

Third Year Committee Report

Sarah Stevens, McMahon Lab
Meeting: July 8th, 2015 in MSB 5503

Research Progress

I currently have a manuscript submitted on the results of my analysis of 30 genomes from metagenomes (GFMs). I mapped the reads from our metagenomic time series of Trout Bog to the GFMs. From the mapping I was able to extract coverage and single nucleotide polymorphism (SNP) data through time. We found evidence for both genome-wide and gene-specific sweeps depending on the sequence-discrete population investigated. I am also currently working on a manuscript concerning the population dynamics of the ubiquitous and abundant freshwater bacterium *acI*. We have 14 single cell genomes (SAGs) from this clade, representing 3 lakes and X tribes. Since these genomes come from a single cell and not an assembly of many cells, like the GFMs, we shredded the genomes and mapped them against each other in order to understand how their relationships would hold up in our metagenomic time series. We found that SAGs from different tribes do not map well to each other. When we mapped reads from the metagenomic time series of Mendota, we found that only SAGs collected from the same lake were representative of the populations in the lake. We also found that members of the same tribe represent ecologically distinct populations in the lake.

Publications

Bendall, M. L.*, **Stevens, S. L. R.***, Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... Malmstrom, R. R. (*submitted*). Genome-wide selective sweeps and gene-specific sweeps in natural bacterial populations.
*Equal contributors

Garcia, S. L.*, **Stevens, S. L. R.***, Crary, B., Martinez-Garcia, M., Oyserman, B., Stepanauskas, R., Woyke, T., Tringe, S. G., Andersson, S., Bertilsson, S., Malmstrom, R., McMahon, K. D. (*in prep*). Genetic populations of abundant and uncultivated freshwater actinobacteria inferred from single cell genomes and metagenomes. *Equal contributors

Stevens, S. L. R., Hamilton, J. J., McMahon, K. D. (*in prep*). Freshwater GFMs and SAGs from the *betI* lineage. **Stevens, S. L. R.**, Hamilton, J. J., McMahon, K. D. (*in prep*). Freshwater GFMs and SAGs from the *BetII* lineage. **Stevens, S. L. R.**, Hamilton, J. J., McMahon, K. D. (*in prep*). Freshwater GFMs and SAGs from the *BetIV* lineage.

Oral Presentations

"Genome-wide Selective Sweeps in Natural Bacterial Populations Revealed by Time-series Metagenomics." 15th International Symposium on Microbial Ecology. August 24, 2014. Seoul, South Korea

"Genome-wide and Gene-specific Selective Sweeps in Freshwater Bacterial Populations Revealed Using Metagenomics." 14 Symposium Society for Aquatic Microbial Ecology. August 2015. Uppsala, Sweden

Poster Presentations

ISME

Microbial Population Biology Gordon Conference

SciMed GRS Poster Session 2014

JGI UGM?, JGI MGM? Raper Symposium 2013?, SciMed GRS 2013?

Professional Development

- Software Carpentry Instructor Training - May 2015
- Helped teach two workshops on campus and hope to instruct more this year.
- Molecular Microbial Ecology and Evolution(MoMiEE) support group - Started Nov. 2014 - Co-chair
- Plan and facilitate our monthly meetings, organize our webpage, and started a biweekly Python study group.
- MoMiEE Python Study Group - Started Dec. 2014 Chair
- Plan and facilitate our bi-weekly meetings.

- Data Carpentry Hack-a-thon - Mar. 2014
- Helped to create instructional material for a genomics workshop

Committees and Outreach

- MDTP Recruiting Committee 2014-2015
- Illinois Mathematics and Science - Academy Intersession Instructor - Bioinformatics Basics, Microbial Evolution and Ecology - Jan. 2015
- Nuestro Mundo Science Night Volunteer - Apr. 2015