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Bacterial and Archaeal Diversity in Sediments of West Lake Bonney, McMurdo Dry Valleys, Antarctica

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Bacterial and archaeal diversity was examined in a sediment core from Lake Bonney, Antarctica. Members of the *Archaea* showed both low abundance and diversity, whereas bacterial diversity was moderately high and some phyla were fairly abundant, even in geologically old samples. Microbial diversity correlated with sample texture and differed in silty and coarse samples.

Several permanently ice-covered lakes exist in the McMurdo Dry Valleys, Antarctica (MCM), with ice covers ranging from 3 to 6 m. The limnological properties of MCM lakes can vary dramatically from lake to lake and are likely a response to local geochemical and climatic factors over time (1, 2). Wind mixing and other major currents do not exist in these lakes, and sedimentation is primarily due to aeolian dust, soil, and weathered rocks that blow onto the ice cover and are transported through the ice to the sediments (3). Benthic microbial mats stabilize and colonize MCM lake sediments (4), and repeated cycles of microbial mat growth and burial by deposition are thus the main sediment-forming mechanisms (3, 4). This process is very slow; estimates of sediment accumulation from sediment traps show a rate of just 0.02 to 0.9 mm year^{-1} (3), and sediments are well preserved on time scales of thousands of years (5).

We have examined microbial diversity in the sediments of west Lake Bonney (WLB), located in the Taylor Valley. From a nearly 4-m core of WLB sediments, we sampled five sections (Table 1); DNA was extracted from each, and 16S rRNA genes were resolved by denaturing gradient gel electrophoresis (DGGE) and/or clone library construction (see the supplemental material).

DGGE analyses of 16S rRNA gene products from members of the *Bacteria* yielded 46 bands (Fig. 1A). The banding patterns in sections 5I, 5II, and 4I were very similar, while section 4II yielded the most distinct pattern (Fig. 1A). Major phylotypes included the *Bacteriodetes* (22 bands) and the *Proteobacteria* (10 total bands, with 4 members of the *Alphaproteobacteria*, 1 of the *Betaproteobacteria*, and 5 of the *Gammaproteobacteria*). Other phyla included the *Firmicutes* (5 bands), the *Actinobacteria* (3 bands), and one member of the *Acidobacteria*. Archaeal DGGE profiles showed very few bands (Fig. 1B), all of which associated with members of the *Thaumarchaeota* and the *Crenarchaeota* from various environments; these likely originated with sediment deposition. The assemblages of the *Archaea* were indistinguishable except for sample 4II. Only one archaeal phylotype was found previously in the Lake Bonney water column, and it was associated with the *Euryarchaeota* (6). Thus, the water column and the sediments appear to support different phyla of the *Archaea*.

Individual clone libraries for the *Bacteria* were constructed for all samples except 5II. The four libraries contained a total of 442 clones (175 operation taxonomic units [OTUs] [Table 1]). Partial 16S rRNA gene sequences were obtained for 290 clones; section 4I yielded 137 clones, 4II yielded 68 clones, 5I yielded 63 clones, and 5III yielded 22 clones. Both the Shannon diversity index (SDI) and Chao-1 analysis showed moderately high bacterial diversities in all

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TABLE 1 Sample characteristics of a 4-m WLB sediment core and clone library analyses for members of the *Bacteria*

Section	Depth (cm)	Texture description	Composition	No. of clones	No. of OTUs	Chao-1 value with 95% confidence interval[a]	Good's coverage (%)	SDI
4I	5–10	Intermediate dryness with silt/sand, few pebbles	Mixture of microbial mat and terrigenous materials	188	111	272 (194, 421)	60.6	4.5
4II	50–55	Solid, large clasts, sand/soil-like	Mainly terrigenous particles	106	60	129 (89, 222)	63.2	3.9
5I	150–155	Very moist, fine-grained material	Microbial mat	106	53	110 (75, 197)	69.8	3.7
5II	250–255	Larger clasts with some fine-grained material	Mixture of microbial mat and terrigenous materials					
5III	350–355	Large dry clasts, coarse material	Mainly terrigenous particles	42	22	78 (35, 272)	64.3	2.8
Total				442	175	383 (294, 538)	76.9	4.7

[a] Chao-1 95% confidence interval lower bound and Chao-1 95% confidence interval upper bound are shown in parentheses following Chao-1 richness estimation.

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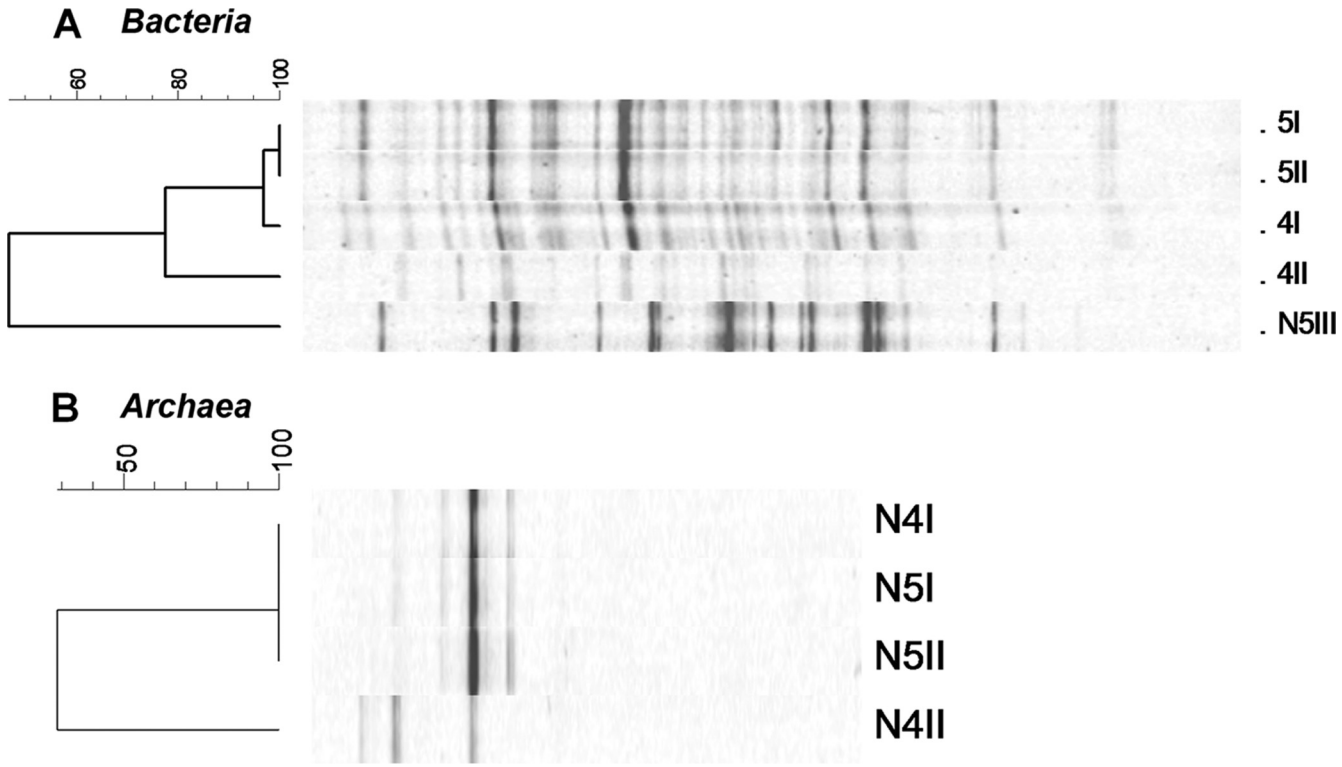

FIG 1 UPGMA cluster analysis of the bacterial and archaeal community structure in each WLB core section based on the DGGE banding patterns and OTU distribution of bacterial clone libraries. Dice similarity coefficients of bacterial DGGE banding patterns (A) or archaeal DGGE banding patterns (B) are shown. "N" in front of the gel label indicates nested PCR. Note that sample 5III did not yield a PCR product for the *Archaea*.

sediment sections (Table 1). Good's coverage varied from 60% to 70%, suggesting that cloning captured the dominant phylotypes. Both Chao-1 and SDI values decreased with depth, while Good's value increased (except in section 5III) (Table 1), signaling a general decrease in bacterial diversity with increasing depth in the sediment.

The *Bacteroidetes* and the *Proteobacteria* were the dominant phyla (~36 and 38%, respectively) (Fig. 2). Low-abundance phyla included the *Planctomycetes* (5.2%) and the *Verrucomicrobia* (4.3%); TM7, the *Chloroflexi*, WYO, and the *Lentisphaerae* had two or fewer clones each (Fig. 2). The bacterial assemblage in core section 5III was clearly distinct from those in the other sections, and each section contained several unique OTUs: 4I, 50%; 4II and 5I, 25% each; and 5III, 57%. The software program TreeClimber indicated that the assemblages in sections 4I and 5I were not sig-

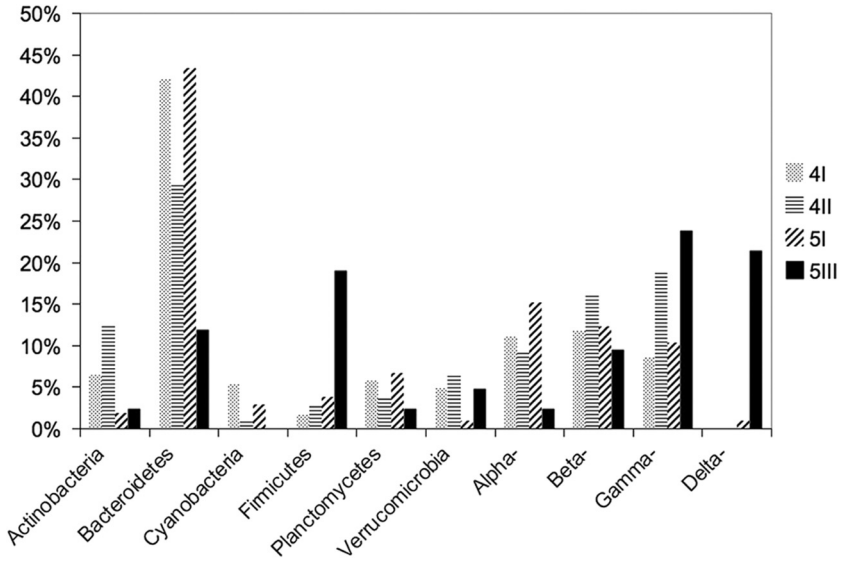

FIG 2 Distribution of bacterial phyla in each individual clone library. The *y* axis represents each (sub)phylum's clone coverage of each section's clone library. Low-abundance phyla not shown included the *Acidobacteria* (3 clones; section 4I had 2 singlets, and section 5I had 1 singlet), candidate division TM7 (section 4I had 2 singlets), the *Chloroflexi* (section 4I had 1 singlet), candidate division WYO (section 5I had 1 singlet), and the *Lentisphaerae* (section 5III had 1 singlet).

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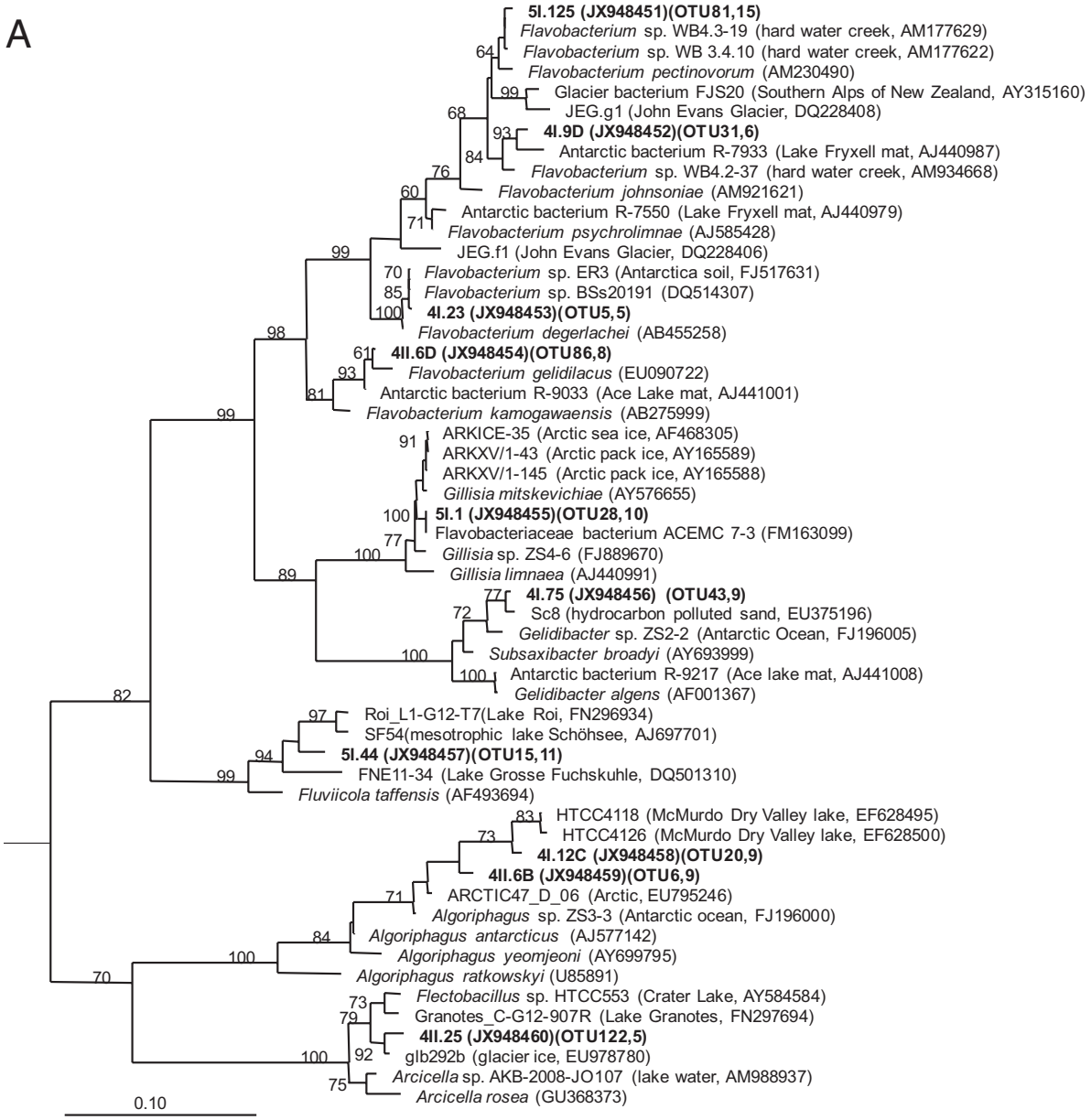

FIG 3 Phylogenetic analysis of major OTUs of the *Bacteroidetes* (A) or the *Proteobacteria* (B) from the WLB sediment core. Bolded sequences are from this study; one representative clone from each major OTU is shown, and in the following parentheses, the OTU name and the number of clones belonging to this particular out, separated by a comma, are listed. Both trees were rooted with *Bacillus subtilis* (D26185) and constructed by maximum likelihood. A mask of 702 (A) or 691 (B) nucleotides with nonambiguously aligned positions was used. Bootstrap values (100 replicates) above 60 are shown above relevant nodes. GenBank accession numbers of sequences from other studies are included.

nificantly different from each other but that the assemblage in 4II was distinct (see Table S3 in the supplemental material). Moreover, the ∫-LIBSHUFF software program indicated that clones from 4II and 5I could be subsets of 4I but those from sections 4II and 5I were distinct (see Table S3).

About 50% of the WLB sediment clones grouped in OTUs having at least five representatives ("major OTUs"). Many of these clustered within clades that contained phylotypes identified in Antarctic or other constantly cold environments (Fig. 3; see also Fig. S1 in the supplemental material). Three major OTUs (OTU 127 and OTU 140 of the *Gammaproteobacteria* and OTU 44 of the *Planctomycetes*) were closely related to phylotypes from the WLB water column (6). Except for members of the *Firmicutes* related to halophilic phylotypes (see Fig. S1), the remaining major OTUs were related to phylotypes identified in diverse environments and are likely derived from external sources.

Bacterial diversity was higher in WLB sediments than in the water column. Major bacterial phyla detected in sediments included all of the phyla detected in Lake Bonney water, such as the *Bacteriodetes* and the *Proteobacteria* (6), plus several minor phyla. The moderately high bacterial diversity found even in old sediment sections underscores the similarity of WLB sediments to stromatolites in preserving a record of prokaryotic diversity. The five sections of the core were of different textures, indicating different sources of sedimentary material. The fine, silty layers were likely derived from relic microbial mats. Phylotypes retrieved from

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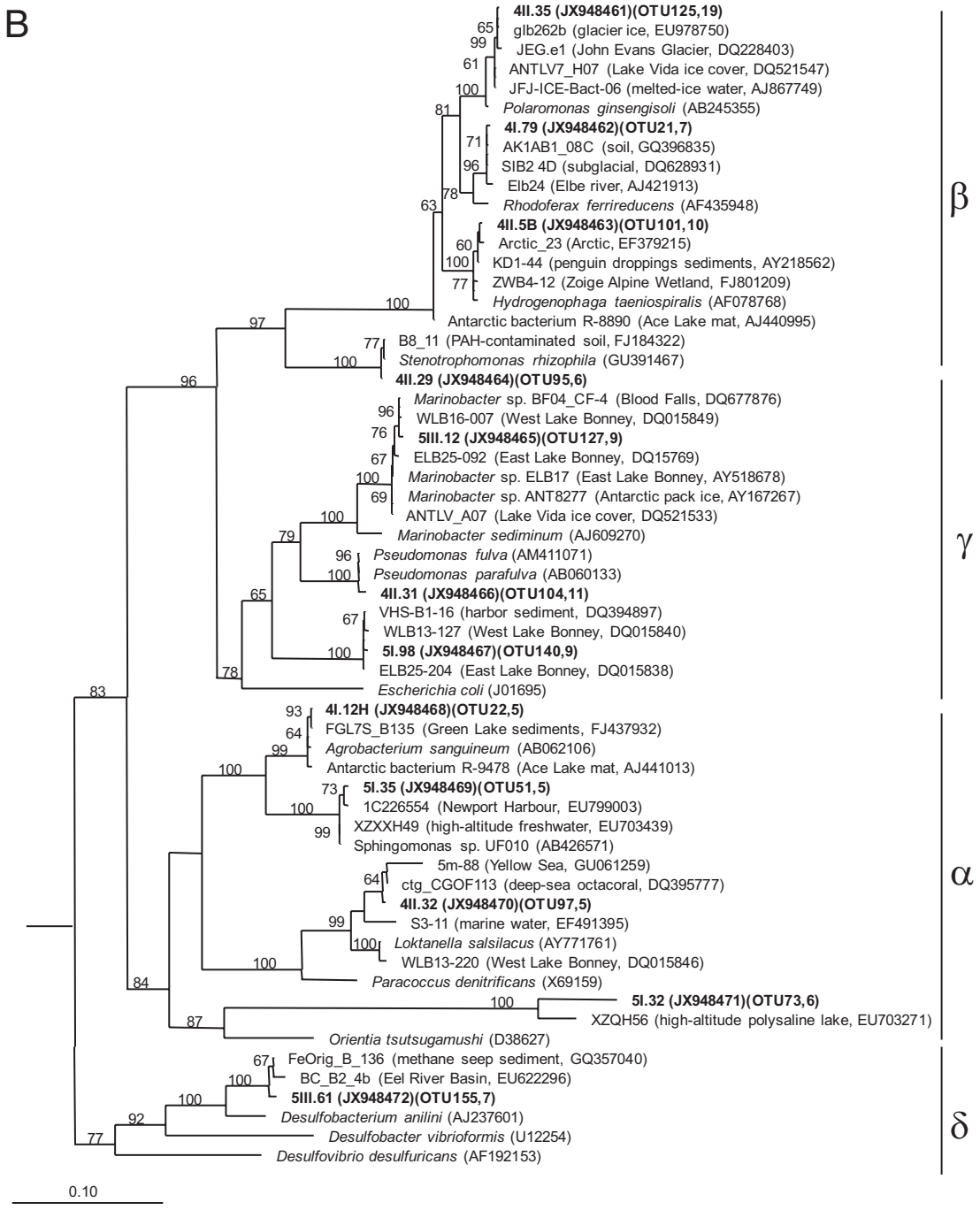

FIG 3 (Continued)

such samples were closely related even though they were physically separated in the core and thus were of different ages. This may reflect the unique composition of microbial mats and underscores the fact that diversity can be preserved over long time periods.

The sandy and clastic layers probably contained more terrigenous materials from episodic depositions of particles blown in from the surrounding hills. We hypothesize that under different climatic conditions, the terrigenous materials that form the clastic samples are probably associated with different bacterial communities. Thus, silty samples would be useful for testing the evolution of microbial mats in MCM lakes, while clastic samples might be useful for examining the effect of climatic conditions on MCM microbial communities.

In summary, WLB sediments appear to be composed of both stromatolite-like mat-derived materials, with their layered structure and long-term record of microbial diversity, and rougher, more clastic materials. Prokaryotic diversity in fine-grained WLB sediment layers varied less with depth than did layers consisting of primarily clastic terrigenous materials. The microbial diversity of the coarse layers may therefore be a better record of climatic impacts and wind-blown materials than are the fine-grained sediments. We conclude that differences in prokaryotic community

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structure among the WLB sediment samples are related to different patterns of sedimentation over time, which are themselves the legacy of past geochemical and climatic events (2).

Nucleotide sequence accession numbers. DDBJ/EMBL/GenBank accession numbers for sequences obtained in this work are JX948451 to JX948742.

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