

## Future of LTER Fungal/Bacterial Environmental Genomics Studies

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Long-term ecological studies have provided meaningful information on diversity and ecology of animals, plants, fungi and bacteria, and the impact of climate change on these communities. In the last decade, new genomic technologies have emerged that are helping with studies of microbial diversity in different ecosystems and substrates. Many of these studies have been undertaken at different LTER sites but little has been done to coordinate cross-site studies and to establish protocols for data collection, management and dissemination. In June 2011, a group of researchers and students met at the Sevilleta Field Station for the first LTER fungal/microbial genomics meeting to exchange information and discuss problems and opportunities.

A total of 43 participants attended the two sections, representing 17 LTER sites. During the first two hours of the working groups, 15 mins. presentations were given. The presentations were:

1. Introduction - Sharon A. Cantrell
2. Microbial/Fungal Genomic Working Group - Summary - Andrea Porrás-Alfaro and Don Natvig
3. Diversity and function of decomposer fungi in a changing climate- Linda van Diepen
4. SRB across ecosystems of Puerto Rico - José R. Pérez-Jiménez
5. Microbial diversity and function in the McMurdo Dry Valleys, Antarctica – Cristina Takacs Vesbach
6. The plant rhizosphere as a habitat for microbial species interactions and coevolution- Dan Schlatter
7. Fungal plant-systems: Sevilleta fungal communities and new tools of analysis - Andrea Porrás-Alfaro

The second two hours of the working group concentrated in the discussion of the following questions:

1. Where do we want to be as a group within the LTER in the next decade?
  - It was agreed that there will be a permanent Microbial WG among LTER sites.
  - We need to take advantage of the major strengths of the LTER including the long-term manipulation experiments to leverage the need to do LTER microbial research.
2. How can we facilitate cross-site studies?
  - Need of common experiments and common methods. We need to take advantage of common experiments at the different LTER sites.
  - Several cross site studies were proposed:
    - Evaluate temporal patterns
    - Evaluate disturbance regime
    - Evaluate nitrogen fertilization
    - Compare archive DNA and soil samples
  - Also, the WG proposed that it is better to archive DNA samples than the actual sample.
  - Is it reliable to store samples in -80C or -20C? What should we save? How much? What kind of metadata do we need?
  - The WG proposed that LTER sites should address ecological questions based on long-term microbial data.
  - There is a need to evaluate the resources available for cross-sites studies.
  - The WG will evaluate the possibility of developing a proposal to LNO for a WG to work toward the development of a RCN proposal.

3. How can we make our presence and simplify genomic data presentation at LTER site webpages?
  - In terms of database, the WG agree to follow the Genomic Standard Consortium MIMARKS specifications. The Genome Consortium needs more input from ecologist to facilitate deposition of LTER genomic and metagenomic data in databases.
  - It was agreed that microbial ecologists should prepared short descriptions about the microbial research done at their LTER sites in order to increase our presence and disseminate better our work.
  - Also, it is important for each LTER site to be aware and request information to those scientists that are not part of LTER but conduct research at LTER sites.

Recommendations from NSF program officer Matt Kane:

1. What can be done with long term data?
2. Seek funding from different programs for example: RCN grant to coordinate sampling and collecting microbial LTER data. There are other opportunities like the Dimensions of Biodiversity Programs and EAGER proposal.
3. Develop microbial questions to address methods and standards for collecting, processing samples, sample storage, etc.
4. Publish information at LTER sites
5. Establish partnerships with people using the new methods to study microbial diversity.

Potential Products:

1. NSF program officer Matt Kane suggested seeking funding from different programs for example: RCN grant to coordinate sampling and collecting microbial LTER data. There are other opportunities like the Dimensions of Biodiversity Programs and EAGER proposal.
2. We organized a pilot project to evaluate the integrity of samples that have been in the -20C for several years. Cristina Takacs-Vesbach will coordinate this effort.
3. We need to identify LTER common manipulation experiments for a potential RCN to coordinate long-term cross-site comparisons of fungal and bacterial communities. We need to name the person that will coordinate this effort.
4. We are currently working on a white paper to summarize major contributions of LTER microbial genomics research. Porrás-Alfaro is coordinating this effort.