

Comparative Analysis of Bacterial Community Composition in Lakes of the Dry Valleys, East Antarctica

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ABSTRACT

In the current study, the community composition of bacteria were investigated the perennial ice-covered lakes in the fine scale using 454-pyrosequencing; Fryxell (FRX), Hoare (HOR) and Miers (MIE). Based on 16S rRNA gene, total 124,803 sequences were quality filtered using 97% similarity cutoff, and 55 phyla were recovered containing the major phyla *Actinobacteria* (29%), *Bacteroidetes* (24.4%) and *Proteobacteria* (14%). In the phylum level, the bacterial taxonomy were highly shown the heterogeneous communities. Overall, microbial community composition varies not only between lakes, but also along the depth gradients within lake. Taken together, the diversity of microbial communities in lakes of MDVs provided a crucial evidence to understand the impact of microbial ecological roles in these ecosystems.

RESULTS

1. Community Structures

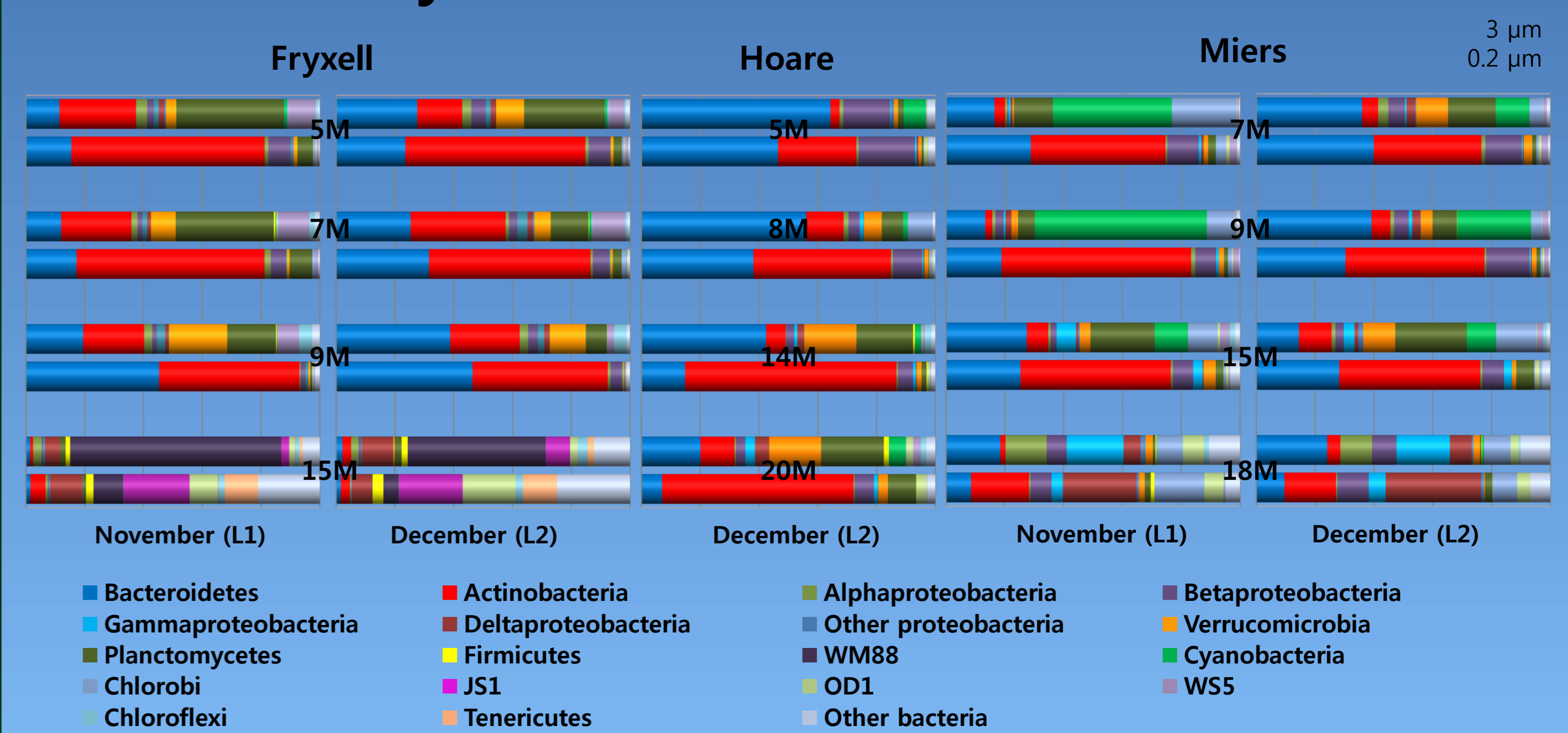


Fig. 4. A comparison of community structures in phylum level

2. Patterns of co-occurrence and unique OTUs

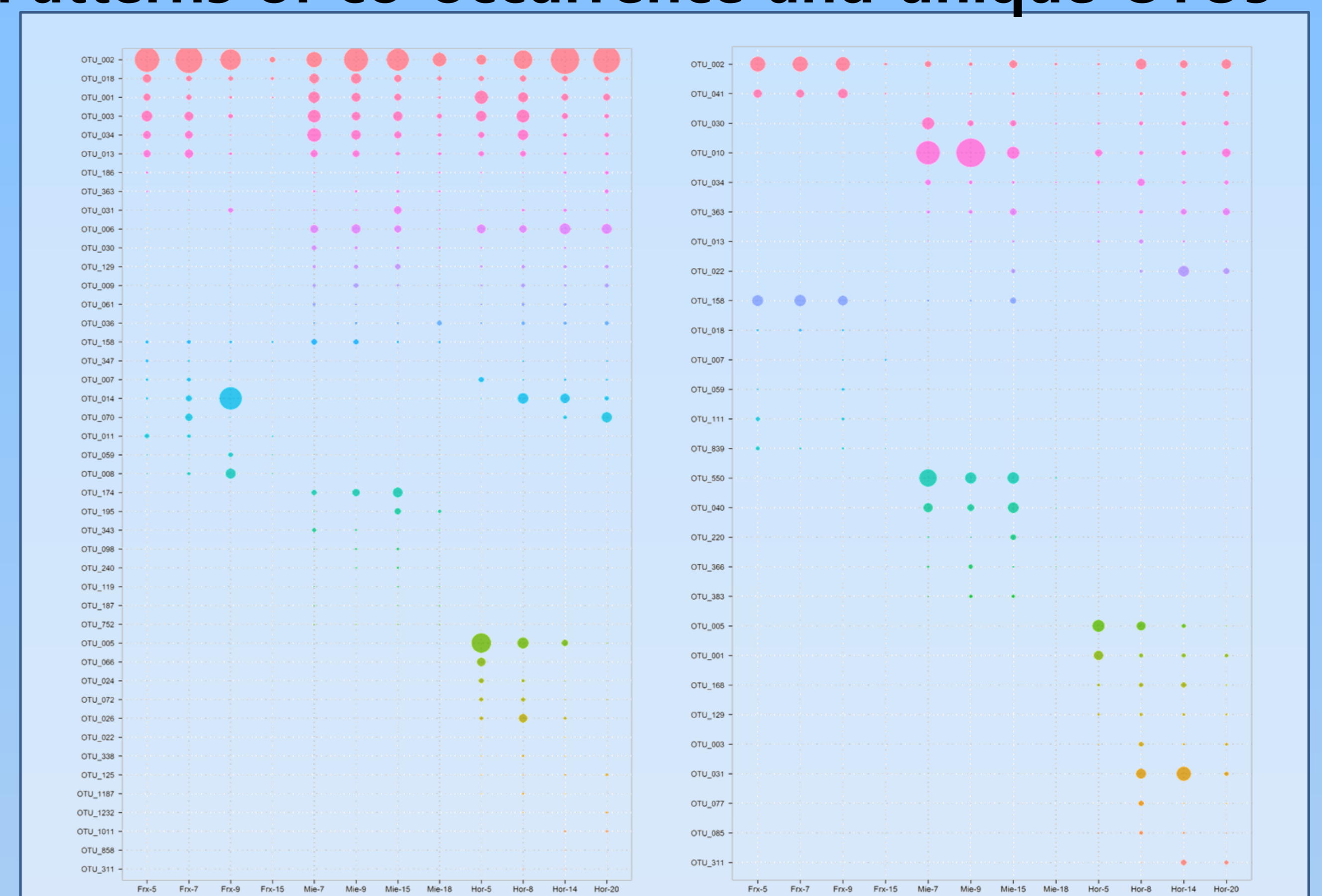


Fig. 5. Relative abundance of bacterial OTUs in 0.2 µm (left) and 3 µm (right) on November

3. Cluster Analysis

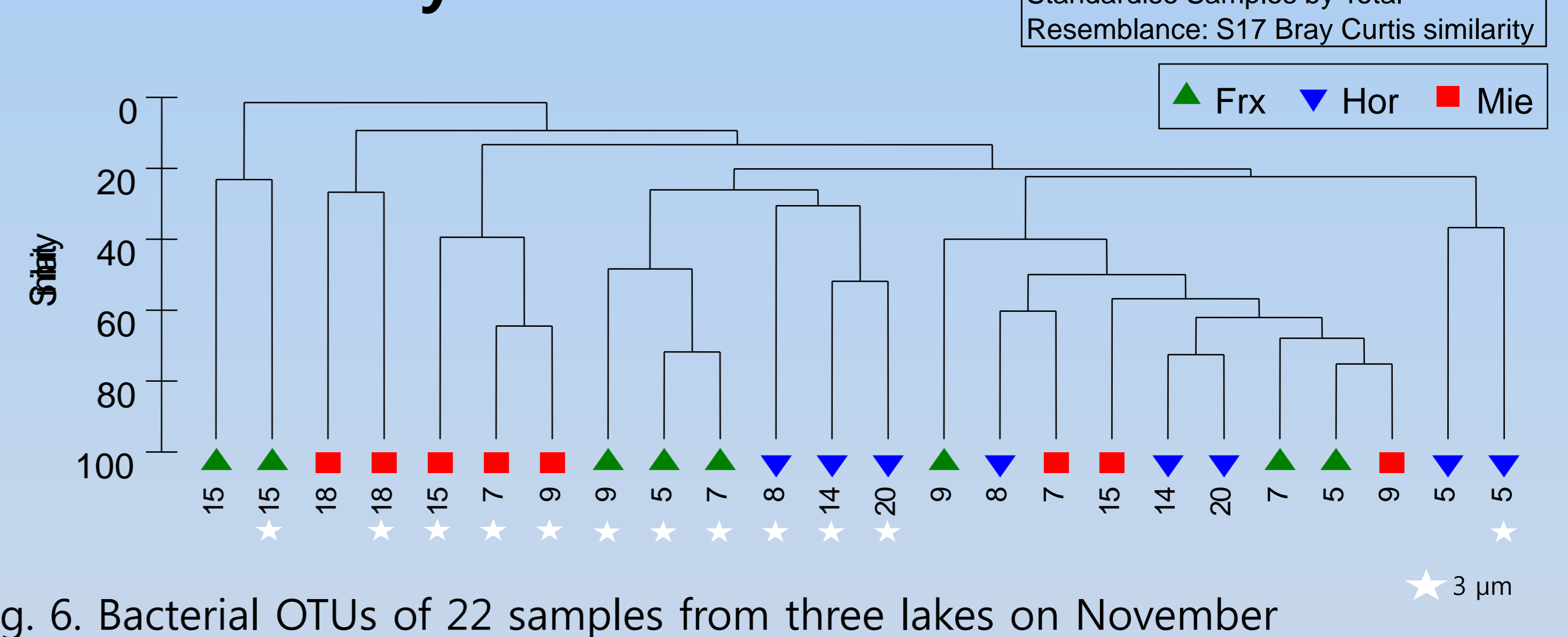


Fig. 6. Bacterial OTUs of 22 samples from three lakes on November

INTRODUCTION

- ◆ McMurdo Dry Valleys (MDVs) are located in the coldest and the driest on earth as the ice-free region (Vick and Priscu, 2012)
- ◆ To date, despite biogeochemical constraints, many studies have shown that the molecular diversity was examined of cold active microorganisms and reported their important roles in these lakes (Karr *et al.*, 2005; Kong *et al.*, 2012)
- ◆ Objective of this study
 - To investigate the bacterial community composition between freshwater habitats in McMurdo Dry Valleys, Antarctica

STUDY SITES & METHODS

1. Sample Collection

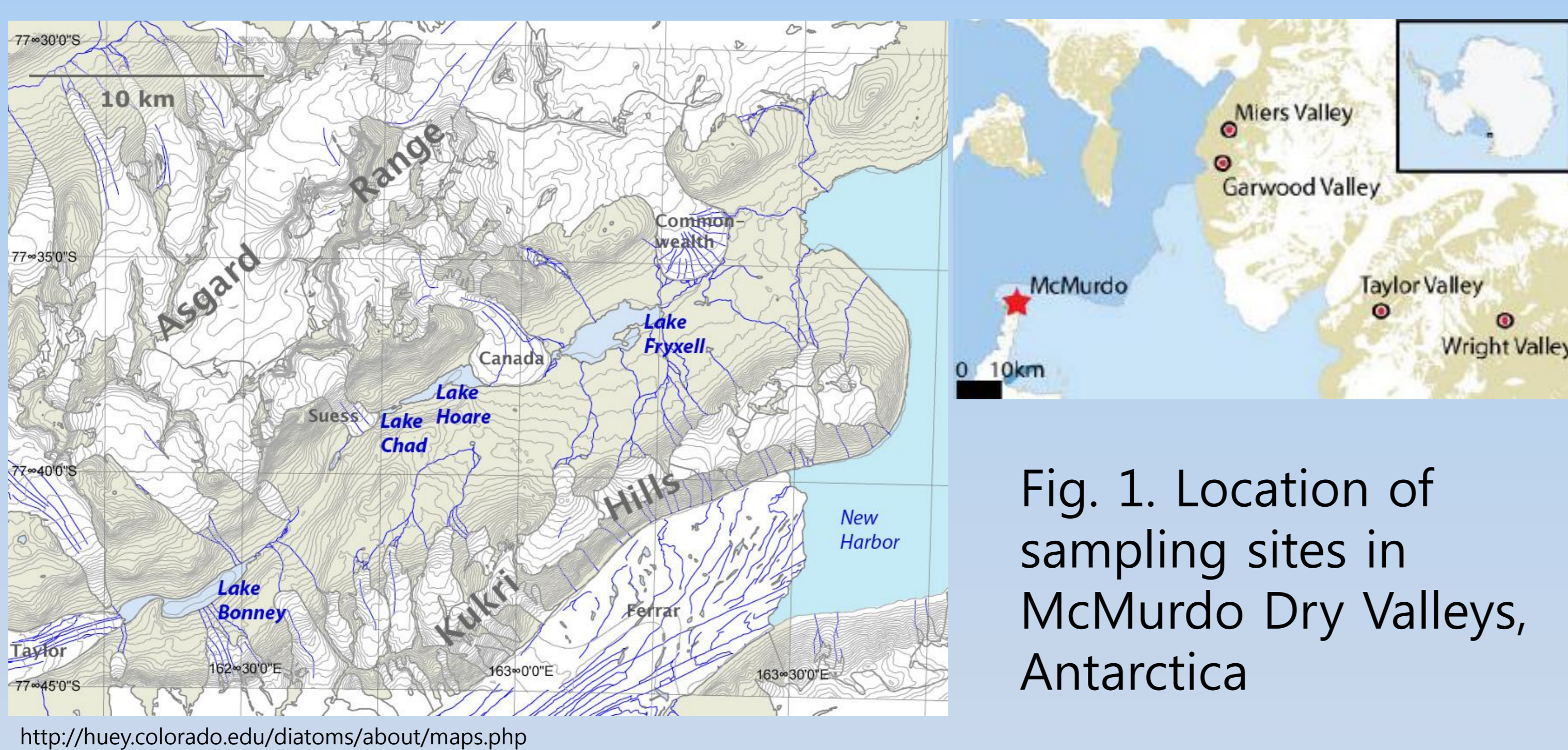


Fig. 1. Location of sampling sites in McMurdo Dry Valleys, Antarctica

2. Methods



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

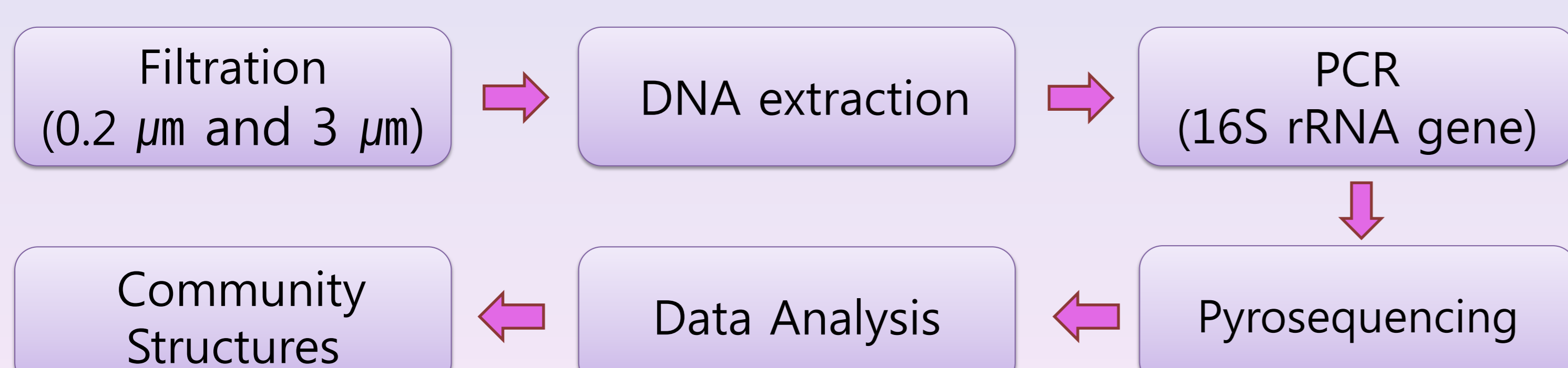


Fig. 3. Flow chart showing overall procedure for analyzing the bacterial diversity in freshwater samples

CONCLUSION

- The most dominant phylum in both of the filters was *Actinobacteria* and *Bacteroidetes* is placed the second abundant phylum in freshwater lakes. *Cyanobacteria* was predominantly found on the first filter in lake Miers. (Fig. 4)
- The trend of detection of bacterial diversity was different in the filters and the lakes. Several OTUs were cooccurred among three lakes. (Fig. 5 and Fig. 6)
- ★ These results present that the lakes in MDV have a diverse group of bacterial communities, and it provides the information of aquatic ecosystem in Antarctica

ACKNOWLEDGEMENT

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