Evaluation of Bacteroidales Host Specific Genetic Markers for Tracking Fecal Contamination Sources in Alabama

The water quality of many waterways in our state and nation is deteriorating due to point and nonpoint source pollution from human and animal wastes. Accurate identification of contamination sources is essential for developing cost-effective pollution control strategies. Direct detection of host-specific genetic markers by polymerase chain reactions (PCR) has been widely used in identifying sources of fecal contamination in environmental waters. In this study, we conducted experiments to validate three genetic markers associated with wildlife and pets for bacterial source tracking in Alabama. More than 430 end-point PCRs were performed on 10 raw sewage samples and 133 fecal samples from nine animal species. Our results show that both avian and deer/elk markers had acceptable specificity and sensitivity and thus can be used for bacterial source tracking studies. The dog marker, however, was found in only 12 of the 22 dog fecal samples and showed cross reactivities with horse and sewage samples. To evaluate the performance of these host-specific markers in environmental water, we collected 12 water samples over a 22-day period from Parkerson Mill Creek, an impaired creek on Alabama's 303(d) list. In addition to the above-mentioned wildlife and pet markers, quantitative PCR was also performed on water samples using a human- and two cattle-specific markers. Human, avian, and dog markers were detected in several water samples; one of the two cattle markers was also detected by qPCR. Samples collected after a significant rainfall event showed higher frequency of host specific marker detection.

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