Abstract

Fecal indicator bacteria (FIB) are an important form of pollution and are of particular concern in tidal creeks, which often serve as conduits of stormwater, transporting high concentrations of bacteria to the aquatic environment. In this study, we conduct a comparison of regulatory FIB (E. coli) to host-specific qPCR assays on direct canine and sea bird fecal grab samples from the Grand Strand of South Carolina to attribute a percentage of the FIB load to a particular host. Temporal variability of the addition of the aquatic environment. In this study, we conduct a comparison of regulatory FIB (E. coli) and host-specific genetic markers in the bacteria unique to the host organism.

Methodology

- Fecal samples collected from selected canines were diluted to 10^{-1} mL final dilution factor, while selected sea bird (Laridae) samples were combined and diluted to 10^{-3} mL final dilution factor.
- Collected samples from an Italian Greyhound and bird mass-fecal sample were incubated (22°C for ~14 days) and dilution and filtering protocols were repeated.
- Bacterial DNA was extracted from filters by mechanical and chemical cell lysis, and quantitative PCR was used to quantify the presence of FIB with the GenBac Assay, the BacCan Assay and the Bird GFD Assay. Additional culturable E. Coli was measured by Colilert-18.

Results

- Concentrations of FIB and species specific genetic markers varied greatly between individuals. Surprisingly some individuals showed no E. coli in fresh feces but had relatively strong genetic marker results.
- A weak correlation existed across individually sampled canines between E. coli and BacCan (R^2 = 0.0366; p = 0.0187), and E. coli and GenBac (R^2 = 0.0366; p = 1.97 X 10^{-6}) determined FIB concentrations.
- Genetic marker decay rates for aged canine fecal sample was rapid and logarithmic in slope. Corresponding E. coli concentrations progressively increased with time to maximum quantifiable level.
- Decay rate for aged sea bird fecal sample was very rapid while E. coli persisted longer with high concentrations.

Conclusion

- There is a great deal of variability in the concentration of FIBs and genetic markers between individuals.
- The source specific signal seems to disappear quickly while FIB concentrations appear to continue to rise after leaving the organism. Thus any detection of a source specific signal should be considered significant.
- This variability between bacterial concentrations in fecal samples limits interpretation of qPCR and culturing results which complicates the assignment of FIB percent load to a particular host.
- These results suggest that a multiple tracer weight of evidence approach including traditional WQ measurements and qPCR methods are necessary for meaningful data interpretation.