

2010 Ocean Sciences Meeting

You may print by clicking on this  button. To return to the previous page, close this browser window or click the 'X' button in the top right corner of the page.

ID# BO25F-11

Location: Poster Hall E

Time of Presentation: Feb 23 5:30 PM - 7:00 PM

A Comparison of Eukaryotic Diversity along a River-to-Ocean Gradient using Molecular and Traditional Tools

P. Kahn^{2, 1}; *L. Herfort*^{2, 1}; *T. D. Peterson*^{2, 1}; *L. McCue*^{3, 2}; *P. Zuber*^{2, 1}

1. Oregon Health and Sciences University, Beaverton, OR, United States.
2. Center for Coastal Margins Observation and Prediction, Beaverton, OR, United States.
3. Pacific Northwest National Laboratory, Richland, WA, United States.

Advances in environmental nucleic acid analysis have fostered a greater understanding of bacterial, archaeal, and viral community structures within coastal margins. However, application of molecular genetic approaches to studying eukaryotic microbial populations is a more recent undertaking. Traditional methods, such as microscopy and pigment analysis, have long been used to characterize larger phytoplankton and heterotrophic protist (5-100µm) community composition. These morphological tools are often unable to distinguish between nano and picoeukaryotes (0.2-5 µm) and thus may lead to an underestimation of diversity. Classification based on pigments is restricted to photosynthetic organisms, and only applies to differences at the class level. Conversely, molecular tools, such as rDNA cloning, have biases inherent in nucleic acid extraction and amplification that may cause misleading assessments of presence and abundance. As the field of eukaryotic metagenomics moves forward, it is important to ground-truth molecular tools with traditional methods to determine relative limitations and strengths of both approaches.

In this study molecular, chemical, and microscopic methods were used to assess the eukaryotic microbial diversity across the Columbia River estuary and coastal zone. Water samples were collected at 0 PSU in the Columbia River, 15 PSU in the estuary, 28 PSU in the plume, and 32 PSU off the coast during April, June, and August of 2007 as well as April, June, July, and September of 2008. Nucleic acid was extracted from the samples for construction of 18S rDNA clone libraries that were subject to sequence analysis, while microscopic cell counts were performed for each sample. Both methods showed that diatoms were the most numerous class of eukaryotic organisms and that a diatom to dinoflagellate transition was evident in the late summer-early fall. However, genus-level resemblances between the clone library and microscopically determined assemblages were weak with only an average of 28% Bray-Curtis similarity. Broadening the comparison to class-level increased the average Bray-Curtis similarity to 50%. Indices of diversity were also higher at the genus-level using cell counts compared to clone libraries, while clone libraries showed a higher degree of evenness. Molecular analysis also revealed the recurring presence of *Katablepharis japonica*, a 5 µm heterotrophic protist that dominated the 15 PSU clone libraries in both April 2007 and 2008. This is likely an important primary consumer during this time that was previously unrecorded in the Columbia River estuary. The detection of *Katablepharis japonica* shows that molecular tools provide essential information about eukaryotic microbial community structure and diversity that microscopy alone does not identify.

Contact Information

Peter Kahn, Beaverton, Oregon, United States, 97006, [click here](#) to send an email