Third Year Committee Report

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

Research Progress

Over the past year I have worked on tracking a set of thirty sequence-discrete populations from Trout Bog, as they are represented by genomes assembled from metagenomes(GFMs), using 63 metagenomes from 6 of years. I called single nucleotide polymorphisms (SNPs) and looked for genes gained or lost by the populations. One genome showed a genome-wide sweep of diversity through the time series. Other genomes show evidence of past gene-sweeps, regions of statistically significant low diversity. From these results, we have propose that diversity within different co-occuring populations may be controlled by different mechanisms(recombintaiton vs. selection). I currently have a manuscript submitted to ISMEJ on the results of this analysis.

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 three lakes and five tribes. We mapped reads from the Lake Mendota time series as 5 of the SAGs are from Lake Mendota. In order to understand how these SAGs would map to one another, we shredded the genomes and mapped them against each other. We found that SAGs from different tribes do not map well to each other. In fact, even SAGs from the SAME tribe don't always map well to each other. When we mapped reads from Lake Mendota to the SAGs, we found that SAGs from collected from different lakes showed a different distribution of identity among the hits. This isn't surprising as the population represented by the SAG has diverged from the allopatric population present in Lake Mendota.

New Questions

Are there related sequence-discrete populations in TB and CB? How closely related are they? Do they share a common gene pool? We now have GFM's from Crystal Bog, which is of similar location and trophic status to Trout Bog. With these genomes, I will see if there are related populations and how similar they are. I will also investigate if these populations are really separated or if they share a common genepool. I will compare the reference genomes and map reads from the opposite source. From the acI SAGs we can see that reference genomes collected from different lakes do not map with high ANI.

Are all populations sequence-discrete? What do non-seq-discrete groups look like? How does ANI structure of sequence-discrete populations compare between different lineages? Most of the populations we have studied must be sequence-discrete in order to assemble into reference genomes from metagenomes. One of my next goals is to investigate and compare population structures using references not assembled from communities. Using both our single cell genomes, in conjunction with our metagenomes, and other marine datasets of metagenomes paired with single cell and sequenced fosmids, I will investigate population structure. I am interested to see if I can find a population which does not fit the sequence-discrete pattern. I have found some preliminary evidence that LD12 and acTH1 have different structures. Along the same lines, I would like to quantify how the population structure, using ANI, is different for different lineages.

Publications

Bendall, M. L.*, **Stevens, S. L. R.***, Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... Malmstrom, R. R. (*submitted to ISMEJ*). 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 for ISMEJ*). 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 for SIGS*). Freshwater GFMs and SAGs from

the Betaproteobacteria lineage betI.
Stevens, S. L. R., Hamilton, J. J., McMahon, K. D. (*in prep for SIGS*). Freshwater GFMs and SAGs from the Betaproteobacteria lineage betII.
Stevens, S. L. R., Hamilton, J. J., McMahon, K. D. (*in prep for SIGS*). Freshwater GFMs and SAGs from the Betaproteobacteria lineage betIV.

Oral Presentations

Stevens, S. L. R., Bendall, M. L., Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... Mcmahon, K. D. Malmstrom, R. R. 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. https://goo.gl/6iunz0
Stevens, S. L. R., Bendall, M. L., Chan, L.-K., Malfatti, S., Schwientek, P., Tremblay, J., ... Mcmahon, K. D. Malmstrom, R. R. 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

Stevens, S. L. R., Bendall, M. L., ... Mcmahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes. 15th International Symposium on Microbial Ecology. August 24, 2014. Seoul, South Korea. https://goo.gl/qsYL32
Stevens, S. L. R., Bendall, M. L., ... Mcmahon, K. D. Malmstrom, R. R. Dynamics of Sequence-Discrete Bacterial Populations Inferred Using Metagenomes. SciMed GRS Poster Session 2014. Sept. 03, 2014. Madison, WI
Stevens, S. L. R., Garcia, S. Stepanauskas, R. Bertilsson, S. Malmstrom, R. R. McMahon, K. D. Time-resolved Metagenomics Reveals Population Expansion and Contraction in Freshwater Bacteria. Gordon Research Conference on Microbial Population Biology. August 2015.

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
- MDTP Steering Committee 2015-2016
- Illinois Mathematics and Science Academy - Intersession Instructor - Bioinformatics Basics, Microbial Evolution and Ecology - Jan. 2015
- Nuestro Mundo Science Night Volunteer - Apr. 2015