Introduction

* Importance of nutrient cycling in lakes
* Eutrophic vs bog lakes
* How bacteria participate in freshwater nutrient cycles
* We used MAGs to investigate genome-level differences between a eutrophic lake and a bog
* Advantages of genome level analysis is better phylogenetic assignment (can use Phylosift and set of core genes, rather than a single gene that may be frequently transferred or highly conserved) and can identify which genes are contained within the same population
* Disadvantages are incompleteness of genomes, we don’t have every single genome from the lake, no data on eukaryotes, and genomes are from populations rather than individuals

Methods

* Sample collection
* Sequencing + JGI’s sequence analysis pipeline
* Assembly
* Metapathways
* Comparison to other genomes?

Results

* Include broad overview of dataset?

1. Primary production
   1. Mendota has mainly Cyanobacteria, Trout Bog has mainly Chlorobi
   2. The Cyanobacteria use the CBB carbon fixation pathway while the Chlorobi use the reductive TCA cycle (more commonly seen in extreme environments) (well characterized in cultured Chlorobi)
   3. Members of Burkholderiales also have chlorophyll a biosynthesis in both lakes (purple bacteria such as Rhodoferax? Check the tags.)
   4. Aerobic anoxygenic photosynthesis?
2. One-carbon compound metabolism
   1. Methylococcales and Methylophilales found in both lakes
   2. Methylococcales consumes methane, also has nitrogen fixation. Methylophilales cannot use methylamines like previously cultivated strains
   3. Incorporate read coverage data showing abundance over time?
3. Nitrogen metabolism
   1. Nitrogen fixation is only found in Cyanobacteria in Mendota, but is phylogenetically widespread in Trout Bog
   2. Urea cycle is the most common method of acquiring nitrogen in both lakes
   3. Polyamine synthesis (putrescine and spermidine) common and widely distributed across taxa in both lakes
4. Polysaccharide degradation
   1. Cellulose degradation – Cyanobacteria in Mendota, Rickettsiales in Trout Bog. Not common in either lake
   2. Bacteroidetes degrades chitin in both lakes
   3. Number of starch degraders in Mendota and Trout Bog hypo, but not Trout Bog epi. Mainly Cyanobacteria, Bacteroidetes, and Verrucomicrobia.
5. Sulfur metabolism
   1. Sulfur reduction and thiosulfate disproportionation found in both lakes, in many taxa
   2. Sulfur oxidation rare in Mendota, common in Trout Bog

Discussion

* Overall, many functions are shared between lakes, despite differences in the taxa performing those functions.
* Many functions are widely dispersed across phylogeny. (Which are not?)
* Trout Bog is energy limited compared to Mendota based on using reductive TCA vs CBB.
* Despite larger methane emissions from bog lakes, one carbon compound metabolism is present in both lakes. Emphasizes importance of freshwater in global carbon cycling. (and physics?)
* Mendota’s only nitrogen fixers are Cyanobacteria. This could contribute to bloom events when nitrogen levels drop (cite Lucas’ paper)
* Sulfur oxidation is an important process in Trout Bog and less important in Mendota. Could be due to high levels of hydrogen sulfide in bogs (related to iron/humic electron transfer?) or due to higher energy electron sources in Mendota. (What S species are in Trout Bog vs Mendota?)

Potential Figures

* Trees showing phylogenetic dispersion of traits
* Community composition by metagenomics reads vs by MAGs
* Pathway maps of primary production (photosynthesis + carbon fixation) in Trout Bog vs Mendota
* Heatmaps of pathway presence/absence by lake