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Multi-tiered approach using quantitative polymerase chain reaction for tracking sources of fecal pollution to Santa Monica Bay, California

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ABSTRACT

The ubiquity of fecal indicator bacteria such as Escherichia coli (E. coli; EC) and Enterococcus sp. (ENT) in urban environments makes tracking fecal contamination extremely challenging. A multi-tiered approach was used to assess sources of fecal pollution in Ballona Creek, an urban watershed that drains to Santa Monica Bay (SMB) near Los Angeles, CA. A mass-based design at six mainstem sites and four major tributaries over a six hour time period was used to assess: Tier 1) the flux of ENT and EC using culture-based methods; Tier 2) ENT using quantitative PCR (QPCR), and detection and/or quantification of additional markers of human fecal contamination including Bacteroides sp. human specific marker and enterovirus, using quantitative reverse transcriptase PCR (QRTPCR); and Tier 3) the specific types of enteroviral genomes found via sequence analysis. Sources and concentrations of fecal indicator bacteria were ubiquitously high throughout Ballona Creek, with no single tributary dominating fecal inputs. The flux of ENT and EC averaged 10^9 to 10^{10} cells hr⁻¹ and was as high at the head of watershed as at the mouth prior to discharge into SMB. In addition, there was a consistent detectable signal of the Bacteroides human specific marker, with 86% of the samples taken over the extent over the study period testing positive. Enteroviruses were quantifiable in 14 of 36 samples (39%), with the highest concentrations at the site furthest upstream, Cochran Avenue. These results indicated the power of using multiple approaches to assess and quantify fecal contamination in freshwater conduits to high use, high priority recreational swimming areas.

Full Text

ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2005_06AnnualReport/AR0506_181-194.pdf

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