

Tracking Microbial Contaminants from Coastal Wastewater Discharges

Goal

- To determine the level of viable Enterococci fecal indicator bacteria and to investigate the abundance of fecal indicators and microbial pathogens in seawater originating from wastewater outfalls based on their genetic signature in the environment.
- Assess the geospatial distribution of fecal indicator bacterial from treated wastewater discharges in along the Southern Florida Coast.



Image of rhodamine dye from the South Central wastewater outfall, Palm Beach County, Florida, July 2008. Vessel shown is R/V F.G. Walton-Smith conducting tracer study for NOAA FACE program.



Image of inter-coastal water exiting the Boynton

Background

- Public health risks in recreational waters and the decline of coral reefs in southern Florida due to human caused contamination are a significant concern in a region where tourism drives much of the economy.
- The first suspects are typically the wastewater outfalls, which discharge up to 300 million gallons of treated wastewater into the ocean 3km off shore each day.
- However, there are a variety of other human pollution sources in the area, including ground water seepage and a number of coastal inlets, which are contaminated with materials from urban stormwater runoff septic tanks, landfills, industrial processes, and agriculture.
- It is important to determine the relative contribution of chemical, microbial, and nutrient pollutants from each of these sources in order to ensure that expensive remediation processes accurately and effectively targets the areas that impact the coastal ecosystem and pose the greatest threat to human and reef health.
- The Florida Area Coastal Environment (FACE) program is carrying out a long term assessment study of the South Florida coastal ecosystems to investigate the transport and distribution of nutrients and microbes from the coastal inlets, treated wastewater effluent, and oceanic upwelling.

Vanninkhof. R.: Sullivan, K. F.: Dammann, W. P.; Proni, J. R.; Bloetscher, F.; Soloviev, A. V.; Carsey, T. P. Environmental Science & Technology **2005**, 39, 8883-8890, Glassmeyer, S. T.; Furlong, E. T.; .Kolpin, D. W.; Cahill, J. D.; Zaugg, S. D.; Werner, S. L.; Meyer, M. T.; Kryak, D. D. nviron. Sci Technol. **2005**. 39. 5157-5169

Molecular Microbial Source Tracking

To address the concerns of microbial water quality and ecosystem and public health risk in coastal waters, it is necessary to determine whether the wastewater effluent contains viable pathogens, how far from the point source these pathogens can travel, and how guickly they dilute out.

- However, there are a large number of potential pathogens associated with fecal matter, and often low microbe levels that are difficult and expensive to detect, but which can still be infectious.
- Instead of testing for each potential fecal pathogen, indicator species are used that are present when fecal contamination is present, and are in large enough concentrations to be easily detected in environmental samples. It is assumed that fecal contamination poses the potential risk of pathogen contamination, and human-specific fecal contamination poses the greatest risk of human pathogens.



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Acknowledgements

Shailer Cummings, Jack Stamates, Joe Bishop, Thomas Carsey, FOCITE II Crew NOAA Hollings Scholarship Program

North Current Results Bacteria Level vs. Distance from outfall Total Enterococci Total HF8 (Human Specific) Map of Southern Florida. Sampling site is outlined in red. ACE July 2008 South Central Outfall ADCP Mooring Distance from outfall (km) South Current Bacteria Level vs. Distance from outfall Total Enterococci Total HF8 (Human Specific) 7/11/08 14:50 - 7/11/08 14:50 - 7/11/08 17:50 - 7/11/08 23:50 - 7/12/08 2:50 - 7/12/08 14:50 - 7/12/08 14:50 - 7/12/08 14:50 - 7/12/08 14:50 - 7/12/08 23:50 - 7/12/08 23:50 - 7/13/08 23:50 - 7/13/08 2:50 - 7/13/08 2:50 - 7/13/08 14:50 - 7 -06 WS-19 WS-18 Outfall WS-17 • • Distance from outfall (km) **Inter-Coastal Bacteria Levels** Total Enterococci Sprobe primer fluorescein 🕞 👩 quencher Total HF8 (Human Specific) Genome iquivalen 2 2) Primer Annealing/ Probe hybridization hybridizes P Maps of sample collection sites (A) during a northern current, (B) from the inter-coastal waterway, and (C) during a southern current, Color corresponds to total enterococci level. Sample • No linear correlation between marker concentration and distance from the outfall indicates that the microbial transport from the boil was not a steady stream. agMan[®] Probe Method Schematic of TagMan gPCR mechanism • The wastewater effluent appears to have exited the outfall as coherent packets of freshwater that may travel along the surface over long distances with little mixing, resulting in the transport of occasional isolated packages of comparatively larger bacterial loads further downstream. • Additional tracer and current data will be used to more fully characterize the discharge pathways. Enterococci and human Bacteroides were highest in the region around the boil, indicating that most of the bacterial load from the outfall may be diluting rapidly within the first kilometer downcurrent. • Observed bacterial loads during this cruise were below levels commonly associated with ecosystem or human health risk. Image of Enterolert Quanti tray under UV • Samples collected during the southward current had a greater ratio of HF8 marker (pink) to lamp. Fluorescent wells enterococci (blue) than did the samples collected during the northward moving current. This may indicate specific presence indicate that the fecal-associated microbial composition of the wastewater (and hence the of enterococci. associated potential pathogen load) of the effluent changes over time. **Enterolert Test Results** Enterococci Level Sample (viable bacteria/100mL **Conclusions and Future Directions** Ocean (85 samples) BD-13 • No viable fecal indicator bacteria were found in the wastewater discharge plume BD-16 Inter-20 Coastal BD-17 Indicator bacterial levels determined by IDEXX EnteroLert[™] and by qPCR analysis were BD-18 61

source. Viral RNA samples will be processed and analyzed to provide information on the distribution of

viral pathogens.

bacteria.

plume.







insignificant from a public health perspective. However this does not address potential health risk by other microbial groups such as pathogenic viruses or protozoan cysts. Dilution and distribution characteristics of viruses especially may not be similar to that observed here for

• Rhodamine and SF₆ tracer data and current profiles will be used to more fully characterize the discharge pathways, and assess the potential distribution of fecal matter from the effluent

• Extracted DNA samples will be further analyzed for additional source tracking and pathogen markers to more accurately determine which bacterial loads originate from the outfall point