

**Title:** Quantitative Real-Time PCR Fecal Source Identification in the Tillamook Basin

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**Abstract:** Rivers in the Tillamook Basin play a vital role in supporting a thriving dairy and cheese-making industry, as well as providing a safe water resource for local human and wildlife populations. Historical concentrations of fecal bacteria in these waters are at times too high to allow for safe use leading to economic loss, endangerment of local wildlife, and poor conditions for recreational use. In this study, we employ host-associated qPCR methods for human (HF183/BacR287 and HumM2), ruminant (Rum2Bac), cattle (CowM2 and CowM3), canine (DG3 and DG37), and avian (GFD) fecal pollution combined with high-resolution geographic information system (GIS) land use data and general indicator bacteria measurements to elucidate water quality spatial and temporal trends. Water samples (n=584) were collected over a 1-year period at 29 sites along the Trask, Kilchis, and Tillamook rivers and tributaries (Tillamook Basin, OR). A total of 16.6% of samples (n=97) yielded *E. coli* levels considered impaired based on Oregon Department of Environmental Quality bacteria criteria (406 MPN/100mL). Host-associated genetic indicators were detected at frequencies of 39.2% (HF183/BacR287), 16.3% (HumM2), 74.6% (Rum2Bac), 13.0% (CowM2), 26.7% (CowM3), 19.8% (DG3), 3.2% (DG37), and 53.4% (GFD) across all water samples (n=584). Seasonal trends in avian, cattle, and human fecal pollution sources were evident over the study area. On a sample site basis, quantitative fecal source identification and GIS land use data provided new information suggesting elevated *E. coli* levels may be linked to specific point and nonpoint pollution sources. Results demonstrate the advantages of combining host-associated genetic indicators and GIS mapping strategies with general fecal indicator bacteria water quality monitoring data to better characterize sources of fecal pollution in environmental waters.

**Keywords:** Microbial source tracking, qPCR, water quality, fecal indicator bacteria

**Disclaimer:** *This abstract does not necessarily reflect U.S. EPA policy.*

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