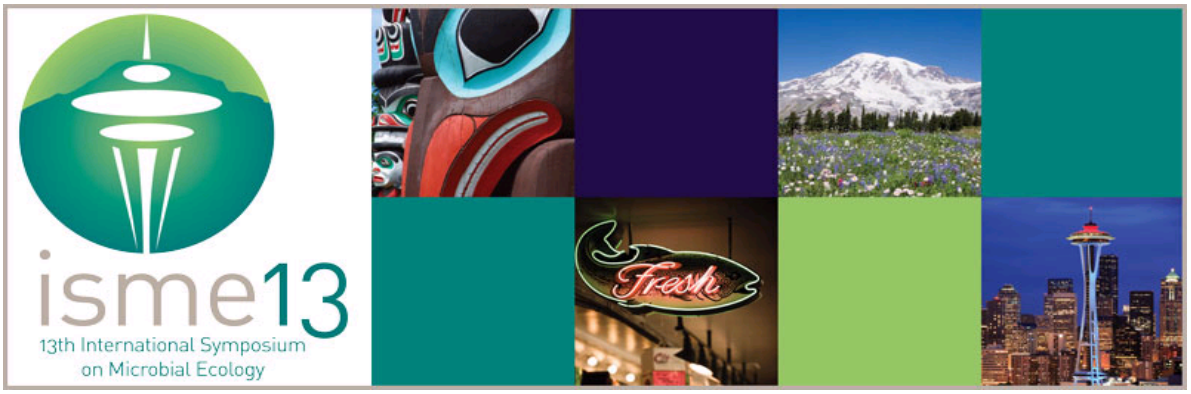
Acknowledgement - The 13th International Symposium on Microbial Ecology 1579033



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Abstract Title (max 150 char):

MICROARRAY ANALYSIS OF MICROBIAL GENE EXPRESSION ASSOCIATED WITH NITROGEN CYCLING IN THE COLUMBIA RIVER COASTAL MARGIN

Abstract text (max 2000 char):

The Pacific Northwest coastal margin is a highly biologically productive system, and the Columbia River system makes an important contribution to this productivity. As the second-largest river in the United States, the Columbia River has profound influence on biogeochemical processes occurring in the coastal ocean through the delivery of nutrients in a massive plume. Physical and chemical

gradients are established in the coastal margin due to varying seasonal discharge volumes, upwelling events, tidal mixing and formation of estuarine turbidity maxima zones. These gradients influence microbial community composition and metabolic activities. We investigated metabolic properties of microbial populations involved in nitrogen cycling (nitrogen fixation, assimilatory nitrate reduction, dissimilatory nitrate reduction to ammonium, denitrification, and nitrification) using microarray analysis of gene expression. Thus, over 80 coastal margin water samples were collected during spring pre-freshet and peak freshet, summer, and late fall in 2007 and 2008; for each, physical, chemical and biological parameters were analyzed. Total RNA was isolated from each sample, reverse-transcribed into cDNA and hybridized to custom-synthesized DNA oligonucleotide microarrays. Microarray probes were designed for 5000 genes involved in carbon and nitrogen metabolisms in environmental bacteria and archaea. Both empirical and bioinformatics approaches were used to determine specificity of the probe set. Hybridization to pooled water samples was done to select a final set of 2226 probes for microarray synthesis, 1648 of which were genes involved in nitrogen metabolism. The microarrays were then hybridized with individual water samples to assess differential microbial gene expression across environmental gradients. Expression profiles of genes involved in nitrogen cycling provide the basis for testable hypotheses about related biogeochemical activities in the Columbia River coastal margin.

Abstract Category

22 Major Biogeochemical Cycles

Presentation Preference

Poster Presentation

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