

Canada

Preliminary Microbial Source Tracking Results from Rouge Beach and the Rouge River Watershed within the Toronto Area of Concern in 2016

T. Edge, Z. Staley, D. He, R. Vender, J. Grabuski, and P. Shum

Environment and Climate Change Canada Canada Centre for Inland Waters Burlington, Ontario

November 14, 2016



Presentation Overview

- Toronto Area of Concern
 - Beach Beneficial Use Impairments
 - Microbial source tracking
- Water sampling in 2016
 - Rouge Beach / Rouge watershed / stormwater outfalls
 - Don River / Toronto Harbour
- Preliminary results from 2016
 - E. coli surveillance
 - Human sewage / gull fecal contamination
- Conclusions / Future Directions





Toronto AOC Beaches





DRAFT – Page 3 – December-16-16



Microbial Source Tracking (MST)

- Detection of *E. coli* in water indicates fecal pollution and the possible presence of harmful waterborne pathogens
- <u>Problem</u>: *E. coli* detection gives no info on fecal pollution source
- Science advances needed to supplement *E. coli* counts and get more info from water samples
- MST: Techniques to detect DNA of microbes in water that are unique to known fecal pollution sources







Water sampling - 2016

- Weekly sampling dates June August (n~14)
 - Rouge Beach, Rouge River (and stormwater outfalls)
 - Don River, Toronto Harbour
- 500mL water sample analyzed for:
 - E. coli (CFU / 100mL)
 - DNA markers from gut bacteria for human, gull, ruminant/cow, and dog fecal sources by endpoint PCR and quantitative PCR
 - Chemical (e.g. caffeine, sweetners) and pharmaceutical (e.g. carbamazepine, acetomenophan) markers for sewage
 - DNA for metabarcoding, metagenomics, eDNA analyses







Rouge watershed sampling sites







DRAFT – Page 6 – December-16-16



Environment Environnement Canada Canada



Don River / Harbour sampling sites





Canada

Environment Environnement Canada

Canada

2016 – *E. coli* results



Log E. coli CFU/100ml

Canada

Canada

2016 – Human/Gull DNA Marker Results



Dry vs Wet Weather – Rouge 2016



Conclusions

- Microbial source tracking can supplement *E. coli* data and provide more information from water samples
- Rouge Beach continuously impacted by accumulating gull/geese fecal contamination; sporadically impacted by human sewage from Rouge River
- In 2016, human sewage DNA marker not detected in the Little Rouge tributary; infrequent and low level detection in the lower Main Rouge River
- Sewage cross-connections detected in stormwater outfalls, particularly at RR1 closest to Rouge Beach
- Human sewage contamination represents highest health risks and a legacy AOC pollution problem to address





Metagenomics Research Directions



- Rouge River DNA samples
- Metabarcoding
 - Taxonomy Who is there?
 - Bacteria, fungi, algae
 - eDNA from animals
- **Metagenomics**
 - Function What can they do?
 - Genes for oil degradation, antimicrobial resistance...
- Genomics benchmark for monitoring future changes



Canada



Acknowledgements

- Thanks to support from Laud Matos, Rimi Kalinauskas, Paul Jiapizian, and funding from ECCC's Great Lakes Action Plan (GLAP), Strategic Technology Applications of Genomics for the Environment (STAGE) program
- Thanks to Meg St John (TRCA), Mahesh Patel and Bill Snodgrass (City of Toronto), and members of the Toronto RAP beach coordination working group
- Thanks to support from Leonardo Cabrera, Parks Canada



