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.

1. Community structures Fryxell 0% 20% 40% 60% 80% 100% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 60% 80% 10% 0% 20% 40% 0% 20% 0% 0

RESULTS

INTRODUCTION

The McMurdo Dry Valleys (MDVs) are located in the largest ice-free region of Antarctica (Vick and Priscu, 2012)

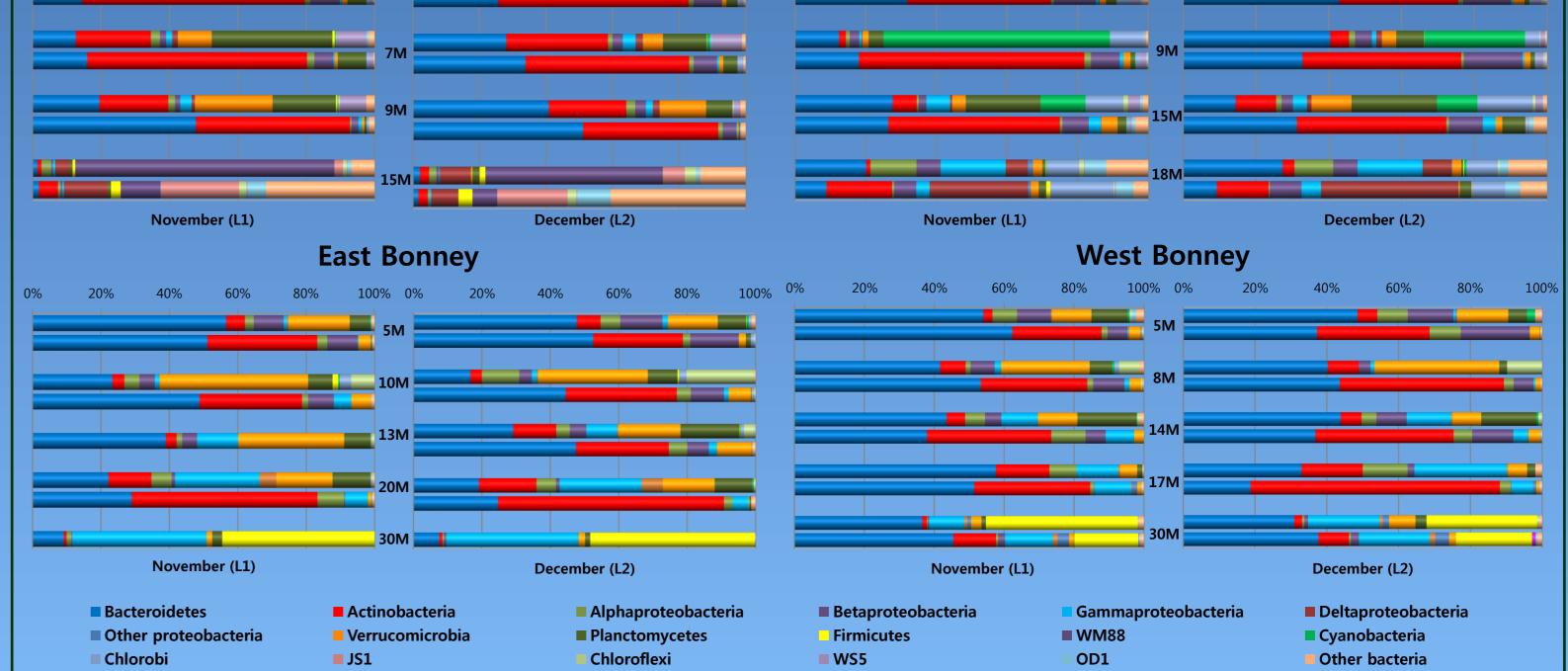


Fig. 4. A comparison of the taxonomic structures in phylum level

2. Patterns of co-occurrence and unique OTUs

	Phylum	Class				Phylum	Class
OTU_015- • • • • • • • • • • • •	Actinobacteria	Actinobacteria_c	оти_136 - 🔴 🔴 🔶 🔸	••••		Actinobacteria	Thermoleophilia
0TU_001- • • • • •	Proteobacteria	Betaproteobacteria	OTU_148 -	• • • • • • • • • • • • • • • • • • • •		WS5	, WS5_c
OTU_137-	Bacteroidetes	Sphingobacteria					_
		Thermoleophilia	OTU_140 -			Verrucomicrobia	Verrucomicrobiae
OTU_003-		Actinobacteria_c	OTU_031 -			Bacteroidetes	Sphingobacteria
OTU_140-		aVerrucomicrobiae	OTU_164 - • • •			Planctomycetes	Planctomycetacia
OTU_017-		Actinobacteria_c	OTU_035 -			Proteobacteria	Alphaproteobacteria
OTU_031-	Bacteroidetes	<i>Sphingobacteria</i>	OTU_226 -				
OTU_126-	Actinobacteria		010_220				Sphingobacteria
OTU_148-	WS5	WS5_c	OTU_023 -			Proteobacteria	Alphaproteobacteria
OTU_005-	Planctomycetes		OTU_004 -			Cyanobacteria	Chroobacteria
OTU_025-		<i>Betaproteobacteria</i> <i>Flavobacteria</i>	OTU_147 -	• • •		Chlorobi	OPB56_c
OTU_149-	Planctomycetes		OTU_020 -			Planctomycetes	Planctomycetacia
OTU_008-		Betaproteobacteria				-	-
OTU_011-		Actinobacteria_c	OTU_079 -	• • •		Bacteroidetes	Flavobacteria
0TU_111-		Thermoleophilia	OTU_137 -			Bacteroidetes	Sphingobacteria
OTU_157 -	Bacteroidetes	Sphingobacteria	OTU_166 -	• • •		Planctomycetes	Phycisphaerae
OTU_009-	Actinobacteria	Acidimicrobiia	OTU_156 -			Bacteroidetes	Sphingobacteria
OTU_020-	Planctomycetes	Planctomycetacia	OTU_286 -				Planctomycetacia
OTU_184-	Actinobacteria	Actinobacteria_c				-	-
OTU_021-	Bacteroidetes	Sphingobacteria	OTU_032 -			Bacteroidetes	Cytophagia
OTU_082 -		Betaproteobacteria	OTU_163 -		• • • • • • • • • • • • • • • • • • • •	Verrucomicrobia	Verrucomicrobiae
OTU_118-	Verrucomicrobi	· · ·	OTU_170-	·····	• •	Proteobacteria	Gammaproteobacteria
OTU_154-	Bacteroidetes		OTU_188 -		• • • • • • • • • • • • • • • • • • • •	Planctomvcetes	Planctomycetacia
OTU_159-		Actinobacteria_c				-	Alphaproteobacteria
OTU_162-	Verrucomicrobi	· · ·	OTU_193 -				
		<i>Gammaproteobacteria</i>	OTU_205 -		• • • • • • • • • • • • • • • • • • • •	Planctomycetes	Planctomycetacia
OTU_014- OTU_293-		Gammaproteobacteria	OTU_207 -		• • • • • • • • • • • • • • • • • • • •	Proteobacteria	Betaproteobacteria
OTU_058-		Alphaproteobacteria Sphingobacteria	OTU_187 -			Actinobacteria	Acidimicrobiia
OTU_163 -		aVerrucomicrobiae	OTU_152 -			Bacteroidetes	Flavobacteria
OTU_032 -	Bacteroidetes	Cytophagia					
OTU_104-		Flavobacteria	OTU_103 -			Flanciomyceles	Planctomycetacia
FRX-5 FRX-7 FRX-9 FRX-15 MIE-7 MIE-9 MIE-15 MIE-18 ELB-5 ELB-10 ELB-20 WLB-5 WLB-8 WLB-14 WLB-17 WLB-3			FRX-5 FRX-7 FRX-9 FRX-	15 MIE-7 MIE-9 MIE-15 MIE-18 ELB-5 EL	B-10 ELB-13 ELB-20 ELB-30 WLB-5 WLB-8 WLB-14WLB-17WLB-30		

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

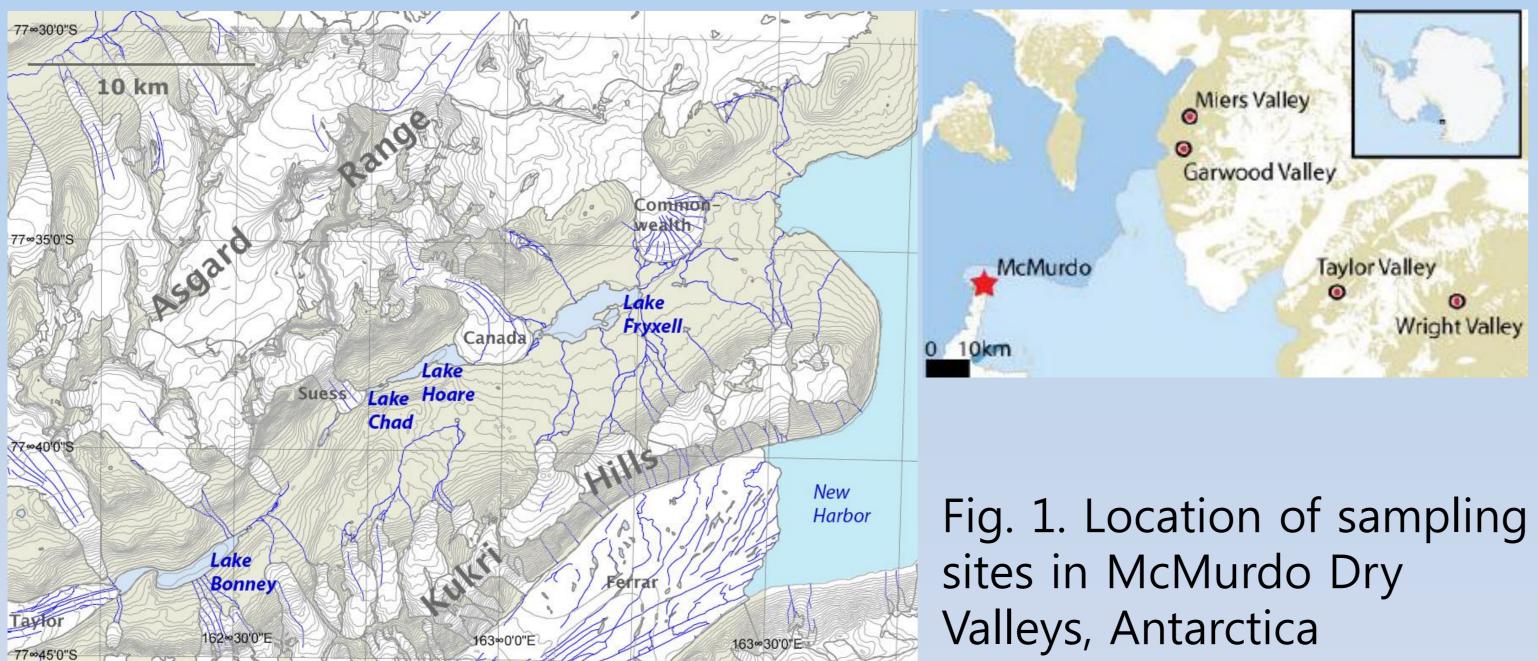
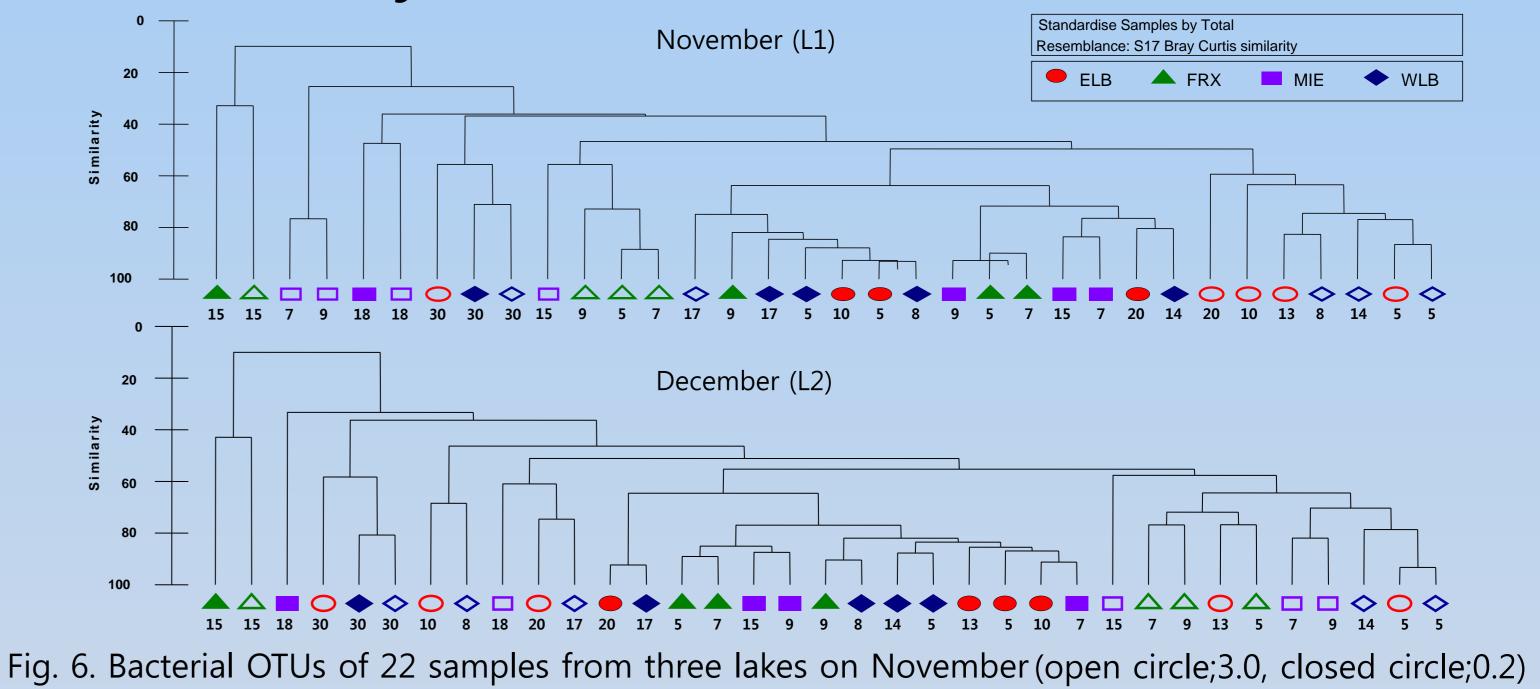


Fig. 5. Relative abundance of bacterial OTUs in 0.2 μ m (left) and 3 μ m (right) on November

3. Cluster analysis



CONCLUSION

http://huey.colorado.edu/diatoms/about/maps.php

2. Methods







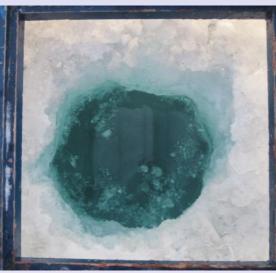


Fig. 2. Drilling of the Ice-cover and sampling in the lakes

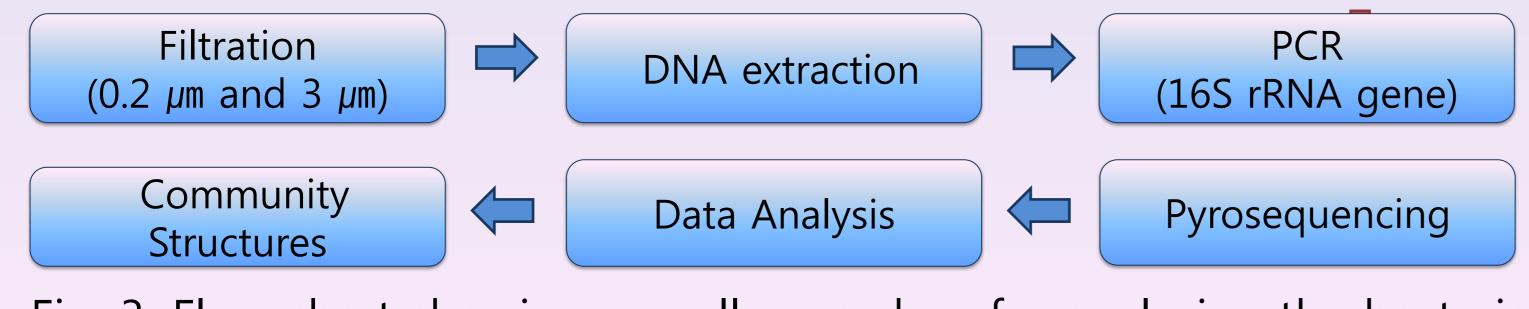


Fig. 3. Flow chart showing overall procedure for analyzing the bacterial diversity in freshwater samples

>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 is 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



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