

REPORT: LTER FUNGAL/MICROBIAL GENOMICS WORKING GROUP MEETING 2011

DATES: JUNE 16-18, 2011

Hosted by THE SEVILLETA LONG-TERM ECOLOGICAL RESEARCH PROGRAM AND SEVILLETA FIELD STATION

ORGANIZING COMMITTEE: Andrea Porras-Alfaro, Donald O. Natvig, Sharon Cantrell, Cristina Takacs-Vesbach, Robert Sinsabaugh

Summary:

This workshop provided an opportunity for LTER fungal/microbial scientists to share current research activities, explore challenges and opportunities to develop new collaborative research questions, and define priorities in terms of microbial/fungal research in the field of ecological genomics.

Goals:

The main objectives of this working group were:

- 1) Review microbial studies in ecological genomics including manipulation experiments along latitudinal gradients and across time scales. Special attention was given to the potential for such studies to inform climate-change predictions. The symposium considered contrasting ecosystems including terrestrial and aquatic systems and all microbial guilds (Fungi, Bacteria and Archaea).
- 2) Discuss the problems and opportunities inherent in coordinating and funding future cross-site collaborations in microbial ecological genomics. We also discussed approaches to annotation and deposition of molecular datasets and metadata.
- 3) Create a draft combination synthesis and position manuscript for publication. We expect this manuscript to inform LTER and the scientific community about accomplishments of LTER in terms of fungal/microbial ecology and future directions.

Workshop summary:

The workshop consisted of a number of short talks given by participants (see program below). In addition, we had two discussion sessions on June 17 and June 18, 2011. The following is a summary of topics discussed and the main points derived from discussions.

1. Microbes (fungi and bacteria) are the only life form common at all LTER sites, and they should become a core measurement at all LTER sites to allow the study of long-term trends. Microbial studies at LTER sites have value over

- such studies at non-LTER locations because LTER provides opportunities for biological replication, standardized methods for handling data and metadata, manipulation experiments, and long-term site histories.
2. Since microbial community measurements are now cost effective, we need to concentrate on improvement of metadata as well as on experimental design, including definition of number of replicates and standardization of protocols. Where do we archive samples? Do we have facilities and infrastructure? How do we handle large datasets that are being generated by diverse groups? Is it possible to compare them?
 3. LTER microbial/fungal scientists need to take advantage of long-term manipulations that make LTER sites unique.
 4. As a group we will put together a synthesis paper that will take into account the five LTER core areas in relation to microbial/fungal genomics studies, and we will make recommendations about future directions of LTER in terms of microbial/fungal research. This synthesis paper will provide new guidelines for potential target areas and ideas for potential collaborations for future proposals to increase microbial/fungal studies at the LTER sites including a potential sequencing proposal to JGI.
 5. Coordination with other programs such as NEON, Terragenome and the Earth Microbiome project will open new opportunities for sequencing efforts and will avoid replication of work. There are seven LTER sites co-located with NEON sites.
 6. Main points that remain to be addressed:
 - a. Where do we want to be as a group in the next 10 years? It is important to define priorities and goals for microbial/fungal sequencing taking advantage of current evolving technologies. What constitute the next generation of questions that LTER microbial/fungal groups should be addressing? How can we move from survey to function?
 - b. How do we establish more cross-site comparisons between aquatic/ terrestrial systems? There is a need for more studies in transition zones.
 - c. There is a need to define core reference genomes representative of different ecosystems that will allow a deeper understanding of keystone and core microbial species and the ecosystem services that they provide.
 - d. There is a need for the use of new technologies such as single genomic sequencing and more expression studies (i.e. transcriptomics, proteomics) to acquire a deeper understanding of the function of these microbial communities and how they respond to environmental changes. There is also a clear need to target other poorly studied groups such a protozoans, slime molds, etc.
 7. We are currently working on a synthesis paper of LTER fungal/microbial research and a summary of recommendations and future directions to advance microbial

research at all LTER sites taking into account main points discussed during this working group meeting.

Main contributions:

1. We supported 34 participants from 19 different institutions including JGI, RDP, NEON, SNL and LANL. The group included six students and three postdoctoral associates. The list of participants, abstracts and details of the program can be found at:

<https://sites.google.com/site/ltermicrobialgenomics/home>



LTFR Fungal/Microbial genomics Working group 2011

2. Presentations: Day one and two included a total of 17 oral presentations about projects at different LTER sites. In addition, there were 9 poster presentations.
3. Website development: A website was developed with information about the workshop and additional information will be added about the meeting outcomes: <https://sites.google.com/site/ltermicrobialgenomics/home>

Budget report: We supported travel of 19 participants with lodging and food for a total of 34 participants.

Additional Support

The organizing committee would like to thank Jennifer Johnson, Anthony Rigoni, George Garcia, Miriam Hutchinson for their helpful support. We would also like to thank the support of the LTER network office, NSF, the Sevilleta Field Station, University of New Mexico and Western Illinois University.

AGENDA – Main talks and discussions

TIME	ORAL PRESENTATIONS
June 16 th , 2011	
4-6 pm	Participants Arrival and Registration
6 pm	Dinner
7:30-8:30 pm	Don Natvig – Opening Remarks Bacterial biodiversity and function in a cold desert ecosystem Cristina Takacs-Vesbach, David Van Horn, Lydia Zeglin, Shannon Fitz Patrick, Michael Gooseff, and John Barrett
8 pm	Reception
June 17 th , 2011 – Oral presentations	
7:30-8:30 am	Breakfast
8:50 am	Introduction
9:00 am	Plant host and plant community diversity impact soil Actinobacterial community structure Matthew G. Bakker, James M. Bradeen, and Linda L. Kinkel
9:15 am	Fungal and microbial community change in response to long-term warming of Arctic tundra Julie R. Deslippe , Martin Hartmann, Suzanne W. Simard, William W. Mohn, and John E. Hobbie
9:30 am	The Luquillo LTER: Understanding effects of climate and land use Sharon A. Cantrell and D. Jean Lodge
9:45 am	Species Diversity of Lava Cave Microbial Mat Communities from the Azores, New Mexico, and Hawai'i Diana E. Northup, J.J.M. Hathaway, M.G. Garcia, M. Moya, M.N. Spilde, F.D. Stone M.L.N.E. Dapkevicius, C. Riquelme
10:00 am	Characterizing the effect of variable precipitation events on root-associated fungal communities on <i>Sporobolus cryptandrus</i> Jose Herrera
10:15 am	COFFEE BREAK
10:45 am	Different environmental factors drive continental-scale eukaryotic and prokaryotic communities in soil Kathryn M. Docherty , Rachel E. Gallery, Rebecca Hufft-Kao
11:00 am	Microbial community structure in an agricultural land use gradient and its impact on nitrous oxide fluxes Tracy K. Teal , Vicente Gomez-Alvarez, Thomas M. Schmidt
11:15 am	Core Organisms and Functions of the Diverse Rhizosphere Microbiome Ari Jumpponen
11: 30 am	Soil Microbial Communities of the H.J. Andrews LTER Site David D. Myrold
11: 45 am	How can metadata standards help the Fungi network Inigo San Gil
LUNCH	12 – 1:40 pm

1:45 pm	Metagenomes with millions of short reads: Current capabilities and challenges <u>Patrick Chain</u>
2:00 pm	Messing with microbes in the boreal forest: a summary of soil fungi studies and manipulations in the Bonanza Creek LTER <u>Lee Taylor</u>
2: 15 pm	Assessing the role mycorrhizal fungi in limiting migrations of interior Douglas-fir and western larch across a latitudinal gradient in British Columbia <u>Suzanne Simard</u> and <u>Brendan Twieg</u>
2: 30 pm	Exploring the biogeography of soil microbial communities at the continental scale <u>Noah Fierer</u>
2:45 pm	BREAK
3:15 pm	Microbial Inventory Research Across Diverse Aquatic LTERS: MIRADA-LTERS <u>Linda Amaral-Zettler</u>
3: 30 pm	The Ribosomal Database Project and Community Standards <u>James Cole</u>
3:45 pm	Fungal Genomics Program at the DOE Joint Genome Institute <u>Robin Ohm</u>
3:30-6pm	Discussion: Potential for new cross-site studies and synthesis
6-9 pm	Poster Session and Dinner
June 18 th , 2011 – Discussion	
7:30-8:40 am	Breakfast
8:50-11:30 am	Discussion Sessions and Planning Groups <ol style="list-style-type: none"> 1. Data management, annotation, metadata 2. Funding strategies and new data acquisition 3. Other topics
11:45-4pm	Lunch to go and LTER Sevilleta Tour

LIST OF POSTERS:

1. Soil fungi: broad-scale ecological patterns and co-occurrence with soil bacteria. Scott T. Bates, Christian L. Lauber, William A. Walters, J. Gregory Caporaso, Rob Knight and Noah Fierer
2. Applications of TRFLP to the study of fungal and bacterial communities in a subtropical rain forest Sharon A. Cantrell
3. Community Profiling of Ammonia-Oxidizing Archaea across Mangroves in Puerto Rico A. Carazo-Carrión, DL Laureano-Córdoba and José R Pérez-Jiménez
4. Root associated fungal communities in two co-dominant plants in an alpine tundra ecosystem Sarah Hicks, Andrea Porras-Alfaro, Katherine Suding, Robert Sinsabaugh
5. Richness and Endemicity of Sulfate-Reducing Bacteria in Neotropical Environments. Laureano-Cordova DL, Latorre-Castro LO, Rodríguez-Ortiz B, Rodríguez-Colón M, José R. Pérez Jiménez
6. Automated Classification of fungal communities. Kuan-Liang Liu, Gary Xie, Stephanie Eichorst, Nick Hengartner, Cheryl R. Kuske, Andrea Porras-Alfaro
7. Semiarid grasslands soil and fungal diversity and community structure. Andrea Porras-Alfaro, Robert Sinsabaugh, Jose Herrera, Donald Natvig
8. Metatranscriptomic inventory of rhizosphere soils in an arid grassland under global environmental change scenarioSAmy Jo Powell, Donald O. Natvig, Andrea Porras-Alfaro, Joanna Redfern, Miriam Hutchinson, Kylea Odenbach, Susannah Tringe, Edward Kirton, Eric Ackerman, Blake Simmons, Scott Collins, Robert Sinsabaugh, Diego A. Martinez, Chris Detter, Ralph A. Dean, Jon Magnuson, Randy Berka
9. Nitrogen amendments have predictable effects on soil microbial communities and processes: A cross-biome experiments. Kelly S. Ramirez, Joseph M. Craine, Noah Fierer