A comparative method for elucidating cyanobacterial diversity in Taylor Valley, Antarctica

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Abstract

The McMurdo Dry Valley (MCM) ecosystem has been a model system for understanding ecosystem dynamics and life at the extremes for more than 20 years (1). Cyanobacteria are key members of this ecosystem and occur in many diverse ecological niches (2). Our study examined the diversity of Cyanobacteria present at several habitats throughout the cold, dry habitat of Taylor Valley, Antarctica. Using the 16S rRNA gene sequence and the 16S-23S internal transcribed spacer (ITS) we compare the diversity of genera detected using each of these phylogenetic markers as well as draw conclusions regarding dispersal and distribution of Cyanobacteria in Taylor Valley.

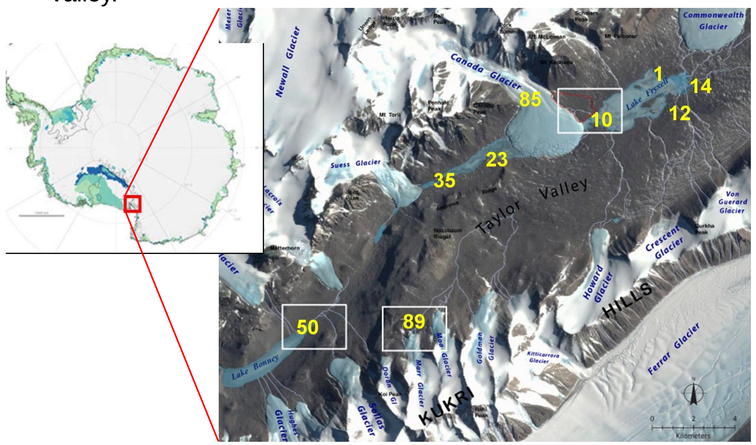

Figure1. Sample sites from the 2007-2008 sampling season. Sample sites are as follows, Sample Site 1 and 10: Lake Fryxell Mats (FRXLS), Sample Site 12: Fryxell Basin Soil (FRXS), Sample Site 14: Fryxell Aeolian Sediment (FRXA), Sample Site 23: Hoare Aeolian Sediment (HORA), Sample Site 35: Hoare Lake Sediment (HORLS), Sample Site 50: Bonney Stream Mats (BON), Sample Site 85: Canada Glacier Sediment (CAN), Sample Site 89: Marr Pond Mats (Marr Pond). Image credits: 2.4 meter QuickBird imagery copyright DigitalGlobe, Inc

Methods

Field Sampling:

Samples were collected during the 2008-2009 field season from several habitats throughout Taylor Valley (Figure 1).

Sample Analysis:

1. DNA extraction using MoBio Power soil kit (Carslbad, CA)
2. PCR amplification of 16S rRNA gene and a section of the 16S-23S ITS region using Cyanobacterial specific primers
3. Generate clone libraries using Invitrogen Topo TA Cloning Kit (Carslbad, CA)
4. Sequencing was performed by Functional Biosciences (Madison, WI)
5. Sequences were organized and queried against the NCBI database using an in house program (Python)
6. Unifrac was used for environment clustering and Jackknife values

Results

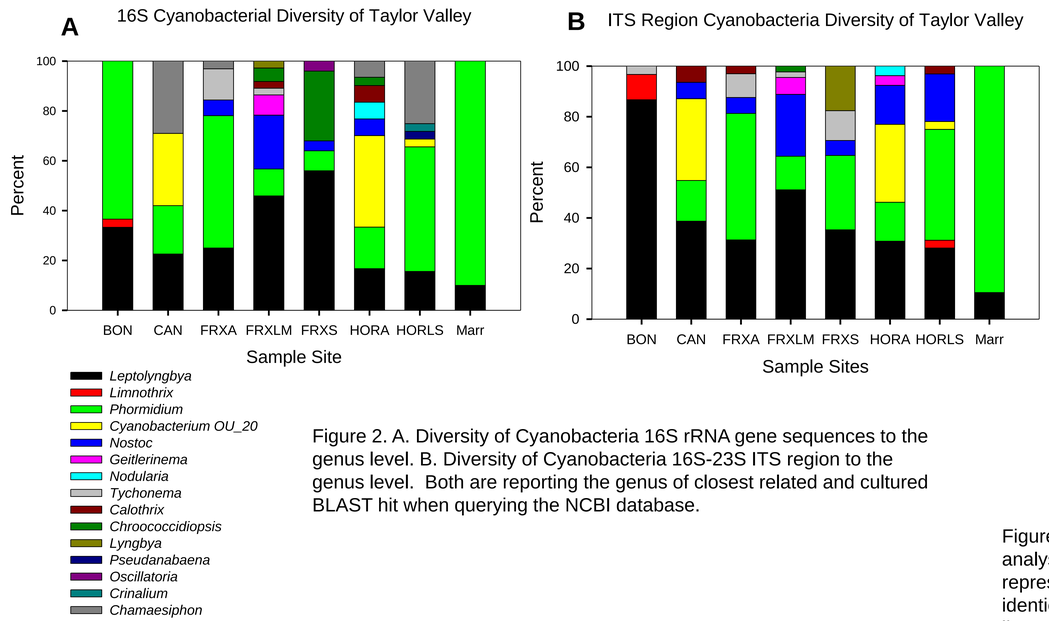

Figure 2. A. Diversity of Cyanobacteria 16S rRNA gene sequences to the genus level. B. Diversity of Cyanobacteria 16S-23S ITS region to the genus level. Both are reporting the genus of closest related and cultured BLAST hit when querying the NCBI database.

Table 1. Shannon-Weaver index of diversity values for each sample site and percent difference between the 16S and 16S-23S ITS region phylogenetic markers

	Shannon Weaver Index		
Sample Site	**16S**	**ITS**	**Percent Different (%)**
Bonney Str. Mats	0.769	0.468	39.2
Canada Glacier Sediment	1.372	1.380	0.6
Fryxell Aeolian Sediment	1.224	1.214	0.9
Fryxell Lk. Mats	1.583	1.306	17.5
Fryxell Basin Soil	1.141	1.452	27.3
Hoare Aeolian Sediment	1.801	1.552	13.8
Hoare Lk. Sediment	1.308	1.357	3.8
Marr Pond Mats	0.325	0.336	3.5

Future Directions

- Determine the assemblages of bacteria associated with the Cyanobacterial mats, allowing us to examine the importance of microbial consortia on microbial survival and transport in the MCM
- Analyze the Cyanobacteria present in sediment traps currently deployed in the MCM to determine the fate of wind dispersion of Cyanobacteria among habitats

References

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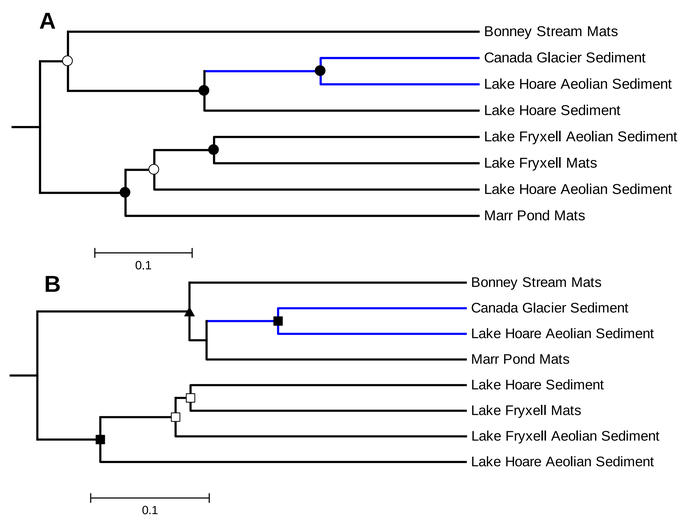

Figure 3. A. Cluster analysis of the eight sample sites using the 16S rRNA gene. B. Cluster analysis of the eight samples sites using the 16S-23S ITS region. The scale bar represents Unifrac units, in which a distance of 0 indicates the two environments are identical and a distance of 1 indicates the two environments contain mutually exclusive lineages. The tree was developed from an environment distance matrix which was calculated using the Unifrac metric, normalized abundance weights, and the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). Nodes are supported by Jackknife values such that, ● = >90%, ○ = >80%, ▲ = >75%, ■ = >60%, and □ = >25%. Blue branches indicate where the two trees exhibit similar clustering of sample sites.

Conclusions

- Phylogenetic analyses using **16S rRNA and 16S-23S ITS region report differing communities from the same sample site**, although the **dominant genera reported were similar** (i.e. *Leptolyngbya* and *Phormidium*)
- **Cluster analyses** infer that **spatially closer sites contain similar lineages**
- **Cluster analysis and sample site profiles infer** that diversity of Cyanobacteria is **greater** in sample sites in the **eastern end** of Taylor Valley
- **Half of the sample sites** have a Shannon-Weaver Index which differs by **less than 5%** (Table 1) between the diversity according to 16S rRNA and 16S-23S ITS region.

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