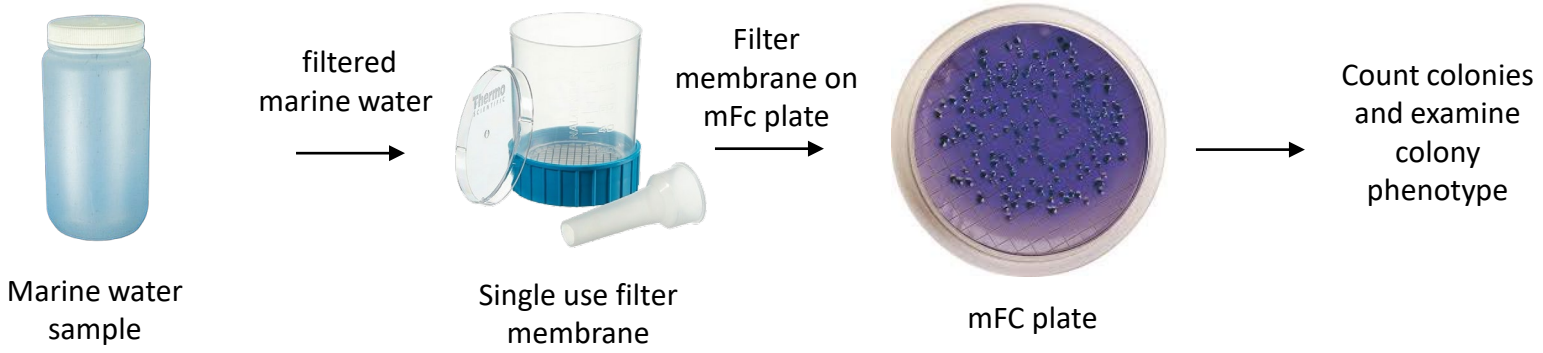
- TS 2 had the highest GenBact detection
- TS 2 also had the highest HumBact detection during this testing period.
- No HumBact detection at TS 3
- No other detections besides Human and GenBact at targeted sites



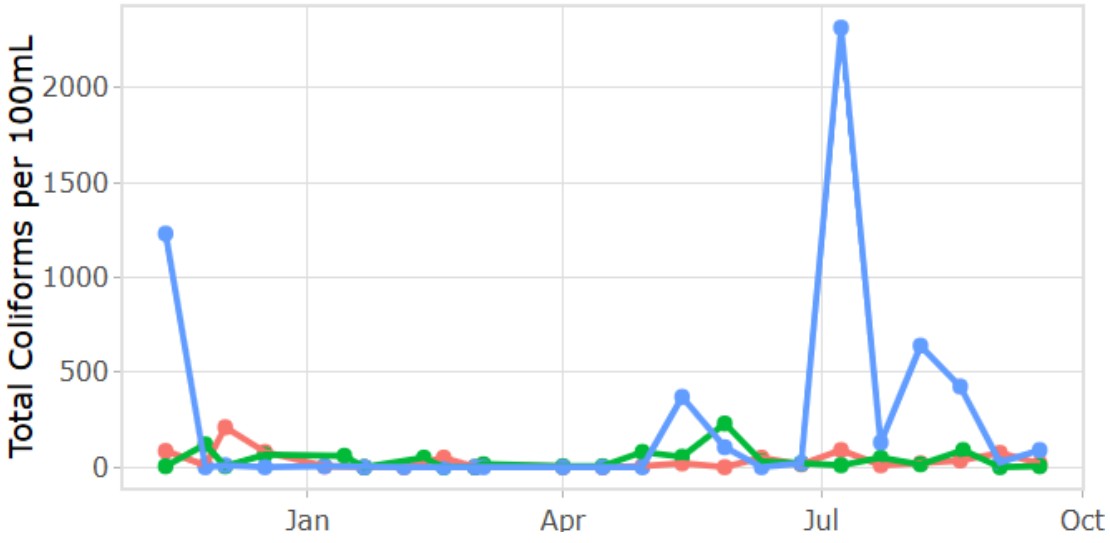
Fecal coliform counts

Utilizing Filtering and mFC plating Method

- Collect marine water samples from partners
- Filter the marine water sample to capture bacteria and DNA on membrane
- Filter membrane is then grown on mFC plates
- Incubate plates for 24 hours and count colonies



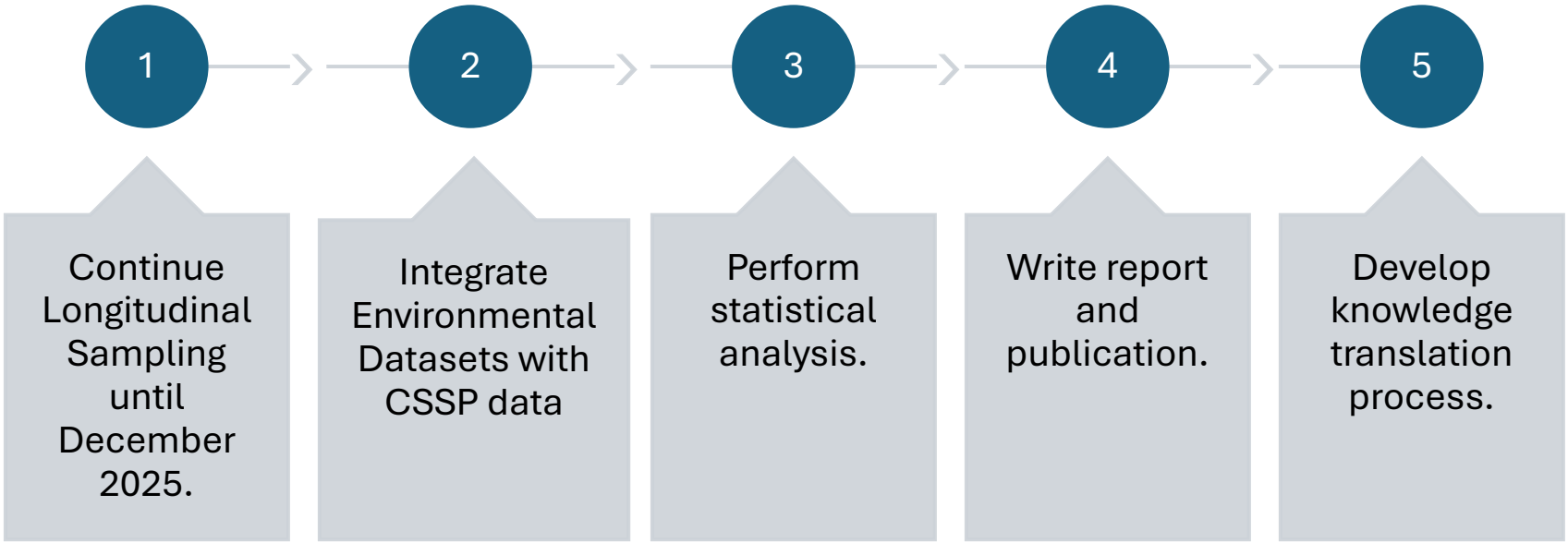
Total coliform counts



Fecal coliforms per 100 ml (2010-2022)				
	Count	Min	Mean	Max
Site A	60	1.9	29	540
Site B	81	1.9	44.5	1600
Site C	64	1.9	17	240

- Total Coliforms per 100mL for Site A, Site B and Site C
- Site B recently had the highest detection in Jul 2025
- Site C experienced increasing fecal coliform counts over May, but tapered off
- Historical CSSP data support our findings: total coliform levels at Site B are both higher and more variable than at other sites.

Next steps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2
3
4
5
Continue Longitudinal Sampling until December 2025.
Integrate Environmental Datasets with CSSP data
Perform statistical analysis.
Write report and publication.
Develop knowledge translation process.

Acknowledgements

- Genome BC
- BC Ministry of Health
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Questions