

Category III – Water Quality

Modeling Non-point Source Contributions of Host-specific Fecal Contamination in San Pablo Bay

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EXECUTIVE SUMMARY

Coastal water quality is affected by increasing anthropogenic uses. Due to a range of water-related recreational activities, microbial contamination is of particular concern to public health officials. Decision makers are plagued with two major difficulties: (i) determination of the presence, abundance and diversity of pathogens and (ii) identification of the sources of fecal contamination. Historically, the obstacles associated with detecting and enumerating pathogens lead professionals to rely on traditional indicator organisms like fecal coliforms, *E. coli*, and fecal enterococci. In recent years their use has come under scrutiny due to the realization that indicator re-growth does occur in natural waters, which negates their use as a predictor of recent fecal pollution. Pathogen and microbial indicator concentrations do not correlate in recreational waters. Recent advances in the development and application of molecular tools have demonstrated that they can be used to enumerate pathogens as well as to differentiate between different sources of fecal contamination such as humans and bovine animals.

Further, monitoring alone is sometimes insufficient in providing a clear picture of the fecal contamination of a water body. Sampling of large water bodies in specific (few) locations, and at certain (discontinuous) times, may prove insufficient in capturing and predicting contamination events that may require public health decisions, including beach postings and closures. Also, it generally provides no information on the sources of fecal contamination. 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). It is relatively easy and inexpensive (as compared with intensive field campaigns) to change boundary conditions in a numerical model in order to simulate non-point sources. It is also feasible to introduce new parameters into the numerical model to assess the relevance and importance of a given process. Therefore, mathematical and numerical transport models can in principle be used together with new molecular techniques to characterize the fecal contamination of water bodies by identifying and quantifying non-point sources, and they can predict the distribution of fecal loads in receiving waters.

Based on these considerations, the present project will focus on 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. A major innovation of the study includes the design of quantitative sea bird-specific molecular DNA assays for the purpose of microbial source tracking to enumerate the contribution of estuarine sources to high traditional indicator counts. Such microbial source tracking will be combined with monitoring of specific pathogens including human adeno- and enteroviruses and the causative agent of *Toxoplasma*; it will also employ a fully validated large-volume water filtration method. The working hypothesis in this study states that a significant portion of the fecal contamination in the estuarine environment is due to non-human contributions such as (i) bird droppings and (ii) urban and agricultural runoff during storm events. The quantitative tools to test this hypothesis are largely in place and additional assays for host-specific microbial source tracking will be developed. To demonstrate the utility of molecular and filtration technology in conjunction with a modeling approach we selected San Pablo Bay, on the basis that there is abundant knowledge about the estuarine system and its tributaries at UC Davis.