

Microbial Community Profiling and Metagenome Analysis in Ice-covered Lake Fryxell of the McMurdo Dry Valleys, Antarctica

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ABSTRACT

Perennially ice-covered lake Fryxell in McMurdo dry valleys is chemically stratified and characterized by its own distinct limnology and biogeochemistry. The bottom of the lake is brackish, anoxic, and high concentrations of sulfide and methane. Despite the long history of microbiological research in these extreme environments, detailed information about what microbes reside and what they have potential function are still little understood. This study investigated bacterial community composition and their metabolic possibility in the bottom depth of lake Fryxell using 16S rRNA gene-based pyrosequencing and Illumina Miseq platform, respectively. Bacterial communities are overall distinctive. For example, all candidate phyla constitute more than half of total bacteria in this bottom depth including WM88, JS1, OD1, SAR406 and WS5, etc. Also, the high quality of 120 million reads were recovered from the sample with metagenome data, and 16S rRNA gene sequences was extracted about four thousands reads. The ratio of each bacterial community in pyrosequencing was differently shown from metagenome data. The metagenome data showed several metabolic pathways, including nitrogen and sulfur metabolism. Strong associations of bacterial community with various physicochemical variables would give additional information about ecology and metabolic potential of these bacteria, which would be consequences of their long-lasting adaptations to the extreme and unique environments of lake Fryxell in Antarctica.

RESULTS

1. Biogeochemical characteristics

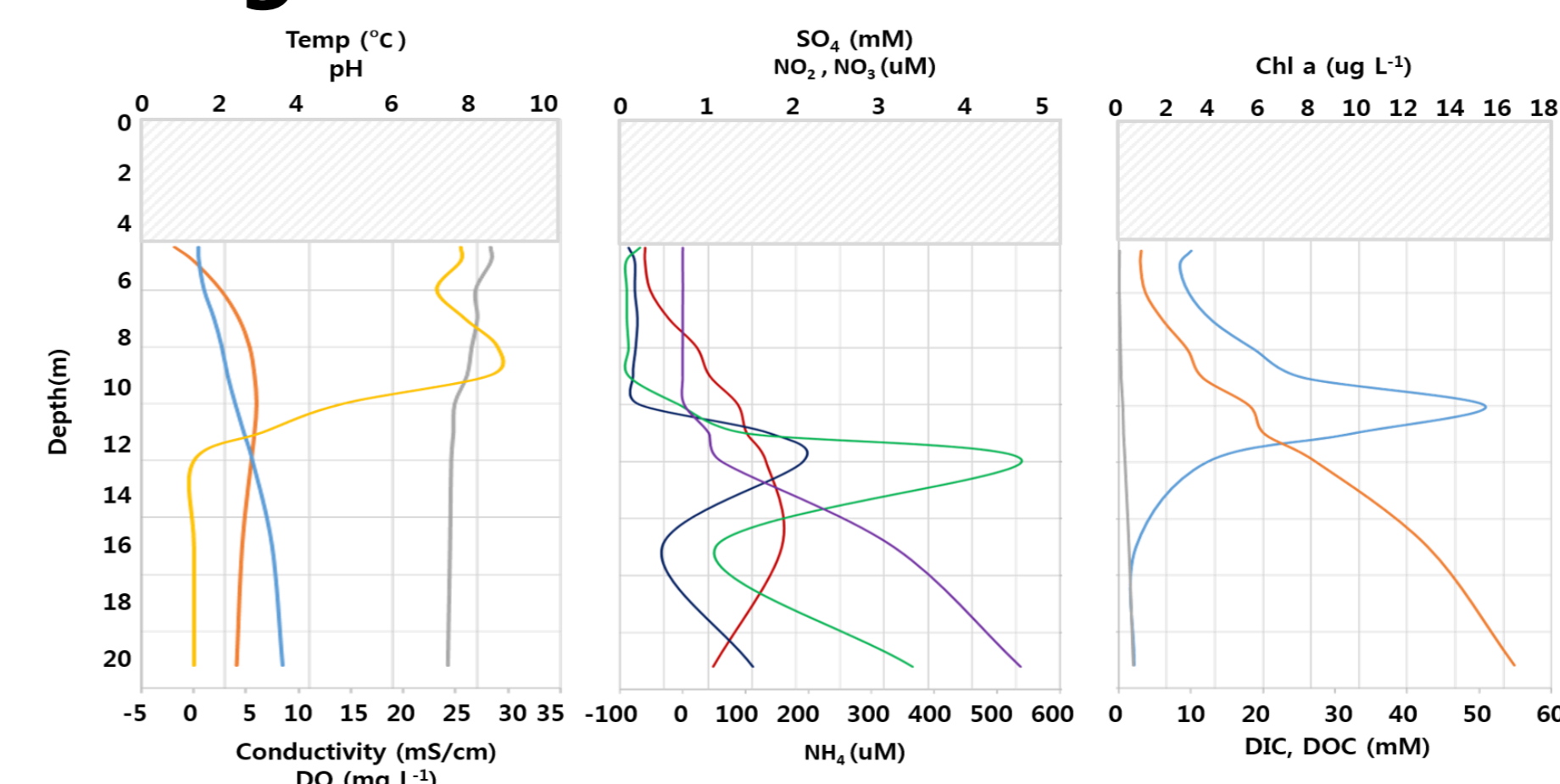


Fig. 4. Vertical shift of environmental parameters. Several factors were highly concentrated with depth, specially NH_4^+ and sulfide. The surface water was supersaturated with DO, but anoxic below 10m.

2. Bacterial community structures

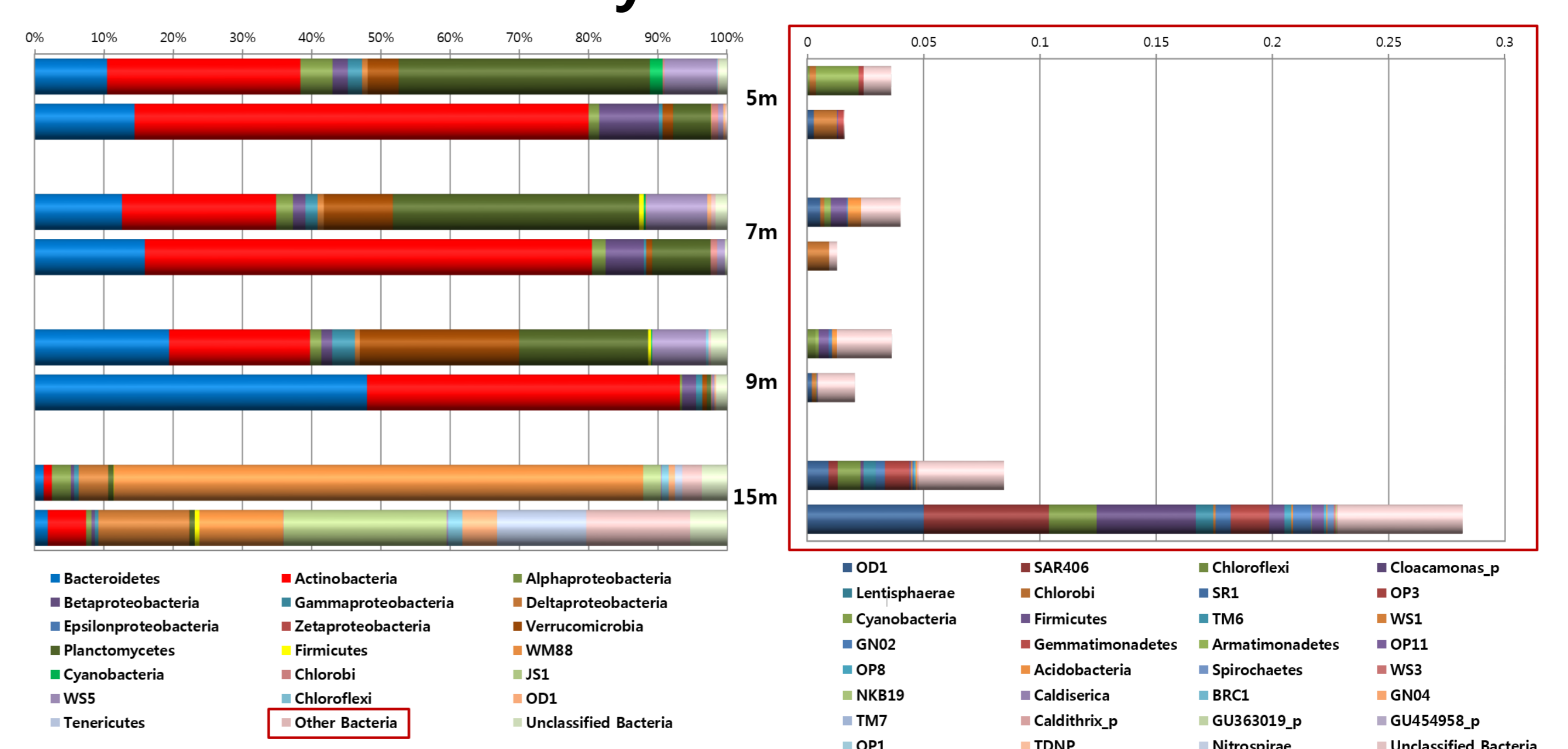


Fig. 5. Bacterial phyla distribution (left) and other bacteria composition (right) by depth and cell size in lake Fryxell. Upper and lower bars denote 3.0 µm and 0.2 µm filters, respectively.

3. Functional category

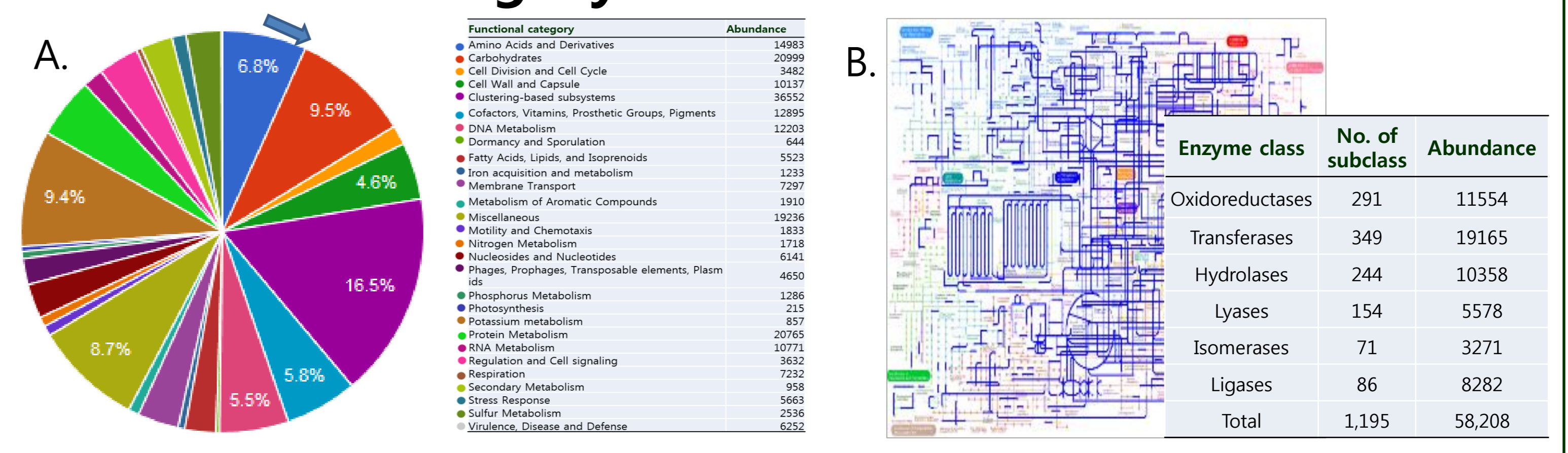


Fig. 6. Pie charts of the distribution of functional categories for at the highest level in the bottom depth of lake FRX: predicted metabolism and functions (A); predicted Enzyme class and metabolic pathway (B); sulfur metabolism (left) and nitrogen metabolism (c)

CONCLUSION

- The higher level of dissimilarities in community composition was found in the bottom depth of lake FRX. Certain members are confined to the 15m depth, which may result from physical change of water column. Also, a variety of candidate phyla were detected than other layers.
- A variety of predicted metabolism and functions related with environmental factors were found in the bottom depth such as stress response, nitrogen, and sulfur.
- Community composition was most closely related to water column geochemistry with particular taxonomic groups inhabiting specific layers in the water columns. Metagenome analysis is important not only for understanding the microbial communities, but also for finding specific function system of descriptors

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REFERENCE

- Karr, et al. 2005. Diversity and distribution of sulfate-reducing bacteria in permanently frozen Lake Fryxell, McMurdo Dry valleys, Antarctica. *Appl Environ Microbiol.* 71: 6353-6359
- Kong, et al. 2012. Evidence of form II RubisCO in a perennially ice-covered Antarctic lake. *FEMS Microbiol Ecol.* 82: 493-500
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INTRODUCTION

- ◆ The McMurdo Dry Valleys (MDVs) are located in the largest ice-free region of Antarctica. (Vick and Priscu, 2012)
- ◆ Recently genomic techniques have been examined microbial and metabolic diversity in these lakes (Karr *et al.*, 2005; Kong *et al.*, 2012)
- ◆ Objective of our study was to investigate bacterial community composition and their metabolic possibility in the bottom depth of lake Fryxell using 16S rRNA gene-based pyrosequencing and Illumina Miseq platform, respectively

STUDY SITE & METHODS

1. Sampling site



Fig. 1. Location of lake Fryxell in Taylor valley of McMurdo Dry Valleys, Antarctica

2. Methods

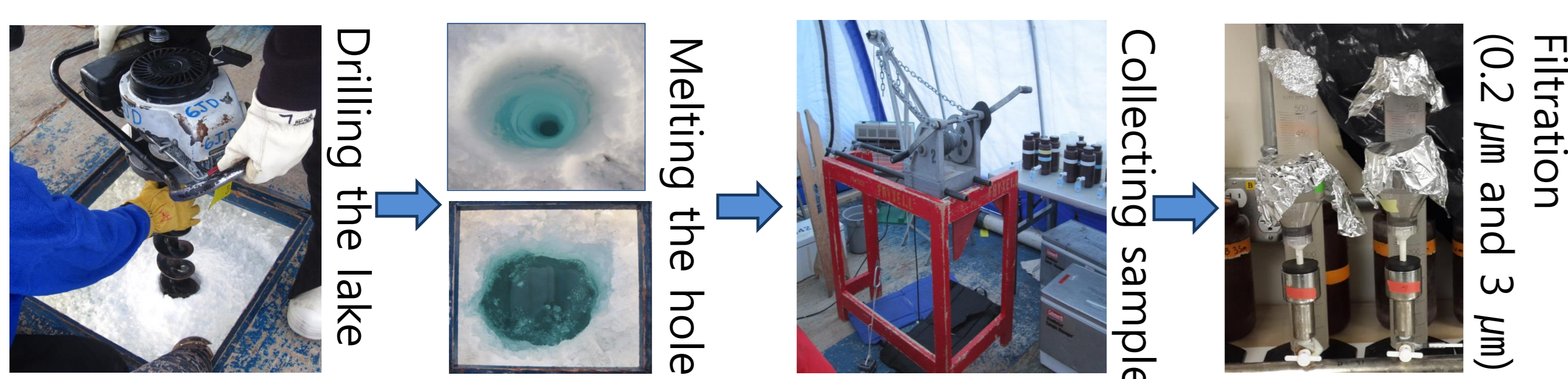


Fig. 2. Sample collection and treatment in the field

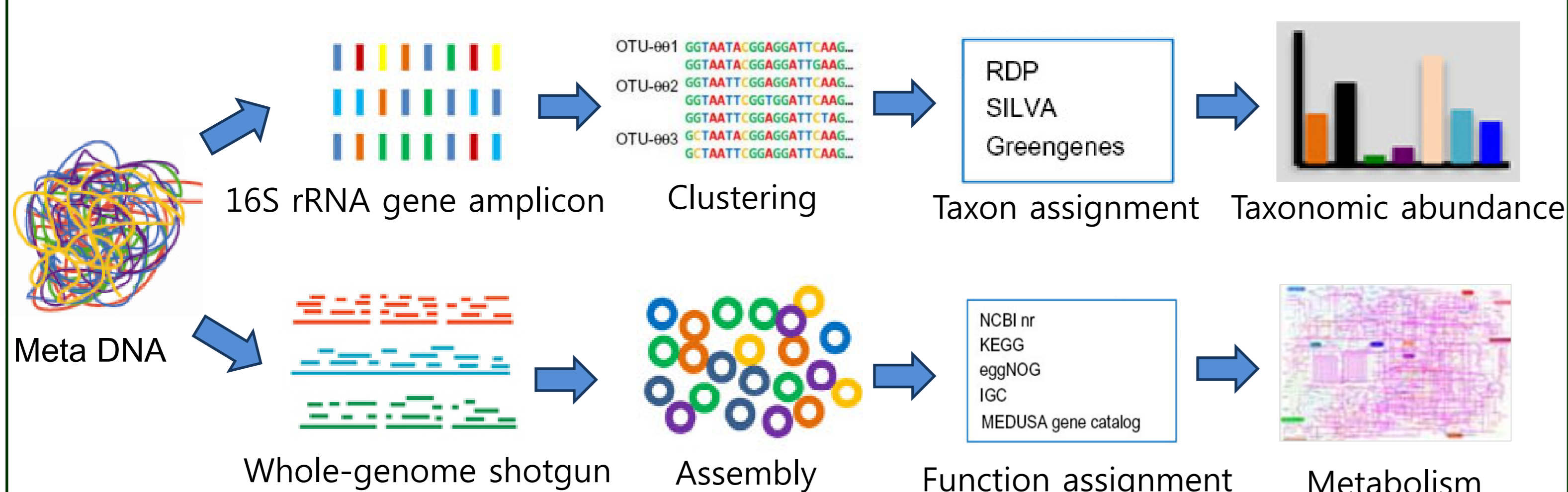


Fig. 3. Flow chart showing overall procedure for analyzing the bacterial diversity and metagenome data