



# Three-Dimensional Spatial Scaling of Microbial Community Diversity Within Aquatic/Terrestrial Interfaces in a Polar Desert

Bobb, M., University of New Mexico, Albuquerque, U.S.A., bobbm@unm.edu ; Zeglin, L. H., University of New Mexico, Albuquerque, U.S.A., lzeglin@unm.edu ; Gooseff, M. N., Colorado School of Mines, Golden, U.S.A., mgooseff@mines.edu, ; Barrett, J. E., Dartmouth University, Hanover, U.S.A., John.E.Barrett@Dartmouth.edu ; Dahm, C. N., University of New Mexico, Albuquerque, U.S.A., cdahm@unm.edu ; Vesbach, C. D., University of New Mexico, Albuquerque, U.S.A., cvesbach@unm.edu



Figure 1. Priscu Stream (M. Gooseff & M.Northcott in foreground) & Lake Joyce.



## Methods

- Samples were collected January 2005 from Lake Fryxell and Green Creek, Fryxell Basin, Taylor Valley.
- Two transects were sampled at each site. The transects were located 3.55 meters apart on Green Creek and 2.8 meters on Lake Fryxell (Fig.2)
- Each transect was divided into four sampling positions: 20 cm. from water edge, the midpoint of the wetted zone, the fringe of the wetted zone, and outside of the wetted zone (fig.2).
- Three depths were sampled at each position: 0-3, 3-6, and 6-10 cm.
- Optimal sampling size was determined by comparing diversity from a single sediment particle, 0.05g, 0.10g, 0.15g, and 0.20g of sediment.
- DNA was extracted using MoBio's Power Soil DNA Extraction Kit with the exception of the mass-based optimization of sample size experiments, for which we used a variation of the CTAB method (2,4).
- PCR was used to amplify the 16S rDNA using Bacteria-specific primers (338F & 519R). The PCR products were analyzed using denaturing gradient gel electrophoresis (DGGE); 20-60% gradient).

## Introduction

The hyporheic zone represents the interface between aquatic and terrestrial systems and is significant in the transformation of nutrients moving both into and out of lotic and lentic environments. In the McMurdo Dry Valleys, because of the lack of vegetation, the hyporheic zone exists as wetted zones that are visible adjacent to streams and lakes (see Figure 1). Despite the low temperatures and ephemeral stream flow, significant nutrient transformations have been measured in these zones (1) and these wetted zones are believed to be an important link between the aquatic and terrestrial ecosystems of the valleys. Presumably, microbial communities are at the basis of these geochemical transformations and the ultimate objective of our research is to characterize the microbial diversity and function in the wetted zones adjacent to McMurdo Dry Valley streams and lakes. Along the gradient of aquatic/terrestrial wetted zones, the microbial community structure would be expected to change as a function of nutrients and hydrological gradients. Because of the low levels of water in the dry valleys, water is expected to be a major determinant of microbial community structure and should also control the diversity of microbes in any particular location within the wetted zone.

As microbial communities change on scales of less than a millimeter, it is important that we determine the spatial scale(s) for sampling that maximizes the microbial diversity observed. Because so little is known about dry valley sediment bacterial communities, we devoted special attention to determining the spatial heterogeneity of this component of the community. We determined community structure variability in both the horizontal and vertical planes using denaturing gradient gel electrophoresis (DGGE, 2,3). This phase of our research shows differing levels of microbial diversity at spatial scales varying from individual particles of sediment to 3.5 meters longitudinally and 10 meters lateral to the water edge.

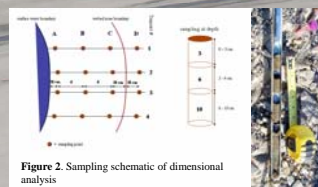
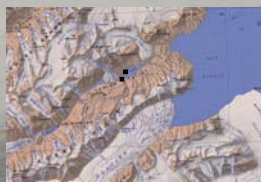
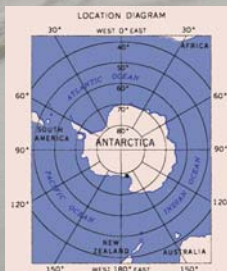


Figure 2. Sampling schematic of dimensional analysis

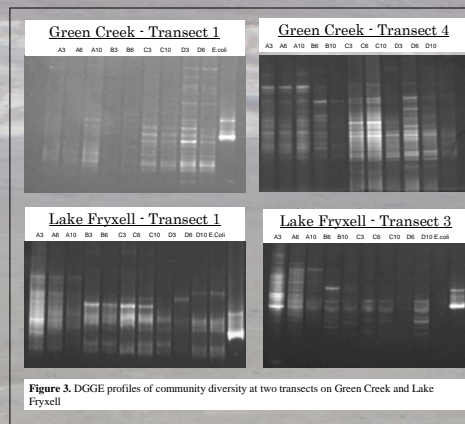


Figure 3. DGGE profiles of community diversity at two transects on Green Creek and Lake Fryxell

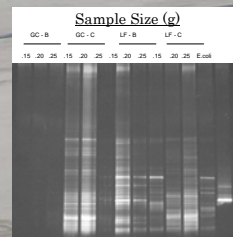


Figure 4. DGGE showing community richness analyzed at differing masses.

## Future Directions

Work will continue by analyzing additional transects from the sites above, as well as analyzing transects from other field sites. In addition, analyses will be repeated with PCR primers specific for Archaea. PCR and DGGE will be further optimized and results will be analyzed statistically to determine if the observed differences between communities are significant (2). Representative samples will be chosen for further analyses, including cloning of full-length 16S rDNA genes and functional genes for phylogenetic analyses.

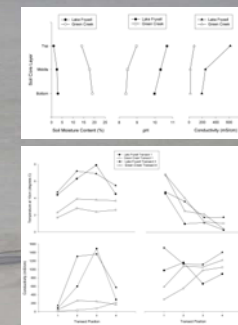


Figure 5. Physical characteristics of the transects analyzed in this study.

## References

1. Gooseff, M.N., McKnight, D.M., Runkel, R.L., Duff, J.H. 2004. Denitrification and hydrologic transient storage in a glacial meltwater stream, McMurdo Dry Valleys, Antarctica. *Limnol. Oceanogr.* 49(5): 1884-1895
2. Mitchell et al. in review
3. Muyzer, G., De Waal, E.C., Uitterlinden, A.G. 1993. Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. *Appl. Environ. Microbiol.* 59: 695-700.
4. Sambrook, J., Fritsch, E.F., Maniatis, T. 1989. *Molecular Cloning: A Laboratory Manual*. Cold Spring Harbor Laboratory Press.

## Acknowledgments

We'd like to thank Melissa Northcott, D. Brad Bate, and Kenneth Hill for field assistance. We are grateful for the outstanding support provided by Raytheon Polar Services personnel and the University of New Mexico's Molecular Biology Facility (NIH Grant Number 1P2ORR18754). This project is funded by NSF and the Office of Polar Programs through grant OPP0338267.

## Conclusions

- Spatial analysis indicates that community structure varies more laterally than vertically. This trend is more pronounced in the lotic than the lentic hydrologic margin (Fig. 3).
- The strong lateral gradient in sediment water content likely relates to observed differences in community structure (Fig's 3,5). Lentic sediment conductivity is higher and more variable than lotic, which may relate to observed differences in lotic and lentic microbial community structure.
- Extraction of the 0.15 g and 0.20 g samples yielded similar DGGE profiles. Because sample size was limited to < 0.25 g, and the smaller masses failed to amplify, we are unable to suggest an optimal sample size at this time. Further PCR and DGGE optimization is required to determine optimal sample size. It does appear as though analysis of samples of different masses may result in different conclusions about species composition and richness (Fig.4).