
Bacterial Sources and Transport in Marin and Sonoma County Estuaries

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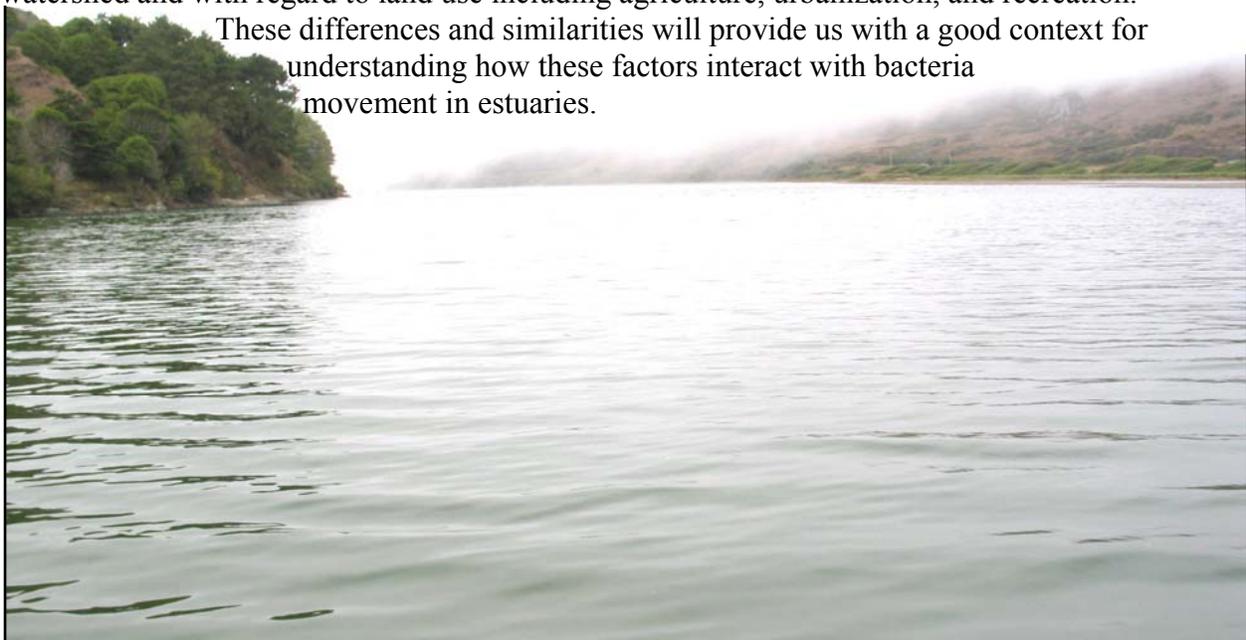
Overview

Beneficial uses of California's bays, estuaries, and near-shore marine environments include shellfish harvesting, swimming, and boating. These beneficial uses are vulnerable to elevated bacterial levels in winter stream flow and suspension of bay or estuarine sediments by tidal currents, stream flow, and wind generated waves. It is very important that water quality monitoring be able to clearly identify sources and reservoirs of bacterial contamination so that remediation efforts such as Total Maximum Daily Load (TMDL) plans and on-farm management practices can effectively reduce pollution of coastal waters. More specifically, when estuaries experience elevated counts of fecal coliforms and *E. coli* during base- or storm-flow conditions, monitoring protocols need to be able to determine if the elevated bacterial counts are due to suspension of estuarine sediments or freshwater inflows from upstream runoff.

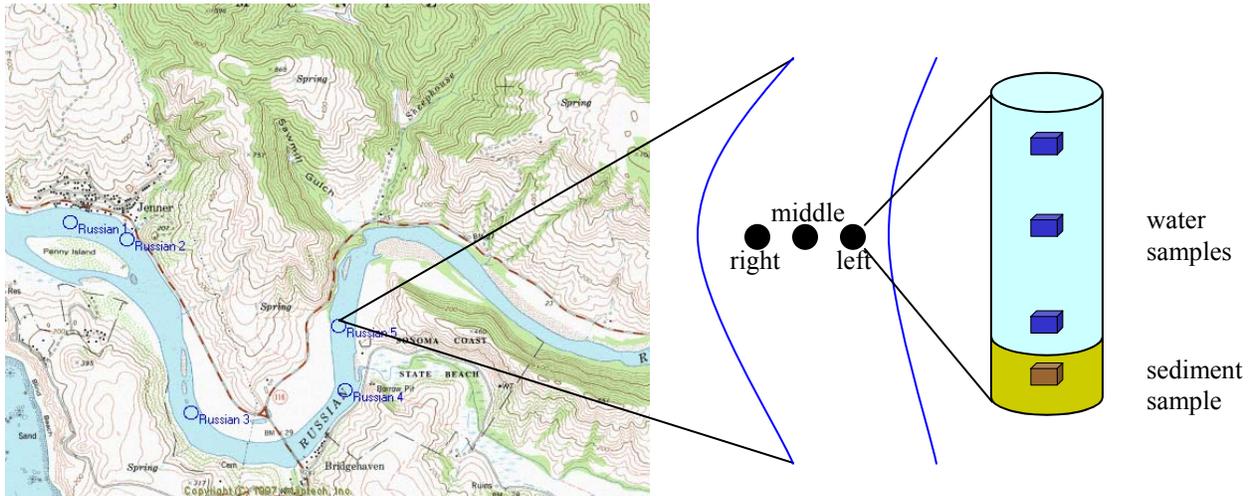
The goal of our study is to develop a comprehensive understanding of these different bacterial sources and develop a water quality monitoring protocol for quantifying sources and transport processes of microbial contaminants (pathogens) in the estuaries. To achieve this goal we are conducting water and sediment sampling and analysis from August 2004 to July 2005 in the Russian River, Salmon Creek, Estero Americano, Walker Creek, and Lagunitas Creek estuaries. We hope this summary provides you with some background information regarding our research project and answers any questions that you may have.

Why were these five estuaries selected? These five estuaries represent a variety of environmental conditions across the coast of Marin and Sonoma Counties. In a general sense, they have similar climate, precipitation, and hydrology. Specifically, this similarity is the result of the Mediterranean climate in California with cool wet winters and dry hot summers. As a result, all five estuaries experience an in flow of freshwater during the winter, flowed by an introduction of salt water in the summer. The five estuaries differ in size, area of contributing watershed and with regard to land use including agriculture, urbanization, and recreation.

These differences and similarities will provide us with a good context for understanding how these factors interact with bacteria movement in estuaries.



Where are samples being collecting? We will collect water and sediment samples from each estuary once a month for ten months. Each estuary will be sampled through a series of five transects. Each transect consists of three sampling locations, right, middle, and left facing downstream. At each location, we will collect three water samples at one foot below the water surface, half the depth of the water column, and one foot above the estuary bottom. A sediment sample will be collected from the estuary sediments at each location.



Map of the Russian River Estuary with the five sampling transect locations identified. Each transect consists of three sampling locations from which three water samples and one sediment sample will be collected.

How will the results from this research be used? The results of this work will be shared with local land owners and managers, resource conservation districts, water quality regulatory staff (e.g., RWQCBs), conservation organizations, watershed groups, and non-profit watershed entities. In addition, we will develop a monitoring protocol to be shared at workshops planned for the Spring of 2006.

What are fecal coliforms and *E. coli*? Bacteria are part of our world and environment, existing in most substances and on most surfaces including our skin. Some of the bacteria that are of significant concern to human health are those of fecal origin. These bacteria and the associated pathogens have the potential to cause disease in human. Indicator bacteria are used as analytical tools to assess this risk of exposure. Fecal coliforms and *E.coli* are two of these indicator bacteria.

Why not conduct research on a specific pathogen or group of pathogens? Testing for a specific pathogen is very expensive and difficult, so water quality investigators often use these more common non-pathogenic bacteria to indicate the potential presence of these pathogens.

How can you tell one bacteria from another? There is increasing ability through the development of new laboratory methods to identify different strains of bacteria from another. These methods rely on genetic differences between bacterial communities. We will be using a method referred to as BOX-PCR to generate a fingerprint of selected individuals from each *E. coli* community (water and sediment). This method of DNA fingerprinting targets interspersed conserved repetitive DNA elements present in multiple copies throughout the *E. coli* genome.

Amplifying the distinct genomic regions located between these repetitive DNA elements generates the distinctive pattern that distinguishes one strain or community from another.

Is sediment really a source of bacteria? Recent research has documented that sediment can be a medium on which bacteria can survive and be transported through a watershed. One of the goals of this project is to measure the amount of fecal coliforms and *E. coli* contained in the bottom sediments of estuaries. Large storm events and wave action have the potential to suspend these sediments and elevate bacteria concentrations in these waters.

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