# Topographic Drivers of Coastal Contamination: Evaluating the Role of Gradient and Proximity in North Shore Dog Parks

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**Abstract:** As pet waste decays, it releases nitrogen and phosphorus into the water, which can cause eutrophication or introduction of ammonia, bacteria, and parasites that endanger the health of humans and wildlife. This study identified different bacterial phyla and species and their relative quantity at four North Shore parks from Glen Cove to Northport and investigated the impact that distance from the shore and grade of dog parks have on the amount of fecal and other bacteria found in nearby water sources. Samples of water were collected of varying grades and distances from the shore, water was then filtered, eDNA was isolated using a Qiagen Power Soil Pro Kit, and the 16S ribosomal RNA region was amplified using PCR and sequenced using a minION flow cell. Crab Meadow Beach had the highest species diversity and abundance, followed by Gold Star Beach, Centre Island, and Garvies Point. Proteobacteria was the most abundant phylum for all four locations. Proteobacteria were abundant in all locations, but fecal coliform or pathogenic bacteria were not present at any location.

**Materials and Methods:** Permission to collect water samples was obtained from Centre Island Dog Park (Oyster Bay), Gold Star Beach Park (Huntington Bay), Garvies Point Dog Park (Glen Cove Creek), and Crab Meadow Beach as a control group (Northport) as there is no dog park there (Figure 1). Gradients of slopes were calculated by using the clinometer app, phyphox, and distances between the dog parks and water were measured using Google Maps. All samples were collected on April 18, 2026. At each location six water samples were collected directly under water surface level with 16.9 ounce sterile water bottles using sterile, disposable gloves. Weather, temperature, tidal phase, and precise location of collection were measured at each location. Samples were filtered with a vacuum pump until the filter became clogged, and after filtration eDNA was then extracted using a Qiagen Power Soil Pro Kit, amplified using PCR, and sequenced using a minION flow cell.

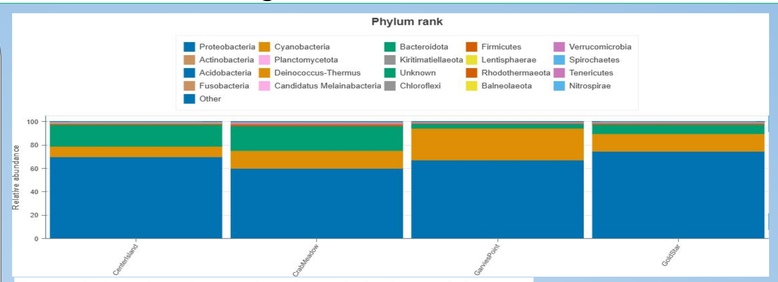


*Figure 3. Barplot of most abundant phyla for each location*

| Indices | Garvies Point (001-006) | Centre Island (007-012) | Gold Star (013-018) | Crab Meadow (019-024) |
|---|---|---|---|---|
| Richness | 1575.0 | 1233.0 | 2590.0 | 3080.0 |
| Shannon diversity index | 4.79 | 4.73 | 4.86 | 5.39 |
| Simpson's index | 0.97 | 0.97 | 0.97 | 0.98 |
| Total counts | 47919.0 | 15657.0 | 80951.0 | 143131.0 |

*Figure 4. Abundance and diversity indices for each location*

**Results:** The collection site at Garvies Point was closest to the dog park (100ft), and the site at Gold Star Beach was farthest (1500ft). The grades of the land at each location also differed: Garvies Point (4.34%), Centre Island (5.38%), Gold Star Beach (17.61%), Crab Meadow (7.29%). Data from the minION sequencing was used to create pie charts in order to depict the amounts and species of bacteria that were found (Figure 2). It was found that Crab Meadow Beach had the highest species diversity and abundance (Figures 3 and 4). Proteobacteria was the most abundant phylum for all four locations, followed by Bacteroidota was the second most abundant phylum for Centre Island and Crab Meadow, while Cyanobacteria was the second most abundant phylum for Garvies Point and Gold Star. Although proteobacteria were very abundant in all four locations, fecal coliform or pathogenic bacteria were not present at any location, specifically *E. coli*, *Salmonella*, or *Campylobacter*.

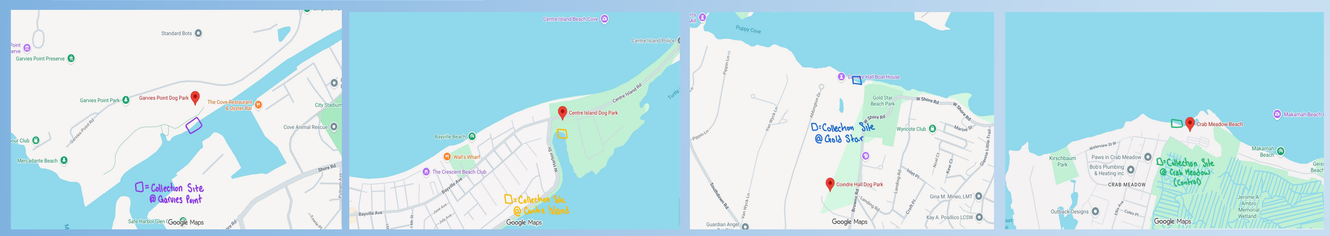


*Figure 1. Collection Sites at Each of the Four Locations*

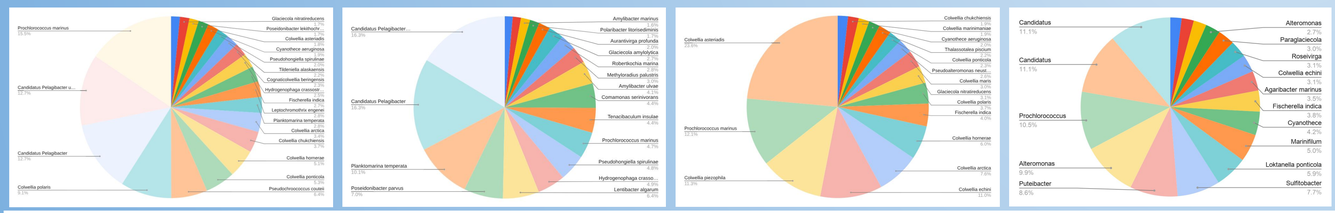


*Figure 2: Abundance of bacterial species present in at least 1% of reads, from left to right Garvies Point, Centre Island, Gold Star Beach, and Crab Meadow, including top 3 genera*

## Top 3 Genera

Garvies Point:
Colwelia (21.4%)
Prochlorococcus, (9.9%)
Candidatus Pelagibacter (8.1%)

Centre Island:
Candidatus Pelagibacter (11.7%)
Planktomarina (7.2%)
Poseidonbacter (5.5%)

Gold Star:
Colwellia (41.4%)
Prochlorococcus (6.6%)
Pseudoalteromonas (3.3%)

Crab Meadow:
Alteromonas (6.2%)
Candidatus Pelagibacter (5.3%)
Sulfitobacter and
Prochlorococcus (5.1% each)

**Discussion:** Among the phyla identified, the ones most strongly associated with fecal contamination are Bacteroidota and Proteobacteria, which were very abundant in all four locations, especially at Crab Meadow. Bacteroidota is considered a reliable and sensitive biological marker for detecting fecal contamination in aquatic environments. Proteobacteria is the most diverse bacterial phylum and is some species within this phyla are commonly found in the fecal microbiota of healthy dogs and cats. The phylum also includes various opportunistic pathogens, such as *E. coli*, *Salmonella*, and *Campylobacter* (Moon et al. 2018). There were no pathogenic species found in our samples, however. Species of proteobacteria that were found have the primary functions of degrading organic matter and serving as a background microbiome (Cottrell & Kirchman 2000). We expected to see *E. coli*, *Salmonella*, and *Campylobacter*, but did not see any in the resulting data within the 1% read cutoff. Some phyla found, including Cyanobacteria, Proteobacteria, and Bacteroidota, have several functions in the ecosystem. Cyanobacteria are mainly responsible for oxygen production, converting inorganic carbon into biomass. Proteobacteria are mainly responsible for organic matter decomposition and nitrogen and sulfur cycling, while some are pathogenic and cause disease infecting fish, shellfish, corals, and humans. Bacteroidota is mainly responsible for organic matter decomposition, marine snow degradation, and nutrient recycling. These results indicate that the four locations differ substantially in microbial biodiversity and therefore differ in environmental conditions as well as water quality. The high species diversity and abundance observed at Crab Meadow Beach likely indicates that this site supports a more complex and stable microbial ecosystem, as greater microbial diversity is commonly associated with increased ecological resilience, functional diversity, and environmental stability (Girvan et al. 2005, Shade et al. 2012). It is possible that the high microbial biodiversity at this location correlates with the absence of a dog park in the area (Garfield & Walker 2008).
Distance from a dog park did not have a significant effect on the abundance of bacteria because the beach with no dog park had the highest bacterial abundance. In contrast with Crab Meadow Beach, the three sites with nearby dog parks have notably lower abundance and diversity of bacteria. Dog parks near shorelines may contribute to the microbial ecosystems of the water through pet waste runoff, and fecal contamination can alter the presence of bacteria by increasing nutrient input and introducing fecal-associated bacteria into the water. This, counterintuitively, can sometimes decrease the level of species abundance and diversity in the site (Maxwell and Bryant 2025). However, because Gold Star Beach showed relatively high abundance and diversity, despite having a nearby dog park, the relationship is likely influenced by various environmental factors such as water circulation, nearby human activity, beach usage, or surrounding vegetation. To receive more conclusive results it would be more advantageous to conduct a wider study across multiple seasons and to measure additional environmental variables such as nutrient levels, dissolved oxygen levels, salinity, or pH.

**Introduction:** Fecal coliform bacteria is a collection of relatively harmless microorganisms found in the intestines of humans and animals that acts as an indicator species, indicating the presence of other pathogenic bacteria such as *E. coli*, *Salmonella*, or *Campylobacter* (Cleveland Clinic 2022). Specifically, waste from pets introduces issues to aquatic environments which can degrade the quality of the water (Water Research Center 2020). As pet waste decays, it releases nitrogen and phosphorus into the water, which can cause eutrophication–the excessive growth of algae that upsets ecosystem balance. This process harms marine life because as the algae dies and decomposes, the water's oxygen levels begin to deplete. This creates hypoxic conditions which can cause aquatic organisms to suffocate and die (NOAA 2024). Furthermore, pet waste contains other harmful matter such as ammonia, bacteria, and parasites that endanger the health of humans and wildlife (Long Island Sound Partnership 2025 and Save the Sound 2025). Ingesting harmful bacteria such as *E. coli*, *Salmonella*, and *Campylobacter* and parasites such as roundworm, tapeworm, and whipworm can lead to health issues including malnutrition, anemia, or organ damage (Ahmed M 2023).
By collecting and analyzing water samples near these parks, water quality can be determined, pathogens can be identified, and steps can be taken to mitigate the negative consequences of water pollutants. Although a positive correlation between dog parks and the presence of bacteria in nearby water sources has been observed in the past, many factors affect this line of study, and a definite conclusion regarding location and grade of dog parks in relation to bacteria found in nearby water sources has been difficult to reach (McKee A, Couch A. 2024).
This study seeks to investigate the impact that the location and grade of dog parks have on the amount and type of bacteria found in nearby water sources. More harmful bacteria are expected to be found at the location in Glen Cove, as this location has the smallest distance between the park and water source, and is assumed to have a steeper gradient, producing more runoff from the park into the water. It is anticipated that Gold Star Beach Park will have the second highest quantity of fecal bacteria, Centre Island Dog Park will have the third highest quantity of fecal bacteria, and Crab Meadow Beach will have the least amount of fecal bacteria.

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**References**