

**WORKING GROUP REPORT**  
**“What is known about bacterial community composition  
(diversity) and its variability in space and time”**

This working group focused on the question, “What is known about bacterial community composition (diversity) and its variability in space and time”. To some extent we also addressed environmental controls on bacterial community structure. The room was packed during much of the morning session (SRO), but the crowds dwindled away after lunch, after the presentations were finished and when it was time for group discussion. The hardy few who stayed talked about cross-site activities and post-ASM proposals for further work. This discussion is noted further below.

Presentations focused on brief surveys of bacterial community composition and ecology at various LTER sites including:

<b>Site</b>	<b>Presented by</b>	<b>Topic</b>
PIE	John Hobbie	Seasonal community succession in Plum Island Estuary
KBS	Tom Schmidt	Physiology, functional properties of bacteria and specific groups, esp denitrifiers.
NWT	Liz Costello	Alpine Microbial Observatory. Community composition, identification of novel phylotypes, dominants, etc. Broad overview presented
NWT	Ryan Jones	Cross-site comparison of KNZ, Peruvian Amazon rainforest, Mojave desert. Emphasis on methods and bacterial species concept.
NTL	Stuart Jones	ARISA assessments of community composition, relationships with phytoplankton species succession in NTL lakes
SEV	Bob Sinsabaugh	Focus on fungal distributions and Fungal denitrification.
MCM	John Priscu	Extensive overview of study site and MCM Microbial Observatory
SBC	Craig Carlson.	DOC dynamics in SB anell, kelp forest as DOC supply, DOC lability
GC	Tim Hollibaugh	Overview of microbial projects at GCE/SIMO. Community characterizations, Spartina-fungal associations, specific functional genes
PAL	Hugh Ducklow	Interannual variability in bacteria-phytoplankton coupling in nearshore marginal ice zone
ARC	George Kling.	DOC/bacteria interactions across the landscape at Toolik Lake site

Following the talks and lunch, discussion centered on several topics. Several participants noted that there is no acceptable or standardized way to store, retrieve and compare genomic sequence data between sites using searchable, queryable database tools. One way to catalyze cross-site comparison and synthesis is to develop such methods of information exchange. GENBANK is not suitable for this purpose.

A related issue is to derive common protocols for conducting molecular genomic surveys of bacterial diversity at different sites. One way to start making consistent surveys across diverse sites is to focus on particular genes responsible for specific, well-characterized biogeochemical processes. Nitrifying bacteria present one example of a relatively well-known and frequently studied group that could be pursued at all aquatic and terrestrial sites.

In general there is been little effort to link microbial research across sites. John Hobbie stated that LTER cannot meet Grand Challenges in Ecology without better attention to microbial processes. There was some enthusiasm for reinvigorating the LTER Microbial Ecology Committee and drafting a new White Paper, and for continuing to investigate better IM tools for answering questions across sites and Microbial Observatories. We resolved to submit a post-ASM mini-proposal to the LNO to hold a workshop to support further discussions and spur some work in the area. Tom Schmidt volunteered to take the lead.

The session broke up when several participants had to leave for the Science Council Meeting.

## LIST OF PARTICIPANTS AND REPORT

**Working Group Title:** Bacterial diversity and dynamics: cross-site contrasts, comparisons and synthesis

**Working Group Organizers:** Hugh Ducklow, Tim Hollibaugh, John Hobbie and George Kling

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