

## Microbial gene expression in the Columbia River

### ISSUE

Biogeochemical cycles in the Columbia River (CR) coastal margin are influenced by the river's freshwater influx and by coastal upwelling, which cause large physical and chemical gradients in water column habitats. They also present very different sources of nutrients and biota, and allow development of abundant microbial communities in the estuary and plume during mixing of coastal seawater with river water. The communities are influenced by water chemistry (which varies seasonally), oceanographic conditions, and transport from both the river and adjacent coastal ocean. Phylogenetic diversity of the CR microbial communities has been analyzed for both bacteria and archaea. Microorganisms respond to changing environmental conditions by expressing (that is, turning on) suites of metabolic genes necessary for survival. This study was a first step toward understanding how different microbial populations respond, at the transcriptional level, to environmental gradients in the CR coastal margin both in space and time.

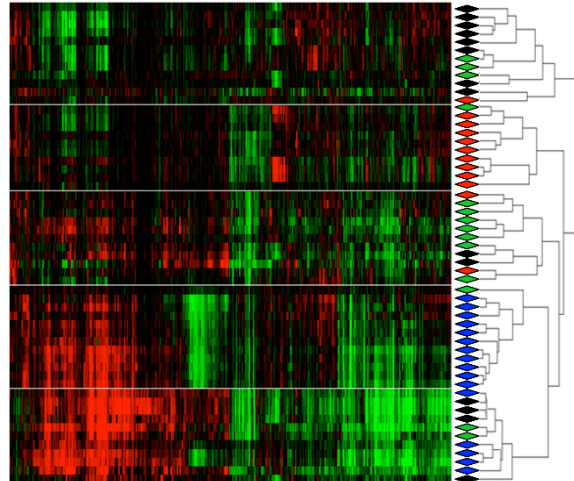
### APPROACH

Drs. Mariya Smit and Holly Simon applied DNA microarrays to generated gene expression profiles of prokaryotic assemblages from the CR coastal margin. Total RNA from a suite of 64 water samples collected during 4 different sea-sons of 2007 and 2008 was converted to labeled complementary DNA, and hybridized to CombiMatrix oligonucleotide microarrays that contained a 2240 probe set designed from ~300 sequenced microbial genomes. For each season, differential gene expression was evaluated in estuary, plume, and adjacent coastal ocean samples relative to the tidal freshwater baseline. The generated gene expression patterns were analyzed in the context of the environmental data-base ([www.stccmop.org/datamart](http://www.stccmop.org/datamart)).

### FINDINGS

The observations revealed that diatoms are susceptible to infection by chytrid fungi in the Columbia River Coastal Margin (CRCM). Infected cells often appeared devoid of contents, indicating that infections could account for diatom mortality. Chytrids occurred in at least three diatom species (*Aulacoseira italica*, *Fragilaria crotonensis*, and *A. formosa*) in the river and estuary from April until at least September – ongoing sampling will reveal whether the

infections persist through the winter months. The specificity of the parasite-host relationship is not clear. Intriguingly, infected diatom cells were also observed within the estuary turbidity maximum, providing a potential mechanism by which chytrid populations may be retained in the system to carry out subsequent infections.



*This 2D clustering diagram shows seasonality in gene expression patterns of the analyzed samples (diamonds colored blue for April, green for June, red for August, and black for November). The heat map shows gene expression ratios calculated for each gene in each sample relative to the seasonal average expression in freshwater. The data are colored red for upregulation and green for down-regulation (with a 4-fold saturation threshold).*

### IMPLICATIONS

The existence of stable, repeating gene expression patterns over relatively long temporal and spatial gradients suggests that expression of microbial genes may vary in predictable ways, and, therefore, prove useful as a “sentinel” for environmental change.

### MORE

A manuscript describing this work and its environmental significance more explicitly has been written and submitted (Smith et al., *Environmental Microbiology*). It is co-authored by a CMOP summer intern who participated in this work. An oral presentation was presented at the Coastal and Estuarine Research Federation 20th Biennial Conference (11/5/2009). The microarray data were made accessible at the Gene Expression Omnibus (GEO) public database with the accession number GSE18303 ([www.ncbi.nlm.nih.gov/projects/geo/](http://www.ncbi.nlm.nih.gov/projects/geo/)).

