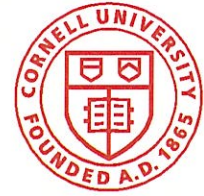


Cornell Cooperative Extension
Suffolk County



FINAL REPORT
Cold Spring Harbor Watershed

**Initial Characterization and Management
of Pathogens Affecting Sanitary Condition of Shellfish Lands
(Spring Street, Laurel Hollow,
and Cold Spring Brook Subwatersheds)**

Phase II – Microbial Source Tracking

Prepared for

Nassau County Soil and Water Conservation District
&
Oyster Bay - Cold Spring Harbor Protection Committee

Submitted by:
Cornell Cooperative Extension of Suffolk County
423 Griffing Avenue, Suite 100
Riverhead, NY 11901-3071

Contact:
Carolyn Sukowski, Water Quality Program Coordinator
E-mail: cs424@cornell.edu
Phone: 631-239-1800 ex.6

PURPOSE

Surface water impairment by fecal coliform bacteria is a water quality issue of national scope and importance. Cold Spring Harbor currently has a year-round shellfish land closure for the area including tributaries south and east of a line extending southerly from the seaward end of the dock serving the Cold Spring Harbor Beach Club to the western extremity of the 'Gale House' located on the shoreline immediately west of Cold Spring Beach, on the campus of Cold Spring Harbor Laboratory. Additionally, the area including tributaries south and east of a line extending westerly from the seaward end of the dock serving the Cold Spring Harbor Beach Club to the flag pole situated near the village hall of the Village of Laurel Hollow is closed to shellfishing seasonally.

The purpose of this project is to characterize and manage fecal coliform contamination in the Cold Spring Harbor Watershed as a first step towards identifying and reducing the sources of bacterial contamination that are causing shellfish closures in southern Cold Spring Harbor with the ultimate goal of opening these shellfish lands. The Oyster Bay – Cold Spring Harbor Protection Committee (OBCSHPC) has committed to pursuing this effort in the Spring Street subwatershed which lies within the Town of Huntington boundary. The Nassau County Soil and Water Conservation District (NCSWCD) has additionally committed to pursuing this effort in the Laurel Hollow and Cold Spring Brook Subwatersheds. This project aligns with the recommended actions identified in the Friends of the Bay Watershed Action Plan and Phase I involved identifying preliminary fecal coliform loads during dry weather and storm events for three significant subwatersheds to Cold Spring Harbor in 2020. Phase II was completed in 2021 and involved processing a prioritized selection of twenty (20) of the preserved dry and wet samples collected in 2020 for microbial source tracking (MST). Additionally, a review of existing fecal coliform data as it compares to the U.S. Food and Drug Administration's National Shellfish Sanitary Program has been conducted incorporating the most up-to-date data collected in 2020 in order to demonstrate current trends.

FINDINGS

TASK I (NCSWCD): Review of Existing Water Quality Data

Existing fecal coliform data from inner Cold Spring Harbor has been compiled and analyzed as it relates to the U.S. Food and Drug Administration's National Shellfish Sanitary Program recommendations. Data review included New York State Department of Environmental Conservation (NYS DEC) Division of Marine Resources Shellfish Harvest Area Classification Unit Report on Cold Spring Harbor Shellfish Growing Area #48 (Triennial Evaluation 2021 (2020 Data), Annual Evaluation 2020 and 2019) as well as data collected by Friends of the Bay (FOB).

Ambient Water Quality Monitoring (FOB, NYS DEC)

A review of ambient water quality monitoring data was conducted in order to highlight most recent conditions. The analysis provided below presents the most recent data available including NYS DEC data from 2009 through 2020 as well as data provided by Friends of the Bay (FOB) from 2011 through 2019.

The NYS DEC conducts an annual sanitary survey and evaluation of Cold Spring Harbor Shellfish Growing Area #48. Systematic random sampling is conducted throughout the growing area. This field sampling and data analysis design presumes that if intermittent, unfavorable changes in water quality occur, they will be revealed in the bacteriological sampling results. These unfavorable sampling results will then contribute to the variation of the data set. Data sets displaying greater levels of variation will consequently exhibit an elevated estimated 90th percentile. The estimated 90th percentile serves as the statistic to measure the variance of a data set. This statistic, along with the geometric mean, is used when evaluating each sampling station for compliance with the National Shellfish Sanitation Program (NSSP) growing area criteria. For fecal coliform, a geometric mean threshold of 14 MPN/100mL and a 90th percentile of 49 MPN/100mL are used as standards to determine an area as approved.

The approved, or 'open', classification for a growing area requires that the sanitary survey has determined that there are no unacceptable concentrations of fecal material, pathogenic microorganisms, or poisonous and deleterious substances. There are no NSSP limitations on the harvest of shellstock from growing areas placed in this classification.

The conditional, or 'seasonal', classifications are designed to address growing areas that are subject to intermittent microbiological pollution. This classification applies

when during certain times of the year or under certain conditions, the shellstock from the growing area may be safely harvested. For example, during periods of low runoff and/or cooler temperatures, these areas may be below thresholds.

The restricted, prohibited, or 'uncertified/closed' area classifications are designed to address growing areas that do not meet approved area criteria and which may be subject to administrative closures such as areas in proximity to waste water treatment plant outfalls. This classification is commonly used for areas affected by non-point pollution from either urban or rural sources that cause the water quality to fluctuate unpredictably or of sufficient frequency that a conditionally approved area is not feasible.

The following map includes NYS DEC and Friends of the Bay (FOB) data going back enough full years to be able to highlight the geomeans and 90th percentiles for at least 30 data points. The extent of the map focuses on inner-Cold Spring Harbor stations only, specifically out to NYS DEC station 48-8 located off of Jennings Beach. One NYS DEC monitoring station, 48-24, was only recently added in December of 2019 so there are only 8 data points. NYS DEC stations located in the year-round closed area (48-11, 48-13, 48-13.1, 48-14, and 48-15) have been marked by NYS DEC as 'inactive' and were not monitored in 2020 nor included in the State's most recent Triennial Evaluation 2021. Additionally, as of 2020 NYSDEC has ceased sampling stations within the seasonally closed areas during closed periods. However, data was collected at these stations in 2019 and prior and is included in our analyses.

Figure 1 represents a seasonally closed (5/1-10/15) NYS DEC and FOB data summary going back to 2010 for NYS DEC data and 2017 for FOB data. This seasonal closed analysis includes the most recent year of data available (2020) whereas the State's most recent Triennial Evaluation 2021 leaves 2019 and 2020 data out for the closed areas as these stations have been marked as inactive. With the inclusion of the most recent year of data (2020), when compared to the NYS DEC Triennial Evaluation, there is still no improvement seen in these stations. All NYS DEC stations and FOB stations, FB-1 and FB-2, in areas closed year-round are failing both the geomean and 90th percentile standards for this period. Seasonal stations, including FOB station FB-3, are also failing both the geomean and 90th percentile standards for this period.

It should be noted that in the 2020 NYS DEC Annual Evaluation, which uses station data from 5/1-10/31 despite the closed period being from 5/1-10/15, station 48-10 is identified as approaching threshold values with a geomean of 8.8 MPN/100mL and 90th percentile of 42.8 MPN/100mL (N=31). As of the NYS DEC Triennial Evaluation

2021, which includes 2020 data, station 48-10 has a geomean of 7.9 MPN/100mL and 90th percentile of 36.1 MPN/100mL (N=36). Our review, which includes data from the seasonally closed window of 5/1-10/15 produced a geomean of 8.6 MPN/100mL and 90th percentile of 40.1 MPN/100mL (N=35). The difference is not significant, but is worth mentioning considering the importance of this year-round open station. This additional analysis of this station was considered as it is the year-round open station closest to the seasonally closed area and therefore could be used to consider potential future extensions of closed areas. As of the NYS DEC Triennial Evaluation 2021, the seasonally closed area has been proposed for extension beyond station 48-10. The changes are effective 11/22/2021 and are expected to be published in the Dec. 8, 2021, edition of the New York State Register. This proposed extension is due to poor water quality being detected at the newly added station 48-24 located on the existing seasonal closure line which showed a geomean of 14.7 MPN/100mL and a 90th percentile of 216.7 MPN/100mL (N=4) in our analysis and a geomean of 14.7 MPN/100mL and a 90th percentile of 151.7 MPN/100mL (N=5) in the NYS DEC Triennial Evaluation 2021.

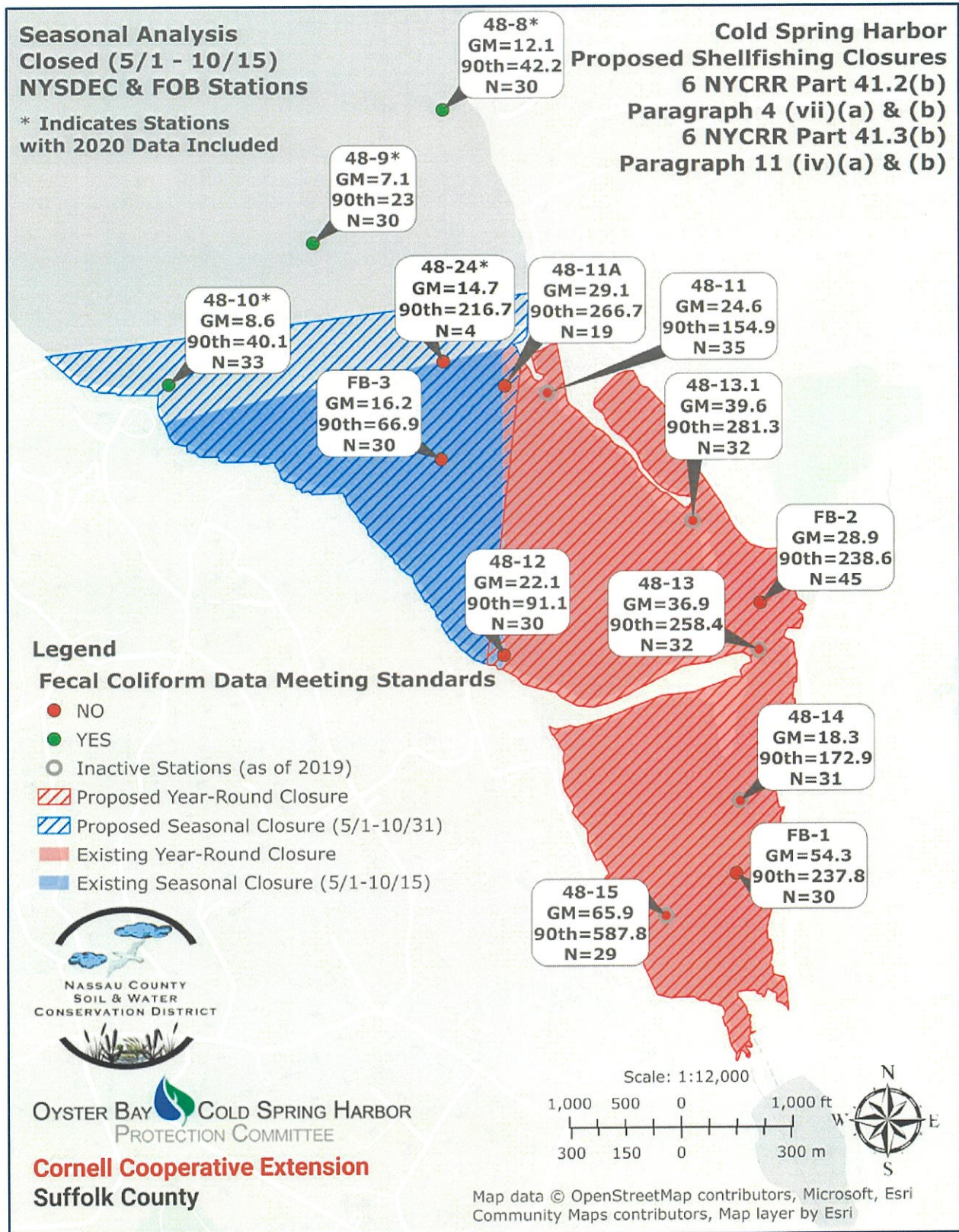


Figure 1. Seasonally Closed Period (5/1–10/15) Analysis: NYSDEC & FOB Fecal Coliform Data in Inner Cold Spring Harbor

TASK II (OBCSHPC & NCSWCD): Microbial Source Tracking (MST) of Preserved Samples Collected from the Major Subwatershed Catchment Areas Prioritized by Fecal Coliform Contribution During Baseflow and Storm Events

Fecal coliform and hydrological data were used to rank tributary contributions of fecal coliform to Cold Spring Harbor in Phase I of this project conducted in 2020. The Cold Spring Harbor Watershed has three major subwatersheds contributing to the impaired segments of Cold Spring Harbor. The Spring Street, Laurel Hollow, and Cold Spring Brook subwatersheds were sampled at significant branches for fecal coliform concentrations. The Spring Street, Laurel Hollow, and Cold Spring Brook subwatersheds, which align with Friends of the Bay's Watershed Action Plan, will be included in this study and can be seen in *Figure 2*. Sampling was conducted during four (4) distinct baseflow events (72 hours of no rainfall) and during four (4) distinct storm events from August through September 2020. CCE sampling procedure involves preservation of all samples for potential future microbial source tracking (MST). CCE in partnership with the OBCSHPC have reviewed the results of the sampling conducted for the purpose of selecting certain samples for potential microbial source tracking (MST). As part of the second phase of the project, a selection of twenty (20) samples collected during dry weather events and wet weather events and subsequently preserved were processed for (MST) based on fecal coliform enumeration results. Selected samples were processed for presence of 3 different potential pathogen sources (human, canine (dogs), Canada goose). It should be noted that while MST is a powerful tool that may lead to actionable results and guide stormwater management, samples are being collected as a snapshot in time. These snapshot samples may not be wholly representative of sources of pathogens being discharged from the system. Data will allow for identification of problem areas and aid in future management planning. This task aligns with the following recommended actions in the Friends of the Bay Watershed Action Plan under section 3.2-Water Quality: Objective 1: Improve Understanding of Estuary and Watershed Conditions; Action 1-2: Continue and Expand Stream and Outfall Monitoring Program

Catchment areas were delineated for each of these significant branches within each subwatershed and can be seen in *Figure 2* along with sampling stations. Flow estimates and fecal coliform enumeration results were used to evaluate fecal coliform loading for each sampling station located in the study watersheds. Catchment areas were delineated in Esri ArcGIS Pro desktop software for each of the 11 sampling stations included in the study using the USGS National Hydrography Dataset High Resolution data.

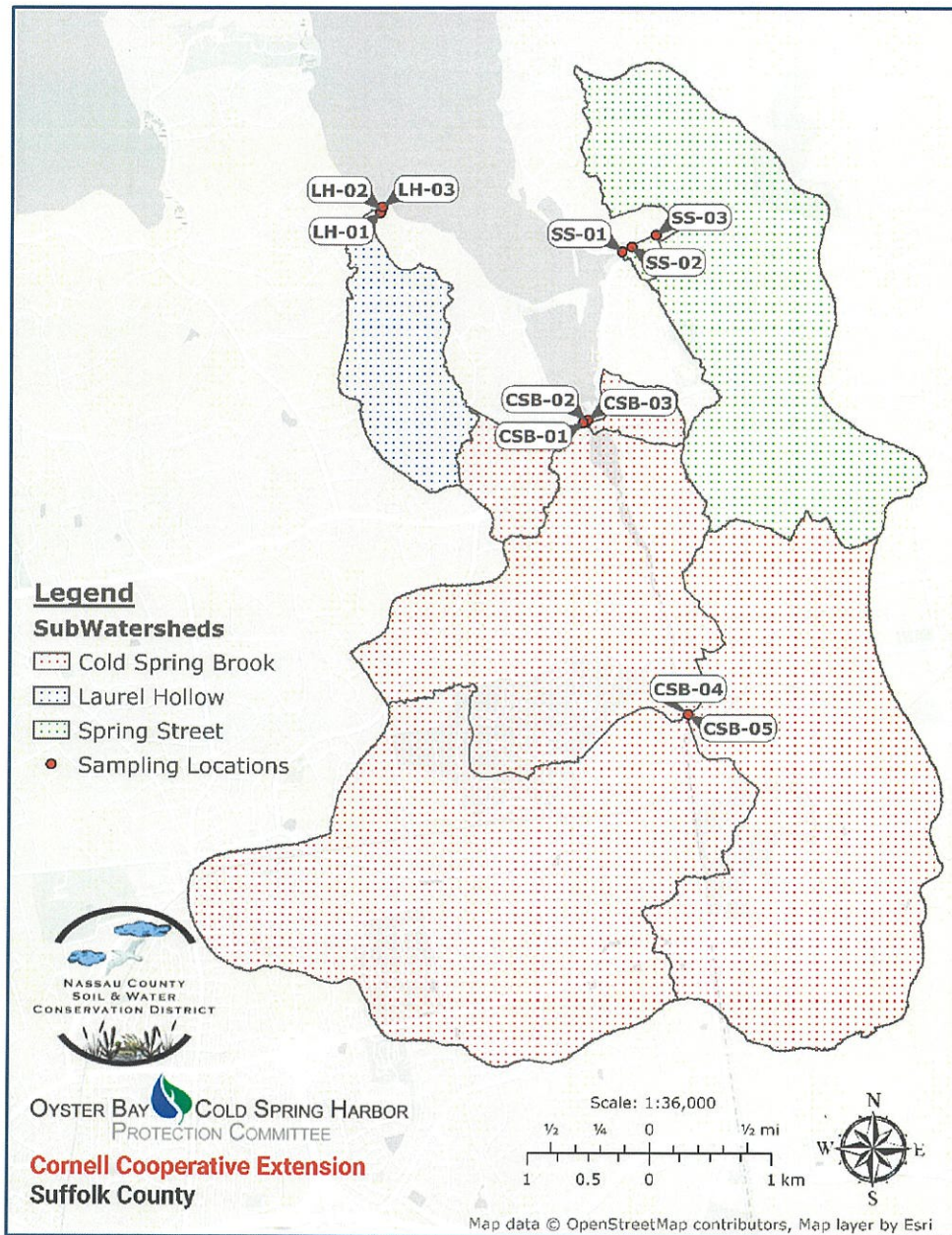


Figure 2. Catchment areas for each of the significant branches within the major subwatersheds of Cold Spring Harbor and Sampling Locations.

Baseflow events occurred on 8/10/20, 8/24/20, 8/26/20, and 9/21/20. Fecal coliform enumeration for baseflow events ranged from <1 MPN/100mL to 1,842 MPN/100mL with a mean fecal coliform enumeration of 215.5 MPN/100mL. Wet weather events occurred on 8/19/20, 8/29/20, 9/01/20, 9/10/20, and 9/30/20. Fecal coliform enumeration for wet events ranged from <100 MPN/100mL to 435,200 MPN/100mL with a mean fecal coliform enumeration of 23,206 MPN/100mL.

Microbial Source Tracking (MST) Results and Station Classifications

Microbes from stormwater samples can be traced back to specific sources using microbial source tracking (MST) techniques to determine if the discharge originated from humans or a particular animal group. Samples were processed by Source Molecular to determine whether or not microbes present in the sample originated from human (e.g., failed septic system) or non-human sources. The non-human sources selected for testing were Canada goose and canine (dog).

Twenty (20) preserved samples from five (5) different stations (CSB-01, CSB-02, CSB-03, LH-02, SS-01) were processed for MST. MST detections for human, canine, and goose biomarkers is indicated in the data table in Appendix A along with fecal coliform enumeration for each sample. 'ND' indicates not detected, 'DNQ' indicates detected but not quantified due to quantities below the limit of quantification, and detected results are indicated by a number that represents a relative quantification.

Stations were classified according to methods described in Tagliaferri et. al (2021) to aid resource managers with potential remediation efforts (Table 1). Class 1 sites have the highest levels of contamination and class 5 sites have the least. This prioritization considers concentrations of fecal coliform above 49 most probable number per 100 milliliters (MPN/100 mL), dry weather discharges, and influences of human sewage and canine waste.

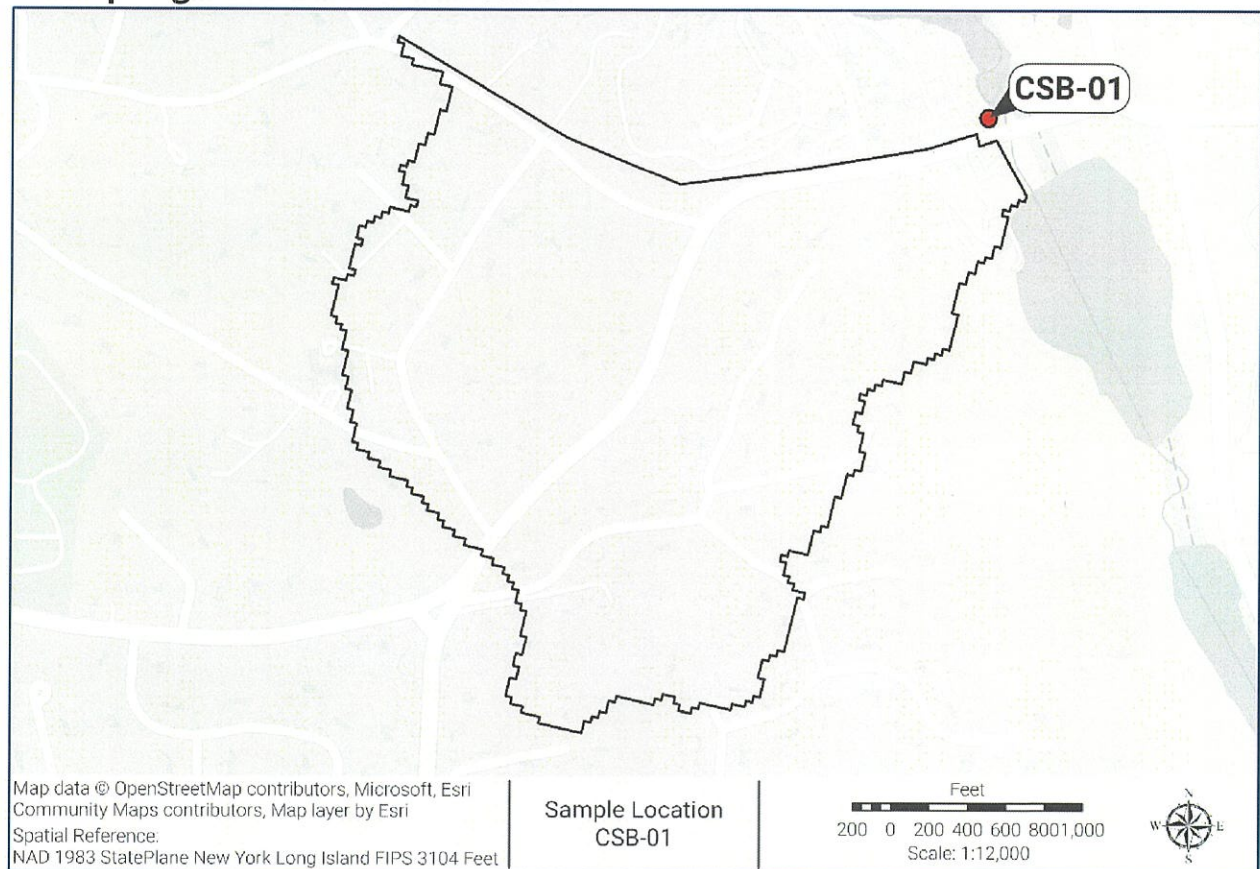
Table 1. Sample results for fecal coliform and microbial source tracking markers by source site type at Cold Spring Harbor on Long Island, New York.

Site Name	Site Type	Number of Samples	Fecal coliform (MPN/100 mL)				Elevated fecal coliform during dry-weather discharge	Sewage affected (HF183)	Canine affected (BacCan)	Class ¹
			Median	25th percentile	75th percentile	Mean				
CSB-01	Channel	8	86	39	548	744	Yes	No	Yes	2
CSB-02	Channel	8	100	39	352	410	Yes	No	Yes	2
CSB-03	Channel	8	280	193	3155	56027	Yes	Yes	Yes	1
LH-02	STS	8	1575	126	3532	7162	Yes	No	Yes	2
SS-01	Outfall	8	5807	208	15670	12797	Yes	Yes	Yes	1

¹Class is rated from 1 to 5, with 1 being the most contaminated and 5 being the least as described in Tagliaferri et. al. (2021)

A summary of each of the 5 stations which are recommended to be prioritized for future retrofits is provided below:

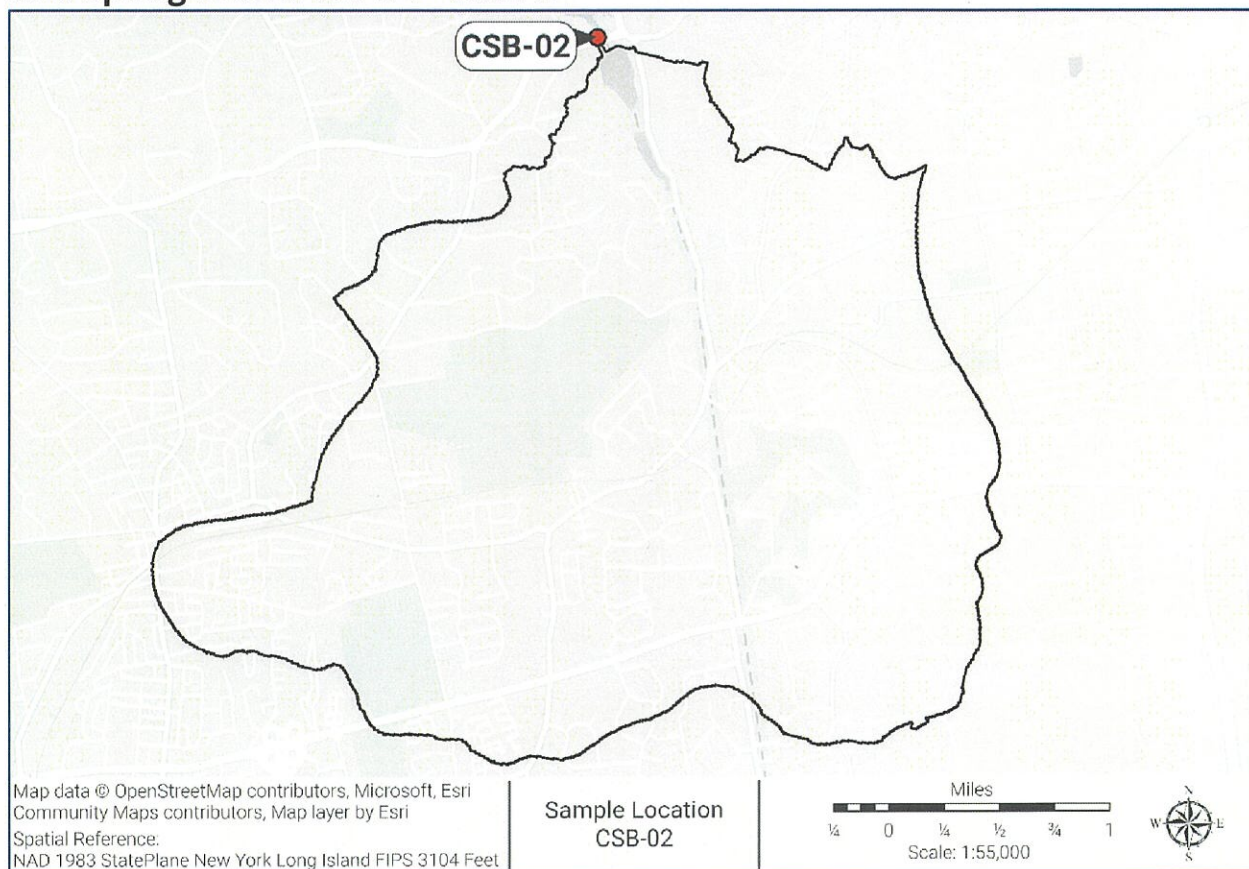
Cold Spring Brook: CSB-01 – Class 2



CSB-01 discharges to the head of Cold Spring Harbor under State Road 25A from the west. The catchment area is about 150 acres and encompasses predominantly low-density residential areas along the 25A corridor. Fecal coliform enumeration for baseflow events ranged from 31 MPN/100mL to 72 MPN/100mL with a mean fecal coliform enumeration of 43.75 MPN/100mL. Fecal coliform enumeration for wet events ranged from 100 MPN/100mL to 3,690 MPN/100mL with a mean fecal coliform enumeration of 1,445 MPN/100mL.

There were four (4) samples processed for MST at CSB-01. One each on 8/24/2020 (dry), 9/21/2020 (dry), 9/10/2020 (wet) and 9/30/2020 (wet). The detections of Human and Canine biomarkers both occurred during wet weather events on 9/10/2020 (0.92in) and 9/30/2020 (0.89in) respectively. Human biomarker detection was not quantifiable. Dog biomarker was detected at 324 copies/100mL. Goose biomarker was not detected in any of the samples.

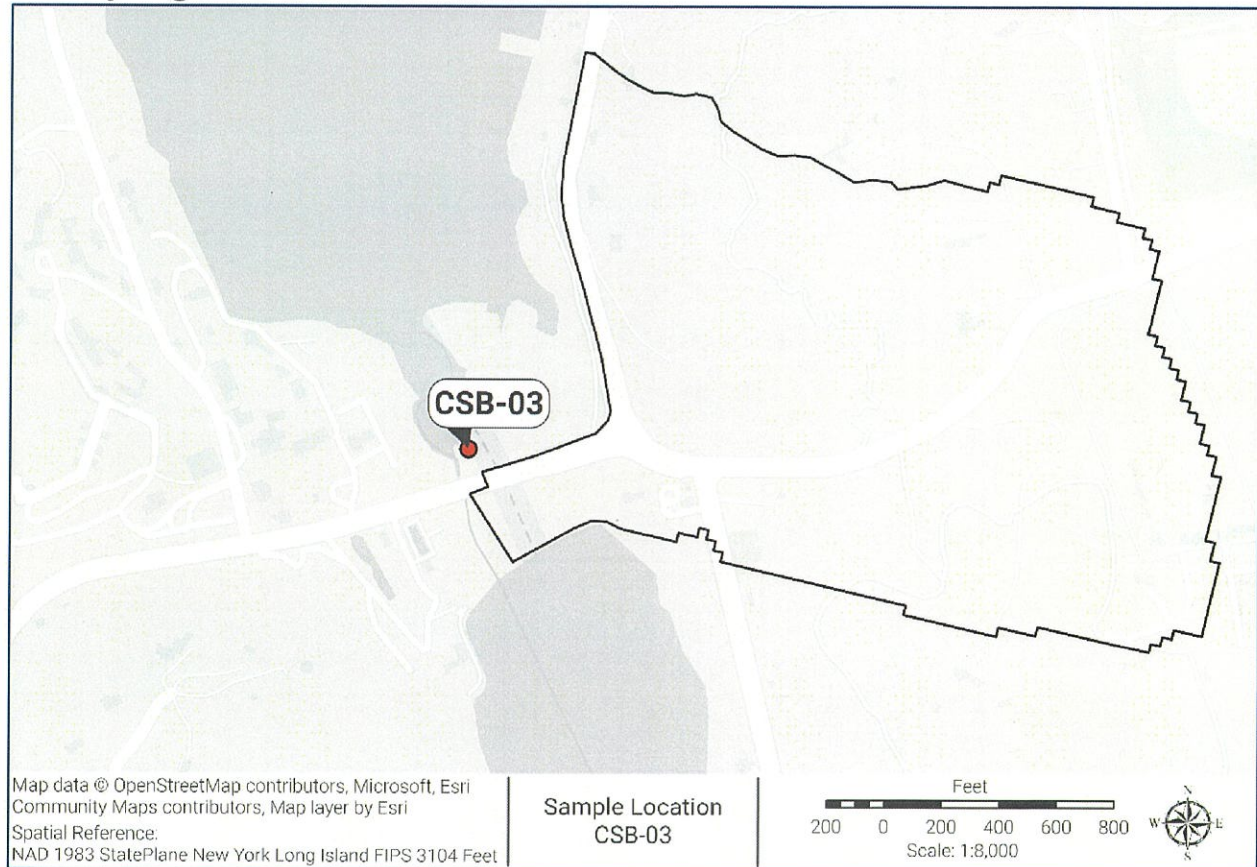
Cold Spring Brook: CSB-02 – Class 2



CSB-02 discharges to the head of Cold Spring Harbor under State Road 25A from the south. The catchment area is about 5,000 acres and encompasses large areas of natural undeveloped land as well as residential areas, St. Johns Pond, Cold Spring Country Club, Oheka Castle, and Town of Oyster Bay Golf Course. Fecal coliform enumeration for baseflow events ranged from 20 MPN/100mL to 299 MPN/100mL with a mean fecal coliform enumeration of 97.75 MPN/100mL. Fecal coliform enumeration for wet events ranged from <100 MPN/100mL to 2,180 MPN/100mL with a mean fecal coliform enumeration of 722.25 MPN/100mL.

There were four (4) samples processed for MST at CSB-02. One each on 8/26/2020 (dry), 9/21/2020 (dry), 9/10/2020 (wet) and 9/30/2020 (wet). Canine biomarker was detected in both wet weather samples. However, the quantifiable detection occurred during 9/30/2020 (0.89in) at 5440 copies/100mL. Neither Human nor Goose biomarkers were detected in any of the samples.

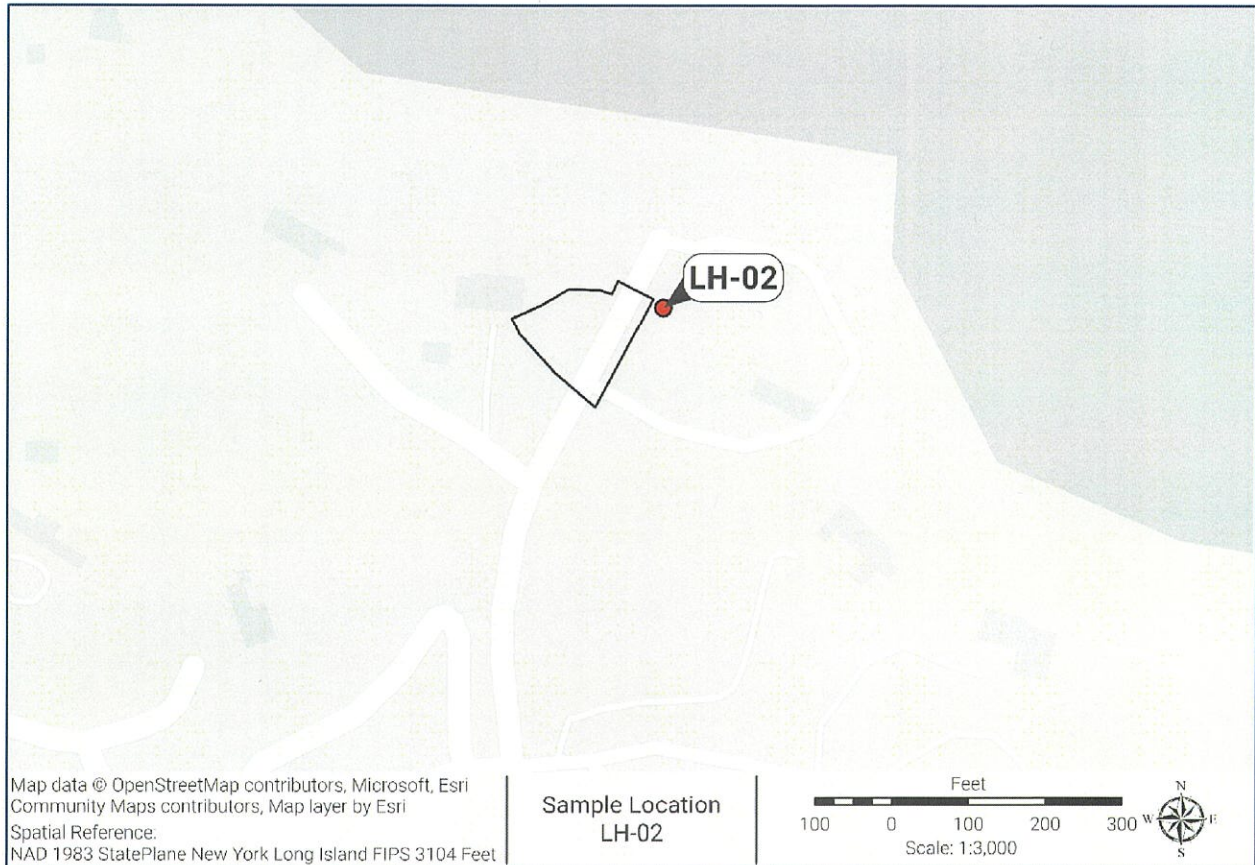
Cold Spring Brook: CSB-03 – Class 1



CSB-03 discharges to the head of Cold Spring Harbor under State Road 25A from the east. The catchment area is about 75 acres and encompasses a portion of Cold Spring Harbor State Park, a portion of Uplands Farm Field Station (Cold Spring Harbor Lab), as well as the intersection of 25A/Harbor Rd/Lawrence Hill Road. Fecal coliform enumeration for baseflow events ranged from 122 MPN/100mL to 259 MPN/100mL with a mean fecal coliform enumeration of 179.75 MPN/100mL. Fecal coliform enumeration for wet events ranged from 300 MPN/100mL to 435,200 MPN/100mL with a mean fecal coliform enumeration of 111,875 MPN/100mL.

There were four (4) samples processed for MST at CSB-03. One each on 8/10/2020 (dry), 9/21/2020 (dry), 9/10/2020 (wet) and 9/30/2020 (wet). Human biomarker was detected during a wet weather event on 9/10/2020 (0.92in) at 328 copies/100mL. Canine biomarker was detected in all samples, but only quantifiable results were obtained during wet weather events on 9/10/2020 (0.92in) at 1220 copies/100mL and 9/30/2020 (0.89in) at 867 copies/100mL. Goose biomarker was not detected in any of the samples.

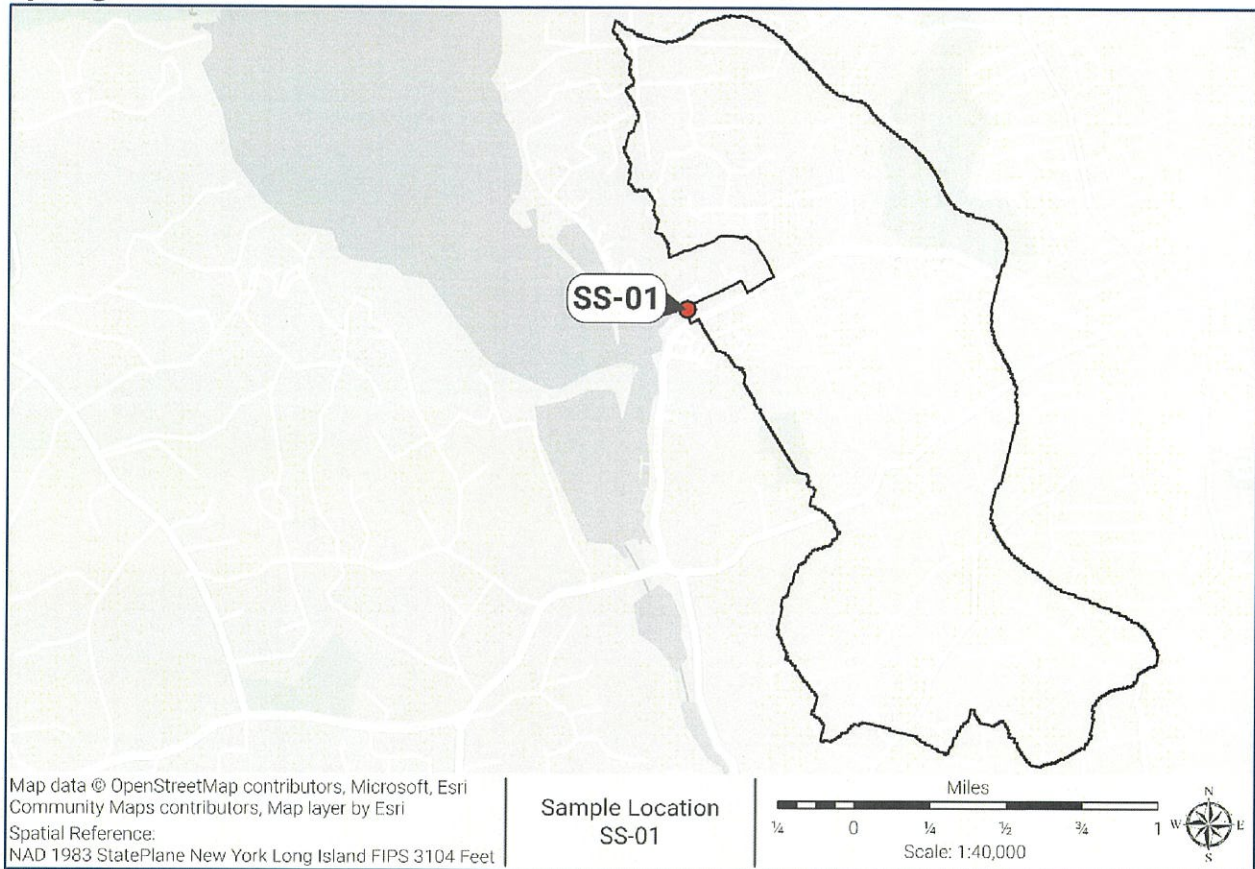
Laurel Hollow: LH-02 – Class 2



LH-02 discharges through a stormwater treatment system to the Laurel Hollow Beach outfall which discharges to Cold Spring Harbor. The catchment area is about 0.37 acres and encompasses predominantly low-density residential areas and a portion of Laurel Hollow Beach Park. Fecal coliform enumeration for baseflow events ranged from <1 MPN/100mL to 1,842 MPN/100mL with a mean fecal coliform enumeration of 506 MPN/100mL. Fecal coliform enumeration for wet events ranged from 1,320 MPN/100mL to 43,520 MPN/100mL with a mean fecal coliform enumeration of 13,817.5 MPN/100mL.

There were four (4) samples processed for MST at LH-02. One each on 8/10/2020 (dry), 8/24/2020 (dry), 8/29/2020 (wet) and 9/30/2020 (wet). Canine biomarker was detected on 9/30/2020 (0.89in) at 899000 copies/100mL. Neither Human nor Goose biomarkers were detected in any of the samples.

Spring Street: SS-01 – Class 1



SS-01 discharges through Spring Street Outfall #273 directly into Cold Spring Harbor and is the first structure in line for this system. The catchment area is about 1,284 acres and encompasses predominantly residential areas, Cold Spring Harbor downtown, a portion of the Huntington Country Club Gold Course, and Goose Hill Primary School. Fecal coliform enumeration for baseflow events ranged from 63 MPN/100mL to 754 MPN/100mL with a mean fecal coliform enumeration of 298.25 MPN/100mL. Fecal coliform enumeration for wet events ranged from 10,860 MPN/100mL to 57,940 MPN/100mL with a mean fecal coliform enumeration of 25,295 MPN/100mL.

There were four (4) samples processed for MST at SS-01. One each on 8/10/2020 (dry), 8/26/2020 (dry), 8/19/2020 (wet) and 9/1/2020 (wet). Human biomarker was detected in all four (4) samples at 1070, 8450, 2000 and 800 copies/100mL. Canine biomarker was detected on 8/10/2020, 8/19/2020 (0.28in) and 9/1/2020 (0.11in). However, quantifiable results were only obtained during wet events at 1220 and 867 copies/100mL. Goose biomarker was not detected in any of the samples.

A summary of average MST concentrations for quantifiable results can be seen in *Table 2*. Quantifiable Human biomarker was found in all four (4) of the SS-01 samples implying a consistent occurrence at this location only. Whereas the remaining locations having at most one (1) occurrence indicates a periodic or inconsistent contribution. While Canine biomarker was present at all locations, it was present in CSB-03 at all four (4) samples collected with two (2) samples having quantifiable results. The remaining locations had varying intensities and frequencies of Canine biomarker indicating a widespread yet inconsistent, albeit significant contribution. Goose biomarker was not found in any of the samples.

Table 2. Summary of Average MST Concentrations by Sample Station

Sample Station	Human_HF183 Average Marker Copies per 100mL			Dog_BacCan-UCD Average Marker Copies per 100mL			Goose_CGOF1 Average Marker Copies per 100mL		
	ND	DNQ	AVG	ND	DNQ	AVG	ND	DNQ	AVG
CSB-01	3	1	-	3	-	324 (n=1)	4	-	-
CSB-02	4	-	-	2	1	5440 (n=1)	4	-	-
CSB-03	3	-	328 (n=1)	-	2	1043.5 (n=2)	4	-	-
LH-02	4	-	-	3	-	899000 (n=1)	4	-	-
SS-01	-	-	3080 (n=4)	1	1	60150 (n=2)	4	-	-

* Please note that concentration of biomarker copies is only relatable to concentrations of the same fecal host, not between different hosts.

CONCLUSION

Cornell Cooperative Extension of Suffolk County (CCE) in collaboration with the Oyster Bay-Cold Spring Harbor Protection Committee, Friends of the Bay, and the Nassau County Soil and Water Conservation District, assessed the potential sources of fecal contamination entering Cold Spring Harbor on Long Island, NY, using samples collected at various storm sewer system (MS4) locations from August through September 2020. Host sources of fecal contamination in Cold Spring Harbor were assessed based on bacterial (Bacteroides) genetic markers.

Quantifiable Human biomarker was found in all four (4) of the SS-01 samples processed implying a consistent occurrence at this location during dry and wet events. As has been suggested in a recent comparable study in Hempstead Harbor, Tagliaferri et. al (2021), this could be attributed to failing on-site wastewater treatment systems (OWTS) adjacent to stormwater infrastructure resulting in over

land flows into storm drains or seepage of contaminated groundwater into cracks in stormwater pipes. Fecal coliform concentrations found during dry weather did not imply traditional illicit connections. Further study would be required to confirm direct locations of sources. The remaining locations (CSB-01 and CSB-03) having at most one (1) occurrence of human biomarker indicates a periodic or inconsistent contribution and could be attributed to sources such as improper disposal of household trash.

While Canine biomarker was present at all locations, it was present in CSB-03 at all four (4) samples collected with two (2) of the wet samples having quantifiable results. The remaining locations had varying intensities and frequencies of Canine biomarker indicating a widespread yet inconsistent, albeit significant, contribution based on fecal coliform enumeration data. Locations where known dog walking corridors exist were found to have higher frequency (CSB-03, SS-01) of occurrence of Canine biomarker or higher average marker copies (LH-02, SS-01).

Goose biomarker was not found in any of the samples indicating that Canada geese were not found to be a source of pathogens in the MS4s discharging to Cold Spring Harbor. Further study would be required to determine if Canada geese are a contributor of pathogens to Cold Spring Harbor through overland stormwater flow directly into the Harbor and presence in the waterway. If Canada geese are a source, it is likely that their contribution would be seen at local bathing beaches or natural areas along the shoreline where they may congregate, but not in MS4s.

Storm sewer systems were the focus of this study, but future study could include assessing other potential sources of fecal contaminated water contributing to Cold Spring Harbor, such as groundwater, marinas (boats), and resuspension of sediment. A recent U.S. Geological Survey (USGS) study of Hempstead Harbor (Tagliaferri et. al (2021)), a nearby waterway on the north shore of Nassau County, has indicated that compared to these other potential sources, stormwater from MS4s were the most likely transport mechanism of fecal contamination into Hempstead Harbor. Furthermore, the most substantial source of fecal contamination to Hempstead Harbor was found to be discharge from sites with constant flow, mainly MS4s throughout the harbor, under both dry and wet conditions. It is important to draw parallels to this recent USGS study, as the purpose is to use findings in Hempstead Harbor as a framework for future water quality regulations on Long Island. It is of

note that of the sites sampled in this study of Cold Spring Harbor, two sites had constant flow (CSB-03 & SS-01) from groundwater seepage into the MS4. These sites had events that showed elevated human and canine biomarker frequency and average marker copies and have been classified as Class 1, meaning within this study they were the most contaminated sites. When comparing to Hempstead Harbor, fecal coliform enumerations during baseflow were not found to be higher than those found during wet weather events at all sites. This further supports that traditional illicit connections (i.e., direct connections from OWTS) may not be as much of a contributor to surface water impairments in Cold Spring Harbor as they seem to be in Hempstead Harbor. Rather, stormwater runoff carries additional pathogens into the MS4 during wet events as opposed to diluting baseflow values. Alternatively, groundwater may be diluting illicit discharges into the MS4s. Further study would be required to determine to what extent groundwater seepage into these MS4s is impacting water quality.

Appendix A. Samples Collected at Cold Spring Harbor on Long Island, New York, for Bacterial Genetic Markers and Fecal Coliform

Table 1. Data summary of all samples collected in Cold Spring Harbor on Long Island, New York, for bacterial genetic markers and fecal coliform analysis.

Site name	Date	Time (EST)	Human_ HF183 (copies/ 100 mL)	Dog_ BacCan (copies/ 100 mL)	Goose_ CGOF1 (copies/ 100 mL)	Fecal coliform (MPN/ 100 mL)	Sample Condition
CSB-04	8/10/2020	9:59	-	-	-	41	dry
CSB-05	8/10/2020	10:03	-	-	-	275	dry
CSB-01	8/10/2020	10:40	-	-	-	31	dry
CSB-02	8/10/2020	10:52	-	-	-	31	dry
CSB-03	8/10/2020	11:03	ND	DNQ	ND	216	dry
LH-03	8/10/2020	11:19	-	-	-	-	dry
LH-02	8/10/2020	11:25	ND	ND	ND	1842	dry
LH-01	8/10/2020	11:42	-	-	-	399	dry
SS-01	8/10/2020	11:57	1070	DNQ	ND	228	dry
SS-02	8/10/2020	12:11	-	-	-	132	dry
SS-03	8/10/2020	12:26	-	-	-	-	dry
SS-01	8/19/2020	11:10	2000	98100	ND	10860	wet
SS-02	8/19/2020	11:25	-	-	-	10170	wet
SS-03	8/19/2020	11:32	-	-	-	13140	wet
LH-03	8/19/2020	11:48	-	-	-	14670	wet
LH-02	8/19/2020	12:00	-	-	-	1830	wet
LH-01	8/19/2020	12:07	-	-	-	2920	wet
CSB-04	8/19/2020	12:23	-	-	-	6970	wet
CSB-05	8/19/2020	12:33	-	-	-	7170	wet
CSB-01	8/19/2020	15:13	-	-	-	100	wet
CSB-02	8/19/2020	15:23	-	-	-	100	wet
CSB-03	8/19/2020	15:36	-	-	-	300	wet
CSB-01	8/24/2020	9:54	ND	ND	ND	72	dry
CSB-02	8/24/2020	10:02	-	-	-	20	dry
CSB-03	8/24/2020	10:14	-	-	-	122	dry
LH-03	8/24/2020	10:33	-	-	-	-	dry
LH-02	8/24/2020	10:42	ND	ND	ND	161	dry
LH-01	8/24/2020	10:56	-	-	-	246	dry
CSB-04	8/24/2020	11:24	-	-	-	62	dry
CSB-05	8/24/2020	11:32	-	-	-	199	dry
SS-01	8/24/2020	11:56	-	-	-	148	dry

Site name	Date	Time (EST)	Human_ HF183 (copies/ 100 mL)	Dog_ BacCan (copies/ 100 mL)	Goose_ CGOF1 (copies/ 100 mL)	Fecal coliform (MPN/ 100 mL)	Sample Condition
SS-02	8/24/2020	12:09	-	-	-	75	dry
SS-03	8/24/2020	12:14	-	-	-	-	dry
CSB-04	8/26/2020	10:35	-	-	-	97	dry
CSB-05	8/26/2020	10:41	-	-	-	399	dry
LH-03	8/26/2020	11:10	-	-	-	-	dry
LH-02	8/26/2020	11:20	-	-	-	20	dry
LH-01	8/26/2020	11:31	-	-	-	199	dry
SS-02	8/26/2020	11:47	-	-	-	10	dry
SS-01	8/26/2020	11:55	8450	ND	ND	754	dry
SS-03	8/26/2020	11:58	-	-	-	-	dry
CSB-01	8/26/2020	12:14	-	-	-	31	dry
CSB-02	8/26/2020	12:24	ND	ND	ND	41	dry
CSB-03	8/26/2020	12:32	-	-	-	122	dry
LH-01	8/29/2020	2:18	-	-	-	200	wet
CSB-04	8/29/2020	13:33	-	-	-	1210	wet
CSB-05	8/29/2020	13:39	-	-	-	9060	wet
LH-02	8/29/2020	14:06	ND	ND	ND	8600	wet
CSB-01	8/29/2020	15:16	-	-	-	100	wet
CSB-02	8/29/2020	15:21	-	-	-	<100	wet
CSB-03	8/29/2020	15:26	-	-	-	310	wet
SS-01	9/1/2020	9:11	800	22200	ND	57940	wet
SS-02	9/1/2020	9:17	-	-	-	141360	wet
SS-03	9/1/2020	9:27	-	-	-	43520	wet
LH-03	9/1/2020	9:47	-	-	-	12540	wet
SS-01	9/10/2020	9:30	-	-	-	15150	wet
SS-02	9/10/2020	9:38	-	-	-	14500	wet
SS-03	9/10/2020	9:48	-	-	-	13340	wet
CSB-04	9/10/2020	10:04	-	-	-	12740	wet
CSB-05	9/10/2020	10:06	-	-	-	27550	wet
CSB-01	9/10/2020	10:27	DNQ	ND	ND	1890	wet
CSB-02	9/10/2020	10:31	ND	DNQ	ND	510	wet
CSB-03	9/10/2020	10:35	328	1220	ND	11690	wet
LH-03	9/10/2020	11:02	-	-	-	200	wet
LH-02	9/10/2020	11:10	-	-	-	1320	wet
LH-01	9/10/2020	11:16	-	-	-	3230	wet
CSB-01	9/21/2020	9:25	ND	ND	ND	41	dry
CSB-02	9/21/2020	9:31	ND	ND	ND	299	dry
CSB-03	9/21/2020	9:37	ND	DNQ	ND	259	dry
LH-03	9/21/2020	10:02	-	-	-	-	dry

Site name	Date	Time (EST)	Human_ HF183 (copies/ 100 mL)	Dog_ BacCan (copies/ 100 mL)	Goose_ CGOF1 (copies/ 100 mL)	Fecal coliform (MPN/ 100 mL)	Sample Condition
LH-02	9/21/2020	10:15	-	-	-	<1	dry
LH-01	9/21/2020	10:28	-	-	-	74	dry
SS-03	9/21/2020	10:40	-	-	-	-	dry
SS-02	9/21/2020	10:48	-	-	-	63	dry
SS-01	9/21/2020	10:58	-	-	-	63	dry
CSB-04	9/21/2020	11:23	-	-	-	52	dry
CSB-05	9/21/2020	11:30	-	-	-	933	dry
CSB-01	9/30/2020	6:09	ND	324	ND	3690	wet
CSB-02	9/30/2020	6:12	ND	5440	ND	2180	wet
CSB-03	9/30/2020	6:17	ND	867	ND	435200	wet
LH-03	9/30/2020	6:55	-	-	-	200	wet
LH-02	9/30/2020	7:02	ND	899000	ND	43520	wet
LH-01	9/30/2020	7:08	-	-	-	7940	wet
SS-01	9/30/2020	7:23	-	-	-	17230	wet
SS-03	9/30/2020	7:36	-	-	-	17890	wet
SS-02	9/30/2020	7:43	-	-	-	14830	wet
CSB-04	9/30/2020	8:07	-	-	-	8200	wet
CSB-05	9/30/2020	8:11	-	-	-	24890	wet

REFERENCES

Tagliaferri, T.N., Fisher, S.C., Kephart, C.M., Cheung, N., Reed, A.P., and Welk, R.J., 2021, Overview and method-ology for a study to identify fecal contamination sources using microbial source tracking in seven embayments on Long Island, New York: U.S. Geological Survey Scientific Investigations Report 2021-5033, 8 p., at <https://doi.org/10.3133/sir20215033>.

Tagliaferri, T.N., Fisher, S.C., Kephart, C.M., Cheung, N., Reed, A.P., and Welk, R.J., 2021, Using microbial source tracking to identify fecal contamination sources in an embayment in Hempstead Harbor on Long Island, New York: U.S. Geological Survey Scientific Investigations Report 2021-5042, 19 p., <https://doi.org/10.3133/sir20215042>.

New York State Department of Environmental Conservation, 2021, Cold Spring Harbor Shellfish Growing Area #48 Triennial Evaluation 2021 (2020 Data).

New York State Department of Environmental Conservation, 2020, Cold Spring Harbor Shellfish Growing Area #48 Annual Evaluation 2020 (2019 Data).

New York State Department of Environmental Conservation, 2019, Cold Spring Harbor Shellfish Growing Area #48 Annual Evaluation 2019 (2018 Data).

Weather Underground, 2020, Cold Spring Harbor - KNYCOLDS14: Weather Underground data, accessed December 21, 2020, at: <https://www.wunderground.com/dashboard/pws/KNYCOLDS14>

U.S. Geological Survey, 2020, USGS NHDPlus High Resolution, accessed September 9, 2020, at: https://hydro.nationalmap.gov/arcgis/rest/services/NHDPlus_HR/MapServer.