

# Bacterial Biodiversity in Permanently Ice-covered Lakes of the McMurdo Dry Valleys, Antarctica

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## ABSTRACT

The ice-covered lakes of the McMurdo Dry Valleys (MDVs) are widely acknowledged as one of the extreme habitats on Earth. Permanently cold temperatures, saline waters and extended periods of darkness in these aquatic ecosystems are considered limiting factors for life. Despite these environmental constraints, certain microorganisms thrive in these harsh-icy environments. To better understand the distribution and diversity of prokaryotes, we conducted 454-sequencing of the 16S rRNA gene on 69 samples collected from distinct depths in four lakes of the MDVs in November and December in 2012: Lake Fryxell (FRX), Lake Miers (MIE), West (WLB) and East (ELB) lobes of Lake Bonney. A total of 1,903 operational taxonomic units were generated from approximately 162,931 sequence reads with 97% similarity cutoff. Sequence reads were clustered into 49 phyla with FRX being the most diverse habitat and WLB the least diverse. *Bacteroidetes* and *Actinobacteria* were the most dominant phylum across all samples followed by *Proteobacteria*, especially the *Beta-* and *Delta-proteobacteria* in FRX and *Gammaproteobacteria* in Bonney. These data show that highly heterogeneous bacterial communities exist among lakes at the phylum level. Statistical analyses demonstrate that community composition was most closely related to water column geochemistry with particular taxonomic groups inhabiting specific layers in the water columns.

## INTRODUCTION

- ◆ The McMurdo Dry Valleys (MDVs) are located in the largest ice-free region of Antarctica (Vick and Priscu, 2012)
- ◆ Only recently have genomic techniques been used to examine microbial and metabolic diversity in these lakes (Karr *et al.*, 2005; Kong *et al.*, 2012)
- ◆ Objective of our study was to investigate the bacterial community composition at distinct depths in 4 major lake basins in the McMurdo Dry Valleys, Antarctica

## STUDY SITES & METHODS

### 1. Sample Collection

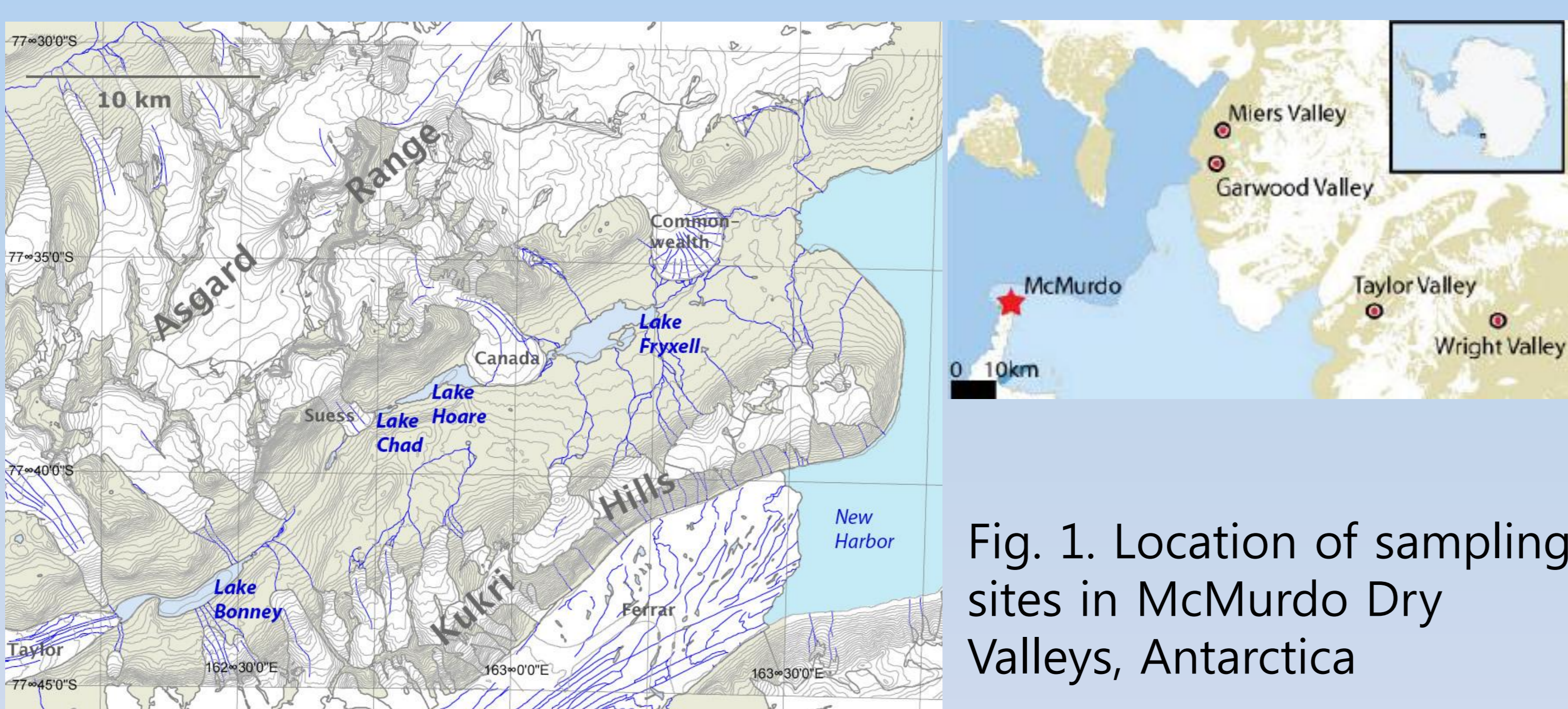


Fig. 1. Location of sampling sites in McMurdo Dry Valleys, Antarctica

### 2. Methods



Fig. 2. Drilling of the Ice-cover and sampling in the lakes



Fig. 3. Flow chart showing overall procedure for analyzing the bacterial diversity in freshwater samples

## RESULTS

### 1. Community structures

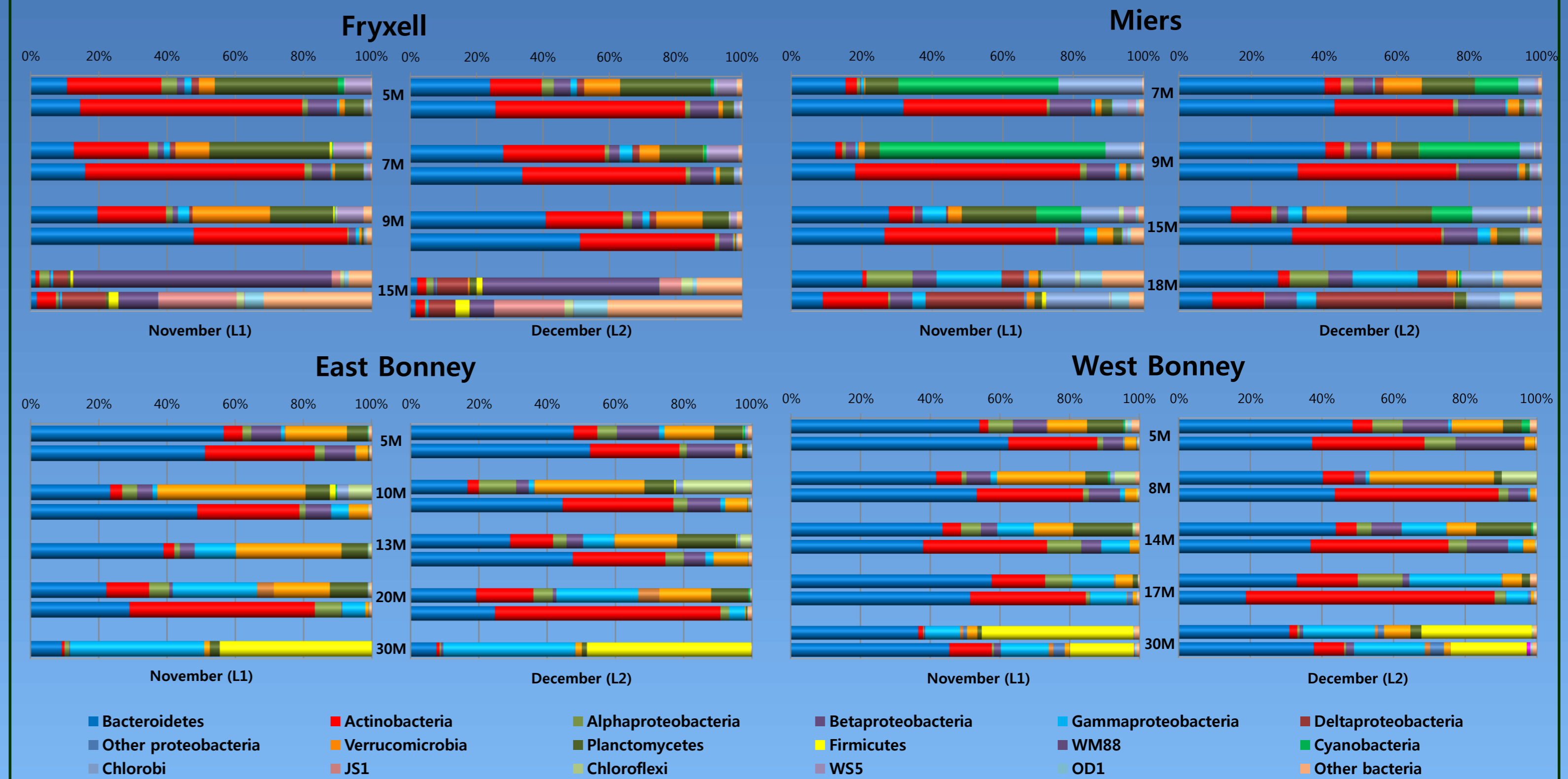


Fig. 4. A comparison of the taxonomic structures in phylum level

### 2. Patterns of co-occurrence and unique OTUs

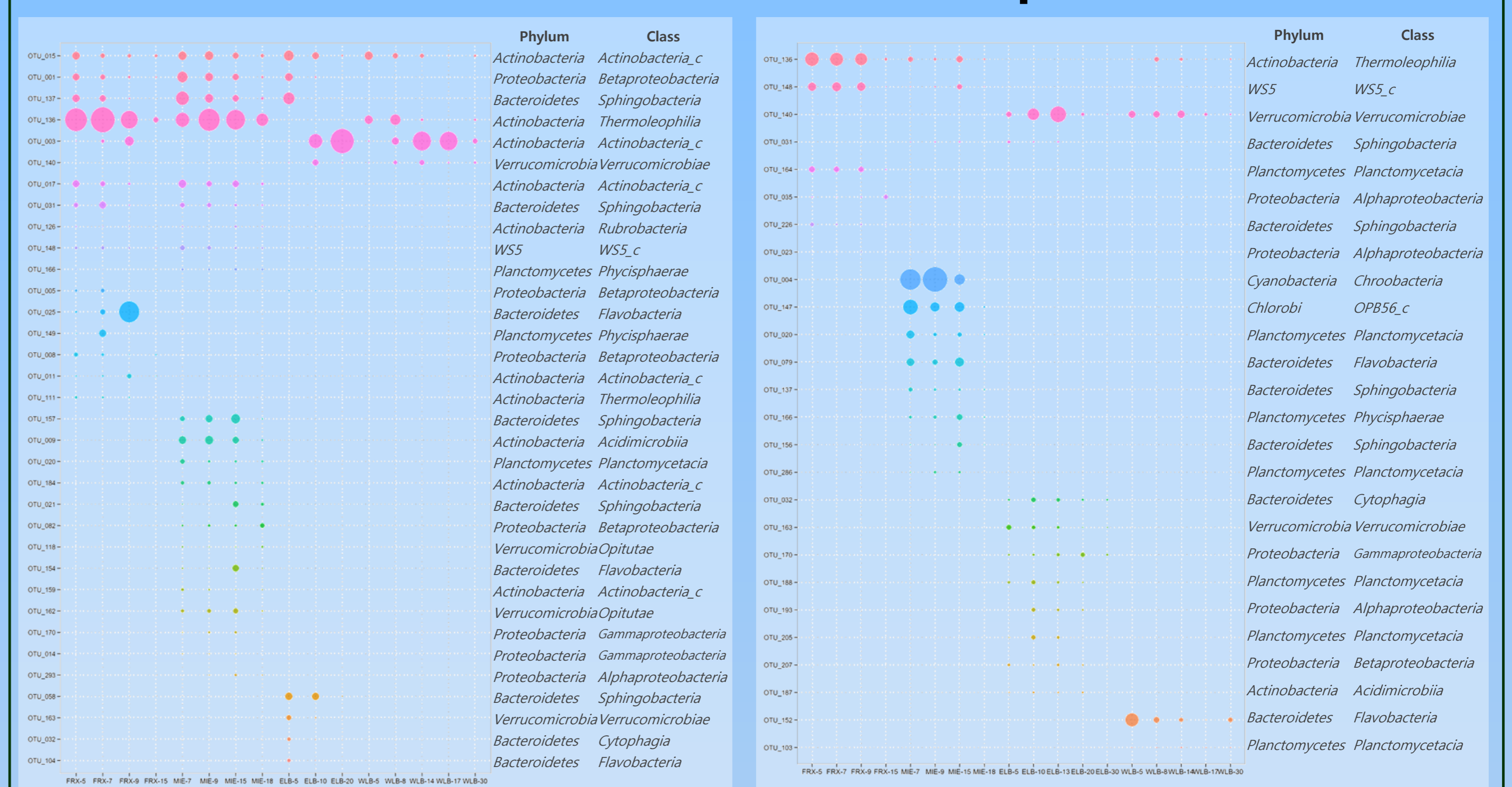


Fig. 5. Relative abundance of bacterial OTUs in 0.2 μm (left) and 3 μm (right) on November

### 3. Cluster analysis

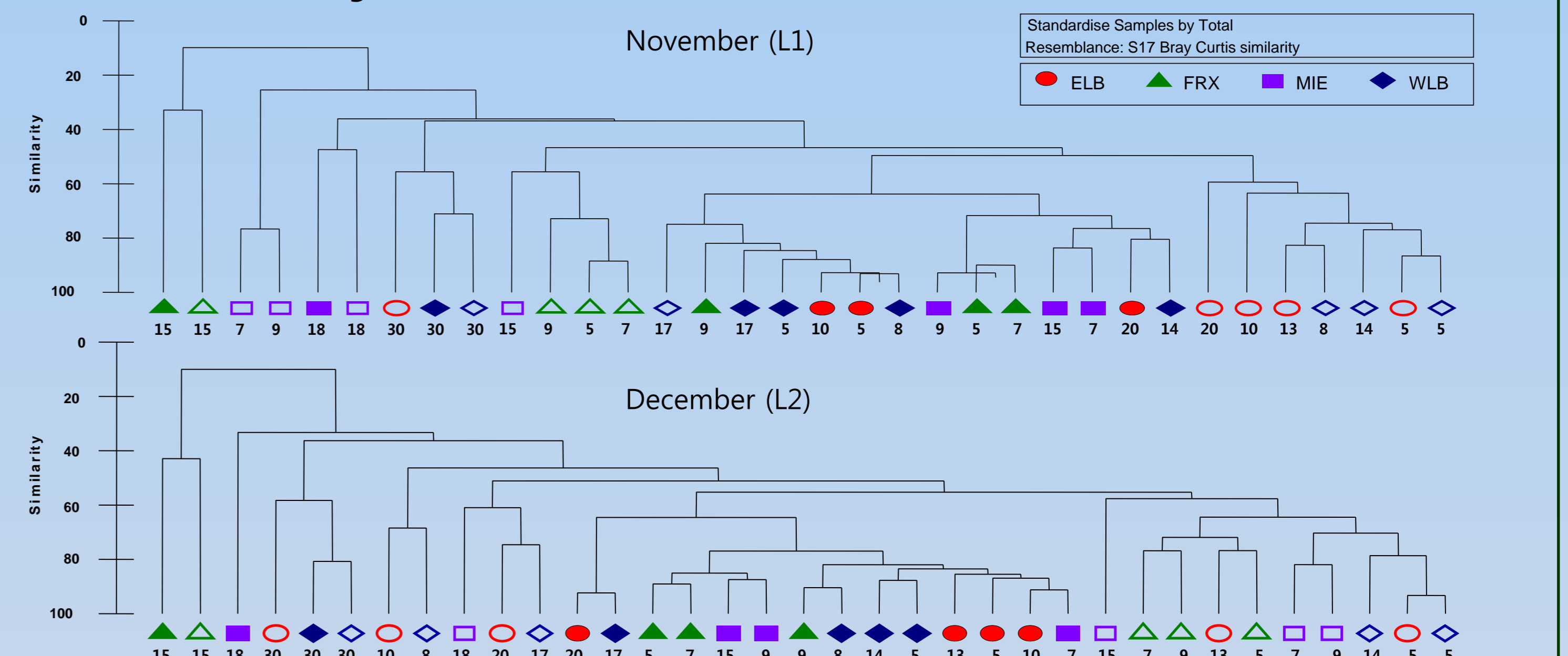


Fig. 6. Bacterial OTUs of 22 samples from three lakes on November (open circle;3.0, closed circle;0.2)

## CONCLUSION

- Lakes in the MDVs support a diverse assemblage of bacteria arranged across biogeochemical gradients.
- The >3.0 μm and 0.2-3.0 μm size classes were dominated by *Bacteroidetes* and *Actinobacteria* in all lakes. *Cyanobacteria* was predominantly found on the first filter in lake Miers. (Fig. 4)
- Although bacterial diversity differed among lakes and size classes, several OTUs co-occurred among the 4 lake basins. (Fig. 5 and Fig. 6)
- Community composition was most closely related to water column geochemistry with particular taxonomic groups inhabiting specific layers in the water columns

## ACKNOWLEDGEMENT

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## REFERENCE

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