

Lake Vanda Microbial Mats Harbor a Diverse Assemblage of Microorganisms K. M. Wall¹, A. D. Jungblut², M. Krusor¹, T. J. Mackey¹, I. Hawes³, D. Sumner¹, ¹ Department of Earth and Planetary Sciences, University of California, Davis, 1 Shields Avenue, Davis, CA 95616, wallkate13@googlemail.com, ²Department of Life Sciences, The Natural History Museum, Cromwell Road, London SW7 5BD, UK, ³Gateway Antarctica, University of Canterbury, Christchurch, New Zealand

Introduction: Lake Vanda is a perennially ice-covered lake in Wright Valley of the McMurdo Dry Valley region of Antarctica. The absence of disturbance, and of grazing metazoans in the lake produce an environment reminiscent of the Earth's early biosphere. The lake waters are very oligotrophic and contain few cells, but within the photic zone, the lake floor is covered with thick microbial mats.

The lake is a microbially dominated ecosystem, with no macroscopic metazoans. Previously, the microbial mats were known to contain abundant Cyanobacteria, as well as diatoms and an aquatic moss (1). This study is the first next generation sequencing study of the mat microbiota.

The mats are covered with pinnacles, tent-like microbial structures. The pinnacles range in size from a few millimeters to ~5 cm (Hawes, 2013). The pinnacles and the prostrate microbial mats are laminated, with approximately annual layers. Overlaying the laminations are characteristic pigmented layers, shown in Fig. 1.

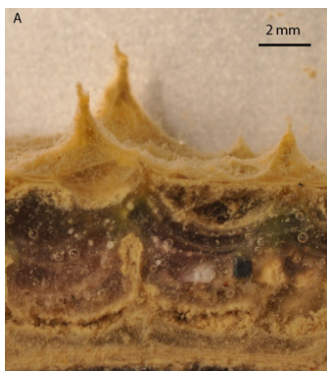


Figure 1 - A cross section of the pinnacled mat from Lake Vanda. The brown/orange outer layer, green middle layer and pink interior layer are apparent.

Results: Pinnacles from Lake Vanda were collected, and dissected into pigmented layers and the DNA extracted. Extracted DNAs were used as template for 16s rRNA PCR, and the barcoded PCR products were sequenced on the Illumina MiSeq.

As expected, the mats were dominated by Cyanobacteria (29%). Proteobacteria (28%) were the next most abundant, with Bacteroidetes (10%) and Chloro-

flexi (6%) also found in high abundance. Unassigned reads made up 8% of the mat. While relative abundances of the various taxa varied with depth in the mat, overall the different mat zones showed the same microbial communities. The pink samples had the fewest Cyanobacteria (5.1%) and the most Proteobacteria (51%). The overwhelming majority of the Cyanobacteria belonged to the Synechococcophycidae (70%), Oscillatoriothycidae (18%) and unclassified reads making up most of the remainder. The Cyanobacterial class 4C0d-2, an enigmatic non-photosynthetic clade (2), made up 3% of the reads assigned to the Cyanobacteria.

The Proteobacteria were dominated by Alphaproteobacteria (44%), followed by Gammaproteobacteria (19%), and Deltaproteobacteria (17%). The most prominent Alphabacterial class is the Rhodobacterales, which are metabolically diverse and include purple non-sulfur photosynthesizing bacteria.

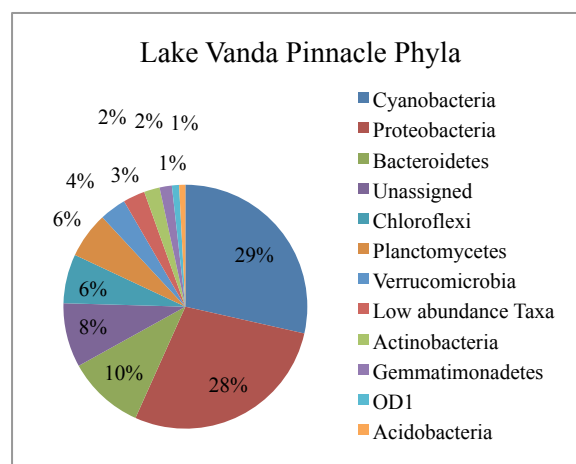


Figure 2 – Major phyla of Lake Vanda pinnacles.

References:

1. Hawes et al, Biology (Basel) 2, 151 (2013).
2. Di Rienzi et al., eLife 2, (2013).