

Application of an integrated community analysis approach for microbial source tracking in a coastal creek

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ABSTRACT

High fecal indicator bacterial (FIB) concentrations signal urban coastal water quality impairments that can threaten public health. However, FIB (total and fecal coliform plus *Enterococcus* sp.) concentrations are not specific to human waste, and thus, microbial source tracking (MST) is employed to assess public health risks and remediation alternatives. Currently, water quality diagnosis requires several simultaneous MST assays. Relatively unexplored is a community analysis approach for MST where the overall microbial community composition is compared, through multivariate analysis, to link sources and sinks of microbial pollution. In this research, an urban coastal creek and drain sampling transect, previously diagnosed as human-waste contaminated, were evaluated for bacterial community composition relative to fecal sources; a laboratory spiking study was also performed to assess method sensitivity and specificity. Multivariate statistical analysis of community profiles clearly distinguished different fecal sources, indicated a high sensitivity for sewage spikes, and confirmed creek contamination sources. This work demonstrates that molecular microbial community analysis combined with appropriate multivariate statistical analyses is an effective addition to the MST tool box.

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