



*A Partnership to Restore and Protect the Sound*

**Watersheds and Embayments Work Group  
Long Island Sound Study**

**June 15, 2021 10:00am – 12:00pm**

website: <http://www.longislandsoundstudy.net>

**June 15, 2021 Meeting Minutes**

**Attendees:** Mark Parker, CTDEEP; EPA; Esther Nelson; Peter Linderoth, Save the Sound; Evelyn Powers, IEC; Chet Arnold, UCONN; Heather Johnson, FOB;; Jimena Viscasillas-Perez, NYSG; Judy Preston, CTSG; Kelly Streich, CTDEEP, Mark Tedesco, EPA; Richard Friesner, NEIWPC; Sarah Deonarine, MBPC; Susan Van Patten, NYSDEC; Victoria O'Neill, NYSDEC/NEIWPC; Jim Ammerman, LISS/NEIWPC; Cayla Sullivan, EPA; Nicole Tachiki, EPA; Alex Huddell, EPA; Stan Stephansen, EPA, Marybeth Hart; Mary C Arnold NYSDEC; Tony Leung, NYSDEC; Alyssa Carroll, NYSDEC; Chris Kephart, USGS; Shawn Fisher, USGS; Jon Morrison, USGS.

**Opening Remarks**

Mark Parker (CTDEEP) began the meeting by emphasizing the importance of microbial source tracking (MST) and thanking Esther Nelson (EPA) for helping him taking on the co-chair role for the work group until NYSDEC gets a replacement.

**Characterizing Fecal Contamination Sources Using Microbial Source Tracking**

Christopher Kephart of USGS OKI Water Science Center gave an overview on MST. Waterborne disease is a persistent public health concern. Across the US, pathogens are the most common cause for beneficial use impairment in rivers and streams. Traditional measures of assessing fecal contamination have relied on fecal indicator bacteria, doing a good job of assessing spatial, magnitudes, and temporal trends, but are not source specific. MST plays on the concept that the intestinal microbes of animal groups are different and can lead to unique host-associated genetic sequences or markers, quantified by techniques such as qPCR. Limitations include that the markers are not identifying specific animals; each marker is strongly associated with, but not exclusive to, the source intended - most have some degree of nonspecificity. Also, concentrations of markers cannot be directly compared to one another. Each MST marker is a unique assay, thus concentrations of the various markers cannot be directly compared to one another. It is most effective when used as one tool in a tiered approach. (Presentation attached).

**Assessment of Fecal Contamination Sources Using Microbial Source Tracking in Long Island Sound**

Shawn Fisher (USGS) shared progress on USGS work with MST, trying to get a better understanding of the source of fecal contamination in LIS. Fecal contamination is pervasive across LIS and upstate NY. Routine sampling has resulted in year-round closings

in shellfishing areas in Long Island embayments. A primary reason for the project was to help better inform potential updates to TMDLs. USGS worked with New York State Department of Environmental Conservation (NYSDEC) to investigate factors affecting pathogen loads. Objectives were to identify the sources of host contribution using MST. Another objective was to understand sources of fecal contamination to each embayment in summer and winter seasons, in both wet and dry conditions. Stable isotopes were utilized to characterize nitrogen sources and transport mechanisms, mainly for groundwater contributions. Hempstead Harbor was presented as an example. There were 8 source sites throughout the harbor. There was no sustainable difference in coliphage among variables. Human and canine markers were detected in roughly half of the samples. Waterfowl marker was most prevalent in the winter. Groundwater results were negative for all fecal indicator bacteria (FIB). Bed sediment may be a potential source of FIBs and MST markers. Resuspension occurs during tidal shifts, storms, and boat activity. Sediment sample collected in South Hempstead Harbor positive for waterfowl marker; negative for coliphage; high fecal coliform and *E. coli* concentrations. Sediment sample collected at the culvert at Glenwood Road was positive for human, waterfowl, and canine markers; positive for coliphage; high fecal coliform and *E. coli* concentrations. Continuous inputs of human markers and fecal coliform to Hempstead Harbor during dry weather were identified. Stormwater is an important conveyance. Note study had small sample size; additional information is needed to better understand sources of fecal contamination to each embayment in summer and winter seasons, during both wet and dry conditions. More information on relative contributions of biological hosts and transport mechanisms would further improve efforts to set effective reduction measures. All data available on National Water Information System (NWIS) Web Interface page (USGS Water Quality Samples for USA: Sample Data). Presentation attached.

#### **Crescent Beach, Glen Cove, Long Island, NY**

Tony Leung and Alyssa Carroll from NYSDEC shared their work on a case regarding a closed public swimming beach due to elevated bacteria levels. The beach has been closed for 12 years. Groundwater does not appear to be contributing to the contamination. Concern was that discharges from the residences were contributing to the bacteria levels. There could be onsite system failures. Sampling was performed in both wet and dry weather and analyzed for *E. Coli* and Fecal Coliform, dye tests were done to conform sanitary systems and stormwater drainage. MST Sampling was done in Summer 2018 & 2019. During the investigation, they did not see as high concentrations as the previous study. Human related fecal coliform was not detected, and low levels of general avian and dog markers were detected. The City of Glen Cove is working with an engineering firm on possible remediation. An engineering report was completed July 2020 recommending the installation of Helix high-flow stormwater filters, conduct ecological restoration, and perform beach management. Interacting with the stakeholders was big challenge; had to find ways to satisfy all parties without compromising the integrity of the investigation. (Presentation attached).

### **Assessment of fecal contamination sources to Alley Creek: Queens County, NY**

Shawn Fisher of USGS, cooperating with New York City Department of Environmental Protection (NYCDEP). NYCDEP wanted to determine the extent of bacterial contamination that was related to humans. Alley Creek receives stormwater runoff and untreated sewage from CSOs and is designated as impaired – 303(d) listed for pathogens by NYSDEC. NYCDEP has been operating under a consent order to reduce CSO contributions and repair infrastructure. Source data was needed to ensure bacteria contributions and assess any decrease in human influences following infrastructure upgrades and repairs. USGS worked with NYCDEP to address components of their Long-Term Control Plan. They identified the relative host contribution of fecal contamination using MST (*Bacteroides* and *Helicobacter*) and chemical analyses in contributing waters to Alley Creek. 8 samples were collected. Fecal contamination sources to Alley Creek were evaluated seasonally, and spatially during both wet and dry conditions, and based on tidal influence. Many sites were high for bacteria, likely related to sewage infrastructure. Pharmaceuticals, sediment FIB and total suspended solids (TSS) were also tested. Bacteria levels at Oakland lake were a bit lower, even with roughly the same TSS contribution. Low tide TSS concentrations were higher at TI-025, the water is more turbid. TI-024 and TI-008 are exposed to sewage at a higher level compared to the other sites. Human markers were low at Oakland lake, most markers were waterfowl markers. Bed sediment revealed human markers for all TI locations. Waterfowl marker was only found at the TI-025 site. TI-007 did not have human markers, it was across from the CSO, but not in its path. Data are available on USGS National Water Information System: Web Interface page (USGS Water Quality Samples for USA: Sample Data). Presentation attached.

### **Microbiological studies of the Bronx and Harlem Rivers – Urban Waters Federal Partnership**

Shawn Fisher USGS, cooperating with the Department of the Interior and USGS NY Water Science Center. This was a coordinated effort between USGS, EPA, NYC, IEC, and Bronx River Alliance. Objective to provide information on likely sources of elevated fecal indicator bacteria observed along the river. Locations with proximity to CSOs were assessed for Fecal Indicator Bacteria and MST markers; temperature, salinity, pH, dissolved oxygen, turbidity, fDOM, and TSS. Assessed the variability in fecal contamination and affects of discharge points along a river with an urbanization gradient. In the Harlem River & Bronx hydrodynamics, boat traffic and water temperature were potential causes for inconsistent bacteria levels. Both rivers underwent transects and microbiological assessment, and shorelines were sampled as well. Currently, they are undergoing continuous water monitoring and sediment resuspension monitoring. In 2017, MST transects were done across five locations. In the Harlem River, bacterial contamination (human and canine) was consistent, with higher concentrations of FIB were found along the shorelines, particularly after boat traffic. At the floating dock there was not much of a change likely due to depth. A continuous water quality monitoring project was set up in Roberto Clemente State Park and Mill Pond Park in 2021. In the Bronx river, at the 6 tested locations, MST markers were high throughout for human and canine. Later in the season there were higher concentration of waterfowl marker. This

information will be used to supplement new management and bacterial monitoring plans in both rivers. (Presentation attached).

### Questions & Comments

- Tony Leung: MST analytical work was done by EPA Region 2 for our Crescent Beach; he thanked EPA. Funding is an issue for MST.
- Shawn Fisher: Sediment resuspension issues should not be underestimated and other environmental indicators should be looked at in conjunction when doing MST.
- Stan Stephansen: TMDLs: The science is not there to calculate loadings from the MST results, are you using those in revised TMDLs?
  - Shawn Fisher: No we are not. They are not actually using the numbers, but the concentration of the markers and their locations, to inform the numbers for the TMDLs.

### Chat Comments

Sarah Deonarine: On MST Study Design: we have a location with a high bacteria concentration and we don't know if it is from failing cesspools or from waterfowl; if we were to use MST to attempt to figure out the culprit, it sounds like we'd have to use a site with lower bacteria concentrations? Or would we still not really be able to get at what the issue is?

Fisher, Shawn C:

Hi Sarah, for the dry v wet weather, we went with DEC considerations for their own designations: >0 ; >0.25" wet within the past 3 days prior to the day of sampling. NYSDEC Division of Marine Resources have been using as guidance (not official by DEC).

Kephart, Chris: Sarah, it seems MST could help w/ cesspools v. waterfowl, we can discuss further after meeting, if you would like. As for needing a site w/ lower bacteria... generally, higher FIB concentrations are better for MST application (more likely to get detections/quantities of the relevant MST markers - more data to work with!).

Peter Linderoth: Shawn, or someone else, could you please elaborate a bit more on the high amplification (of the human marker) near STP effluent outfalls. I get the presence in the tests; more specifically, is there a general baseline that can be used based on GPD? For example, consider a narrow portion of an embayment that has numerous potential illicit discharges, an STP effluent outfall meeting its FIB permit, and high hits for *Entero* fairly consistently. Meeting the FIB requirements in its NPDES permit

Tony/Alyssa - Can you share more on how you managed expectations from various stakeholders. Any suggestions to others who are starting an MST project?

Chris/Shawn/Alyssa, can you talk to uncertainty and limitations which may inform future planned sampling effort. e.g., frequency of sampling, number of samples, number of samples frozen for potential future analysis?

Kephart, Chris: Hi Peter, although I can't speak as well to the specific sites and scenario you are describing as Shawn can, I can say... qPCR for MST markers does not discriminate between genetic sequences from live or dead microorganisms. Thus, a portion of MST markers may originate from non-viable fecal bacteria or even free DNA in the water column – esp. downstream from WWTP effluent e.g. ... Not sure if this helps.

Peter Linderoth: It does help and I follow that logic. I am curious if anyone has developed a sort of baseline for the dead microorganisms near an WWTP outfall based on the gallons per day in the permit. I get flows change, so talking in general.

Kephart, Chris: That's a great question. I have not come across that being investigated, but I think it's worth another look through the literature. Would be useful supporting data, even if general, for when this situation comes up.

Tony Leung, NYS DEC: We set the table at the initial meeting with all involved that we should remain open minded and let the science, *i.e.*, the results of our dye test, fecal tests as well as MST results speak to the source of contamination. Results were shared as they are finalized with all. And in the end, everyone was on board except one individual. Nassau County Dept. of Health and EPA was great in sharing the info and supporting our conclusion.

Carroll, Alyssa D (DEC): To add to Tony's response. As mentioned, the City requested to have their inspector on-site and he had a lot of suggestions that we explored. We included additional sampling locations (as requested) to ensure the stakeholders we were thorough in our investigation. We tried to make our relay of results as comprehensive as possible using maps and tables of results. NCDOH was helpful in interpreting some of the data to the stakeholders.

Kephart, Chris: .... there are no magic numbers in terms of frequency and total n at each site/overall. Each study is going to be different in terms of the setting complexity, the magnitude of the fecal contamination (which will influence number of detections vs. nondetects of MST markers) and the questions that investigators hope to answer. If you have a particular potential study to discuss, we can talk after meeting to get more into this. If just for discussion topic, of course funding is going to drive sampling scope in addition to the factors already mentioned.

EPA: Anything you would like to add?

What is needed to have microbial source tracking efforts result in identifying and remediating specific microbial sources? Are complementary data or parallel management

approaches needed? How has MST influenced our understanding of human versus wildlife contributions?

Please suggest topics for workgroup to consider.

**Next Meeting:** Wednesday, August 18<sup>th</sup> from 10-12pm

Thanks for a productive meeting. Have a great day and stay safe!

**Related Resources:**

LI embayments (NYS DEC): <https://www.usgs.gov/centers/ny-water/science/using-microbial-source-tracking-identify-pollution-sources-pathogen>

UWFP (NYS DEC, NYC DEP/Parks): <https://www.usgs.gov/centers/ny-water/science/urban-waters-initiative-bronx-harlem-rivers>

Alley Creek (NYC DEP): <https://www.usgs.gov/centers/ny-water/science/assessment-fecal-contamination-sources-alley-creek-queens-county-new-york>

USGS: Using Microbial Source Tracking To Identify Fecal Contamination Sources in an Embayment in Hempstead Harbor on Long Island, New York:  
<https://doi.org/10.3133/sir20215042>