

Microarray analysis of microbial gene expression in Columbia River estuary, plume, and coastal ocean

Maria W. Smith^{*}, Lydie Herfort^{*}, Kaitlin Tyrol^{*}, Victoria Campbell^{*}, Byron C. Crump^{**}, Peter Zuber^{*}, Holly M. Simon^{*}

^{*}The Center of Coastal Margin Observation & Prediction (CMOP), Oregon Health & Science University, 20000 NW Walker Road, Beaverton, OR 97006 USA.

^{**}University of Maryland Center for Environmental Science, Horn Point Laboratory, Cambridge, Maryland 21613 USA.

The major goal of this project is to provide detailed molecular portraits of microbial functions along the Columbia River coastal margin. This is being done through characterization of temporal and spatial variations in prokaryotic gene expression across high gradient regions. This information will be used to identify microbial sentinels that foretell of climate-induced or anthropogenically-mediated impacts on Pacific NW coastal margins. DNA microarray analysis was performed for 66 water samples collected along salinity gradients in 2007 and 2008. These samples were analyzed for gene expression changes associated with (a) seasonal differences, and (b) transition from freshwater to the coastal ocean. Oligonucleotide probes were designed for 5000 genes involved in carbon and nitrogen metabolism in bacteria and archaea. A subset of 2240 probes selected for high signal-to-noise ratios was synthesized on custom CombiMatrix microarrays. Gene expression patterns were analyzed by calculating expression ratios for each gene in individual samples versus a baseline sample of pooled freshwater across all 4 seasons. Based on similarity of gene expression patterns, all samples separated into two major clusters corresponding to sampling season. One cluster was dominated by August 2007 and June 2008 samples, and the other contained November 2007 and April 2008 samples. In contrast to the striking similarities observed in gene expression patterns during similar seasons of different years, the conspicuous differences between April 2008 and June 2008 samples, collected only 1.5 months apart in the same year, were unexpected. Our observations suggest that microbial gene expression along the Columbia River coastal margin may be represented by a relatively small number of different seasonal states that are stable year-to-year. If true, such stability should facilitate recognition of deviations from normal expression patterns caused by climatic events or anthropogenic factors.