Biodiversity – Peter Doran and Cristina Takacs-Vesbach

With the application of molecular biology techniques to investigate MDV biodiversity, a surprising level of bacterial (Cary et al. 2010, Takacs-Vesbach et al. 2010; Van Horn et al. 2013) and protist (Bielewicz et al. 2011; Xu et al. in review) richness has been revealed Although bacteria comprise a significant proportion of MDV biomass (Takacs and Priscu 1999; Foreman et al. 2007; Stanish et al. 2012), we know relatively little about their physiology and thus about their ecology and roles in biogeochemical cycling. To truly understand connectivity within the MDV (and hence, to address our hypotheses in MCM4) requires an understanding of the biodiversity, distribution, and functional roles of specific organisms within the environment and their responses to climate driven pulses and presses. Our approach is to determine spatial and temporal variations of microbial diversity, distribution, and function across all major habitats (cryoconites, streams, lakes, and soils) and determine changes in response to experimental manipulations (see sections on LakeICE and P3). Previous microbial 16S and 18S rRNA gene assays in the MDV have produced a large diversity of sequences from specific terrestrial and aquatic habitats (e.g., Gordon et al. 2000; Glatz et al. 2006; Barrett et al. 2006; Porazinska et al. 2009; Vick-Majors et al. 2013, Michaud et al. 2012). In MCM4, we are using our molecular data to investigate the role that microbial distribution and function play in ecosystem level process MDV-wide.

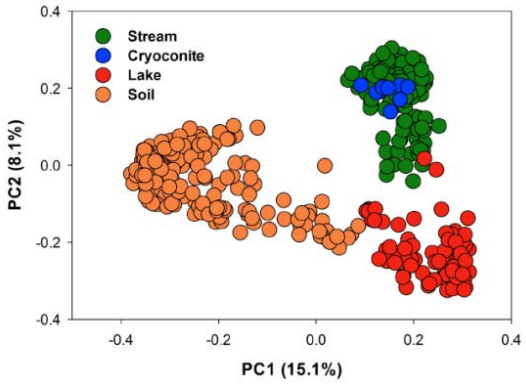

Fig. 1. PCoA of MDV bacterial communities (unweighted Unifrac) from all major habitats.

In Y1 of MCM4, we collected 425 samples from cryoconites, streams, lakes and soils throughout the Taylor, Wright, and Miers Valleys and analyzed 16S rRNA gene diversity to determine a baseline distribution of microbial communities throughout the McMurdo Dry Valleys. The data showed that bacterial alpha, beta, and gamma diversity is greatest in streams, followed by lakes and soils, and that phylogenetic diversity does not differ significantly between lakes and soils. Significant habitat filtering is observed among the samples (Fig. 1, Anosim significance of weighted and unweighted Unifrac clusters $P<0.05$) suggesting a lack of community connectivity despite physical connectivity among habitats. This result is surprising given that diel stream pulses transport significant amounts of mat biomass into lakes (Cullis et al. 2013) and that large flow events as in 2001/2002 resulted in a two-fold reduction of stream biomass (Stanish et al. 2011). Distributions of abundant and rare sequence types among the habitats indicate that the most abundant sequences from each habitat comprised 5 to 40% of the sequence types in other habitats, but the rare sequence types are most often restricted to one habitat type. We intend to repeat similar collections this year (Y3) and in Y6 to address temporal variation. Additional analyses we are exploring include variation partitioning to assess the relationship between beta diversity and environmental and spatial gradients (Sokol et al. 2013), which has revealed contrasting taxon specific distributions for soil communities.

We are using stable isotope probing (Schwartz et al. submitted), metagenomics (Fierer et al. 2012, Takacs-Vesbach et al in prep.), and metatranscriptomics (Buelow et al. in prep) in our work to assess how MDV organisms respond to simulated connectivity within the context of our experiments. Preliminary results suggest that our modest metagenomic sequencing effort includes data from all three domains of life, in addition to viruses, and that using a comparative metagenomics approach, spatial variations in the datasets are discernable. We have also successfully extracted RNA from soils and lakewater and completed Illumina sequencing of eight metatranscriptomes (six from a soil amendment experiment described in Van Horn et al. submitted and two from the primary productivity maxima of Lake Bonney). Ongoing analyses of these datasets are focused on identifying how community function changes with increased moisture and nutrients by identifying over- and under-represented transcripts in relation to experimental amendments performed during MCM4. Ultimately, our goal is to determine how ecosystem function will be altered in response to increased connectivity.