

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



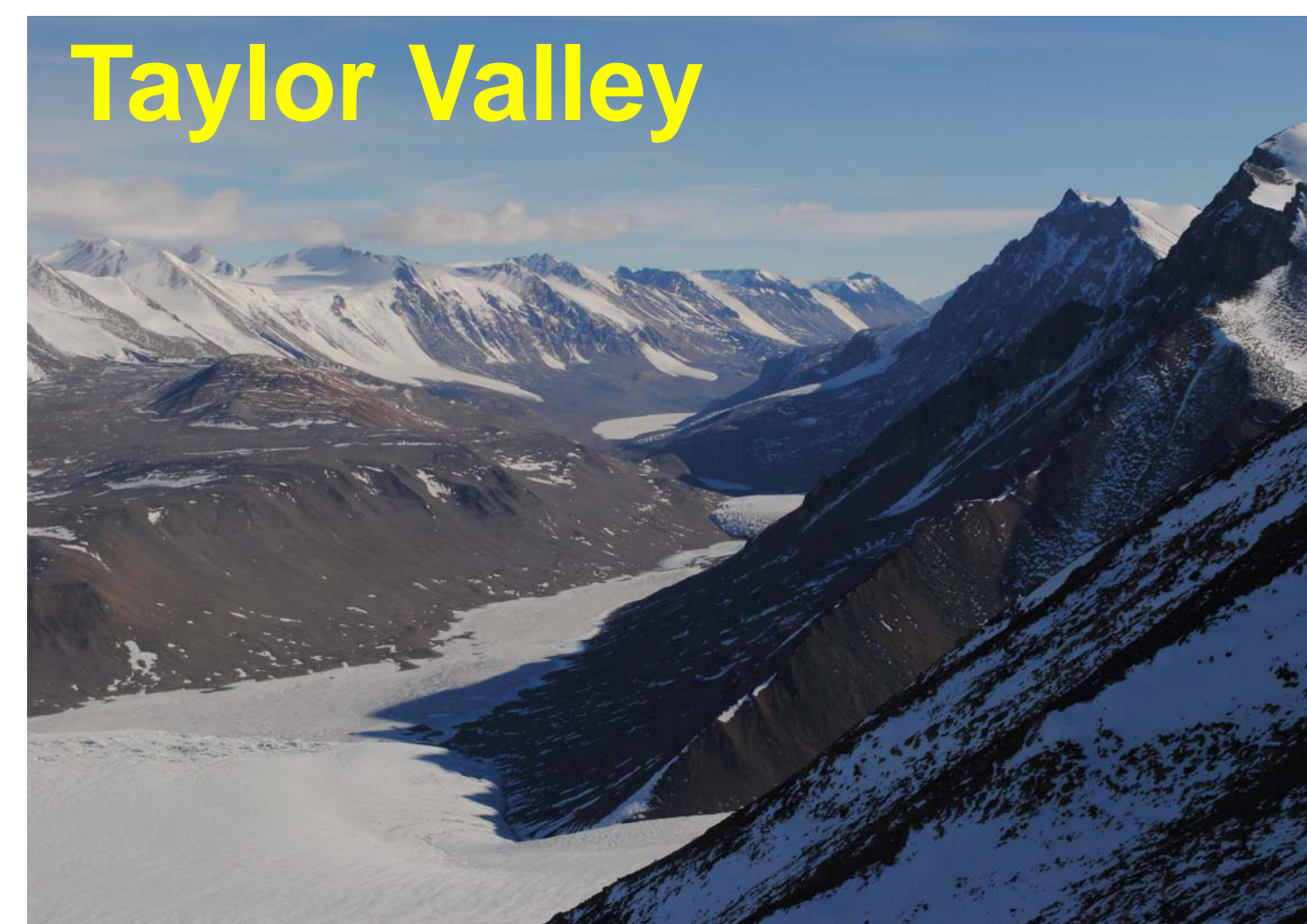
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16S and ITS region phylogenetic markers report similar alpha-diversity, but identify different genera.

Abstract:

Cyanobacteria are key members of the McMurdo Dry Valley (MCM) ecosystem and occur in many diverse ecological niches. Our study examined landscape-scale cyanobacterial diversity using the 16S rRNA gene sequence and the more rapidly evolving 16S-23S internal transcribed spacer (ITS) as independent phylogenetic markers. A comparison of these two markers revealed similar diversity, but with disagreements in genera detected. The faster evolving ITS region does not resolve higher taxonomical (Order) diversity, while the 16S distinguishes Order-level comparisons at this landscape-scale.



Hypothesis: The 16S and ITS phylogenetic markers will report similar alpha-diversity and genera present in each habitat sampled.

Methods:

- Lake mats, glacier sediment, aeolian sediment, soil, and lake sediment samples collected

- 16S and ITS clone libraries constructed

- Sequence data processed using MEGA v.4

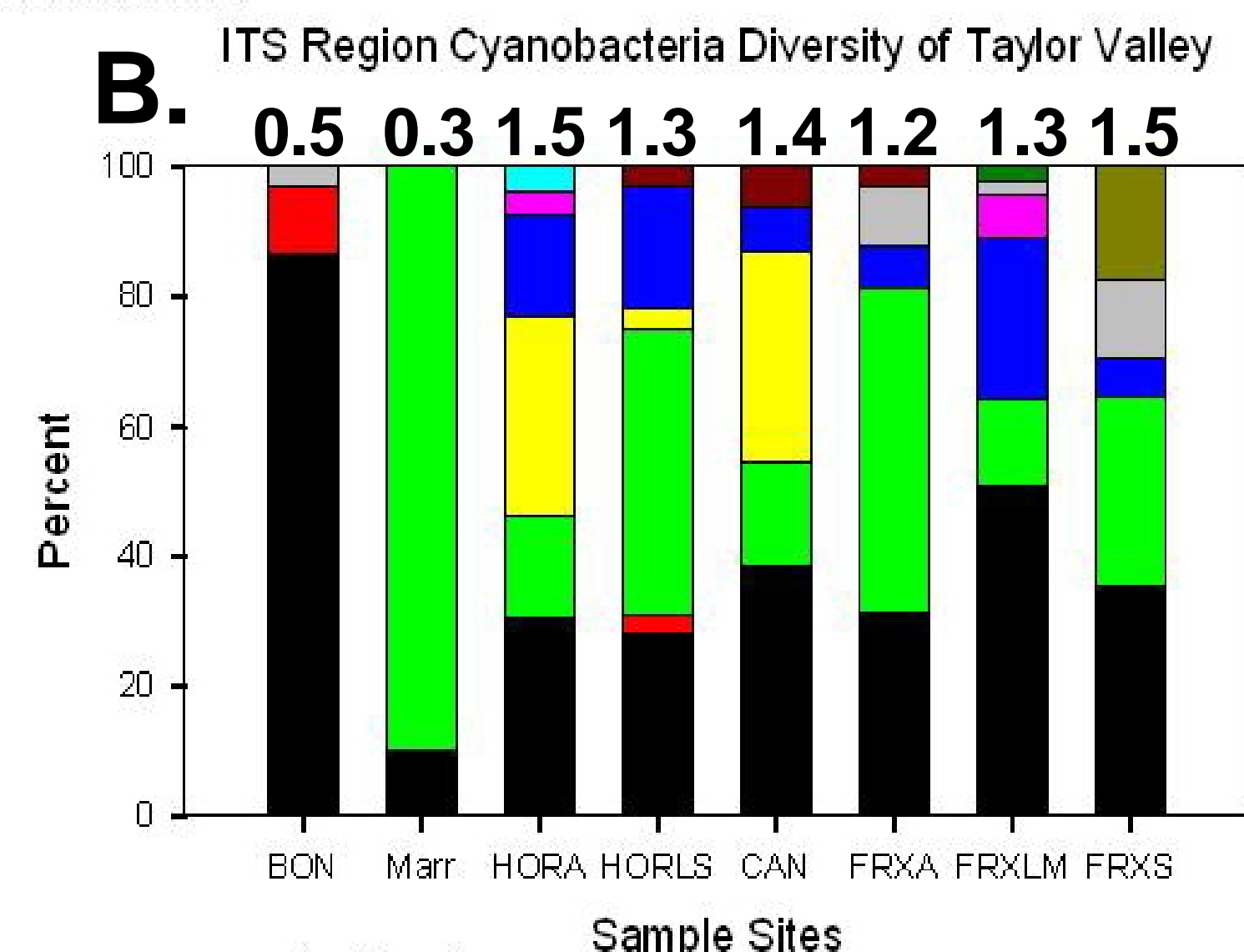
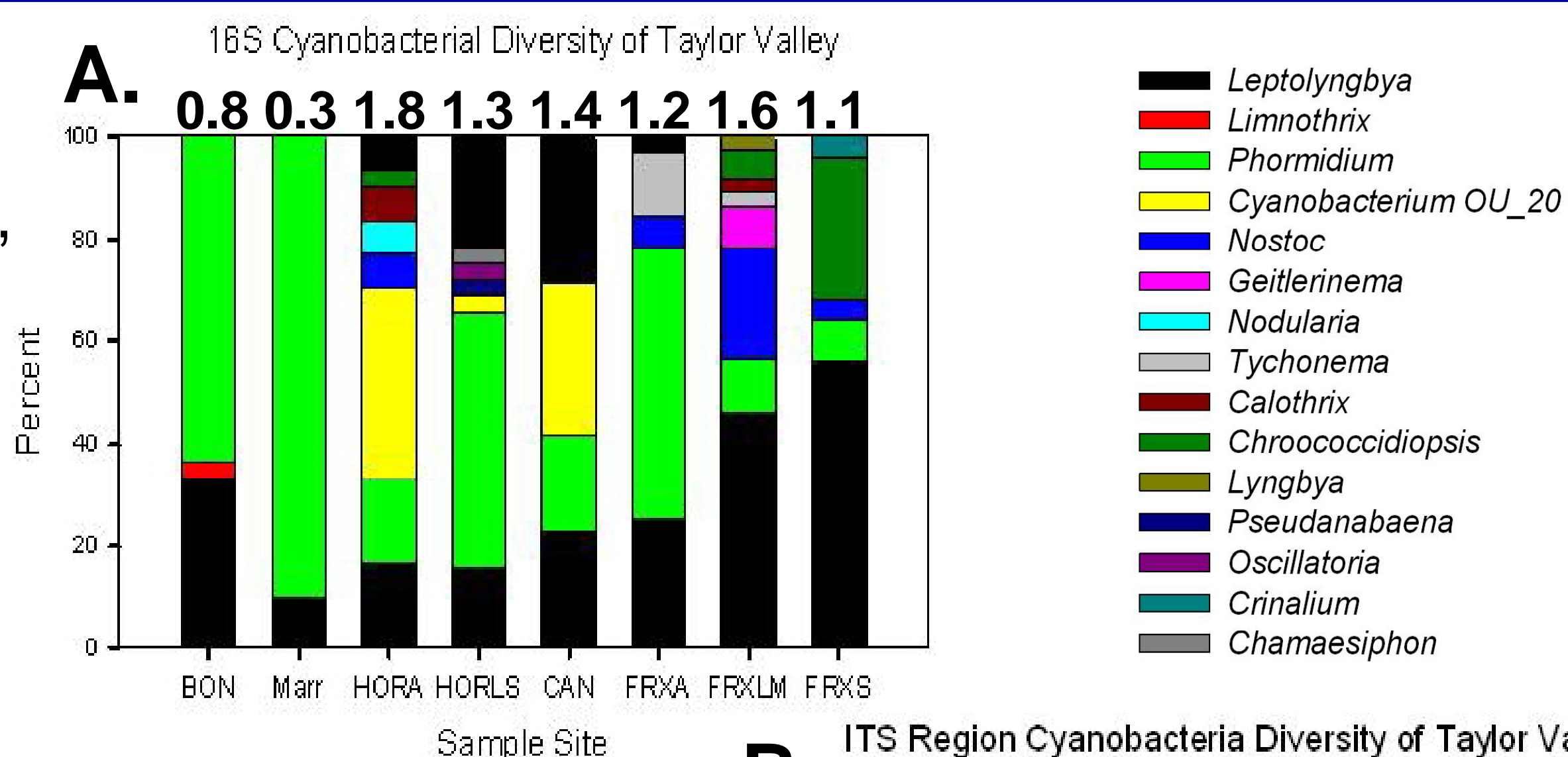


Figure 1. A. Diversity of Cyanobacteria 16S rRNA gene sequences. **B.** Diversity of Cyanobacteria 16S-23S ITS region. Numbers above bars are Shannon-Weaver indices of diversity

Implications:

Landscape scale studies, in which a wide range of taxa are expected, should be conducted using the 16S rRNA gene sequence rather than the ITS.