

## **Quantitative Pathogen Detection & Microbial Source Tracking Combined with Modeling the Fate and Transport of *Bacteroidales* in San Pablo Bay**

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Fecal contamination from non-point sources in coastal and estuarine water bodies is a problem of increasing concern. Water monitoring alone is sometimes insufficient in providing a clear picture of the fecal contamination of a water body. Well-formulated and developed mathematical and numerical transport models, on the contrary, predict continuous concentrations of microbial indicators under diverse scenarios of interest, and they can quantify fecal source contributions on a land use basis (human versus livestock or wildlife).

The present project has demonstrated the utility of quantitative analyses of fecal contamination in water bodies via new experimental measurement techniques as well as mathematical/numerical modeling of the fate and transport of biological contaminants. San Pablo Bay was selected because there is abundant knowledge about the estuarine system and its tributaries and because of the availability of an existing 3-dimensional model. Environmental monitoring of San Pablo Bay was performed with a Microbial Source Tracking (MST) approach that utilized a validated large-volume (100 L) hollow-fiber ultrafiltration method to concentrate water, which was then tested with quantitative real-time PCR assays to identify and quantify fecal contamination contributed from general and human-, cow- and dog-specific sources. Monitoring of human viral pathogens (adeno- and enteroviruses) was also performed. Additional samples were also collected to enumerate microbial indicators (*E. coli* and enterococci). This was the first time that DNA-based molecular assays, which had been previously validated with fecal samples and wastewater effluents in freshwater studies, were applied to an estuarine environment.

Monitoring results indicated low-level general and human-derived fecal contamination in the bay, while cow- and dog-derived contamination was not detected, except for one sample which contained dog-specific genetic marker. Human viruses were also below the sample detection limit. The pollution was more likely to come from surrounding urban areas or wastewater treatment facilities than from agricultural farm land or wildlife areas. Another application of the study included the validation of a quantitative sea bird-specific molecular DNA assay for the purpose of microbial source tracking to enumerate the contribution of sea birds to fecal contamination. The assay was found to possess adequate sensitivity and specificity and could be applied in the future to archived environmental samples from San Pablo Bay and its tributaries.

A suite of theoretical and computational tools, ranging from one-dimensional (1-D) to three-dimensional (3-D) models, was developed during this project for the analysis of the fate and transport of *Bacteroidales* gene markers. These models were paired with existing visualization tools. Flow conditions for the sampling dates were simulated and results compared with velocity observations. Exploratory assessments of water quality in the San Pablo Bay allowed for an incipient characterization of the transport conditions in San Pablo Bay. Future work includes the optimization of the water-quality sub-module of the code in order to a) include sediment transport in the bay; b) obtain more reliable results under a wide set of boundary conditions; and c) be able to simulate a wider set of water-quality parameters. Also, the authors would like to add a user-friendly interface to the code to facilitate decision making by coastal managers.