

Survey of pathogens and human fecal markers in stormwater across a highly populated urban region

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ABSTRACT

Microbial contamination of urban stormwater, rivers, and creeks during rainstorms is a persistent and widespread problem. Remediation of these waters has proven to be challenging since there are many potential sources for the fecal indicator bacteria on which water quality is regulated. Microbial source tracking markers have allowed for improved identification and quantification of the sources of contamination, but the majority of the source-attributed microbial targets are not responsible for causing the illnesses associated with waterborne human fecal contamination. Thus there is a need to better understand the relationships of human pathogens and human fecal markers in stormwater. In this study, we used a spatially-intensive sampling approach (31 sites) across southern California for the analysis of stormwater. During three storms from 2021–2023, we used droplet digital PCR to quantify the human fecal markers HF183 and Lachno3 along with human adenovirus, human norovirus, *Campylobacter* spp., and *Salmonella* spp. This spatially intensive sampling design captures information from a 5900 km² area with ~22 million people. We detected human markers HF183 and Lachno3 genes at 90% and 97% of the sites; concentrations ranged from below detection to 10⁴ and 10⁵ gene copies per 100 mL, respectively. We found variable concentrations of human bacterial and viral pathogen genes. HF183 was significantly correlated to human adenovirus and Lachno3. Lachno3 was also significantly correlated with *Salmonella*. We reported PCR inhibition in 83–90% of the samples but found that separating sediment and adding proteinase K during lysis improved DNA/RNA extraction efficiency and reduced inhibition.

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