# One Health Surveillance for antibiotic resistant *E. coli* in the Salish Sea ecosystem

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## BACKGROUND

Antimicrobial resistance (AMR) is a global threat. The surveillance of AMR in the environment can inform us about contaminations in the shared environments, and how it impacts animals the rely on it and the humans who live near it.

The objective of the study was to take a One Health approach to identifying AMR patterns in the Salish Sea through sampling marine water, marine animals, river otters, and freshwater sources, and isolating and analyzing *E. coli* isolates using antimicrobial testing and whole-genome testing.

Figure 2. Map of all resistant and intermediate *E. coli* isolates in Salish Sea



Table 1. Total number isolates characterized and antibiotic susceptibility testing results for each source.

Sample Source (n=305)	Isolates Characterized	Intermediate	Resistant	Susceptible
Marine Water	212	7 (3.3%)	7 (3.3%)	198 (93.4%)
North Puget Sound	49	3 (6.1%)	4 (8.2%)	42 (85.7%)
<b>Central Puget Sound</b>	55	0 (0%)	2 (3.6%)	53 (96.4%)
South Puget Sound	56	3 (5.4%)	0 (0%)	53 (94.6)
Strait of Juan de Fuca	52	1 (1.9%)	1 (1.9%)	50 (96.2%)
Freshwater	5	1 (20%)	3(60.0%)	1 (20.0%)
Marine water by beaches	3	0 (0%)	0 (0%)	3 (100%)
Harbor Seal	52	6 (11.5%)	8 (15.4%)	38 (73.1%)
Dead Seal	35	6 (17.1%)	3 (8.6%)	26 (74.3%)
Live Seal	17	0 (0%)	5 (29.4%)	12 (70.6%)
Harbor Porpoise	7	2 (28.6%)	0 (0%)	5 (71.4%)
River Otter	24	4 (16.7%)	13 (54.2%)	7 (29.2%)
Sole	2	0 (0%)	0 (0%)	2 (100%)
Total	305	20 (6.6%)	31 (10.2%)	254 (83.2%)

Figure 1. Salish Sea sampling locations from all source types



## **MATERIALS & METHODS**

> Sampling of *E. coli* from marine and freshwater

Figure 3. Map of ExPEC strains of *E. coli* isolates in Salish Sea



## RESULTS

> Higher proportions of resistant and intermediate *E. coli* isolates were found among marine mammal and river otters when compared to marine water samples (p-value < 0.0001; OR=5.334 [95% CI: 2.728-10.648]).

> ExPEC strains (ST10, ST38, ST58, ST69, ST73, ST117, and ST405) were detected in 37 *E. coli* isolates.

## CONCLUSION

Marine mammals can serve as potential sentinels for ecosystem surveillance of antimicrobial resistant E. coli in the Salish Sea ecosystem.

> Monitoring of the marine mammal microbiome may lead to information about how AMR persists in the local environment.

> Continued testing of both marine water and marine mammals can reveal the prevalence of potentially pathogenic strains of *E. coli* in the Salish Sea ecosystem.

using EPA Most Probable Number/100 mL, and fecal samples using IDEXX

> Isolates of *E. coli* from marine water were gathered for shellfish monitoring, and feces was collected from harbor seals (*Phoca vitulina*), North American River otters (*Lontra canadensis*), harbor porpoise (*Phocoena phocoena*), and English sole (Parophrys vetulus)

> *E. coli* isolates were screened using *fumC* sequences to increase variability

> Antimicrobial susceptibility testing was performed and whole genome sequencing was used for characterization of *E. coli* isolates

> Phylogenetic trees and single nucleotide polymorphism (SNP) matrices were created for ExPEC strains

> 6 statistical comparisons were made using Fishers exact test to analyze difference in proportions of susceptibility by sample source

> After mapping non-susceptible *E. coli* isolates, we did not find resistant or intermediate samples around the Strait of Juan de Fuca.

#### RESULTS

> **305** *E. coli* isolate characterized from marine water, freshwater, marine mammals, river otters, and sole

> 20 (6.6%) isolates were intermediate and 31 (10.2%) were resistant

> **196** unique MLST were identified from marine water, freshwater, and mammal samples

> 37 isolates were found to be extraintestinal pathogenic *E. coli* (ExPEC) ST

> Most common ST occurrence was ExPEC strain, **ST10 (n=12)** 



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