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Activity: Abstract

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Microarray analysis of bacterial and archaeal gene expression in the Columbia River coastal margin

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Abstract:

Background: Microbial populations mediate the impact of high gradient regions on ecological function and productivity of the Columbia River coastal margin (CRCM). To address questions about microbial responses to changing environmental conditions, gene expression profiles were generated for archaeal and bacterial assemblages in the CRCM. **Methods:** Total RNA was isolated from a suite of 64 water samples collected during 4 different seasons over two years. The RNA was converted to labeled cDNA, and hybridized to CombiMatrix DNA microarrays against a set of 2240 oligonucleotide probes. The probes were designed from 300 microbial genomes for functional genes involved in nitrogen and carbon metabolism, housekeeping, and light perception. **Results:** In general, the highest similarity in gene expression patterns was observed for samples collected close together in space and time. For each season, differential gene expression was evaluated in the estuary, plume, and adjacent coastal ocean relative to the tidal freshwater baseline. Analysis of these data together with environmental metadata indicated that bacterial and archaeal gene expression patterns in the CRCM were associated with complex environmental factors that varied with seasons. Trends involving light, phytoplankton biomass, proximity to the river mouth, and availability of nitrate, phosphate, and dissolved organic carbon were observed in the gene expression profiles. For example, two functional gene groups involved in nitrate assimilation and dissimilatory nitrate reduction produced enhanced microarray signals coincident with higher nitrate to phosphate ratios observed in the river in spring. **Conclusions:** 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, may be a useful indicator of environmental change. Overall, our results indicate that environmental data and gene expression data may correspond in ways that facilitate our understanding of the drivers - physical, chemical, and microbial - of estuarine processes.

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