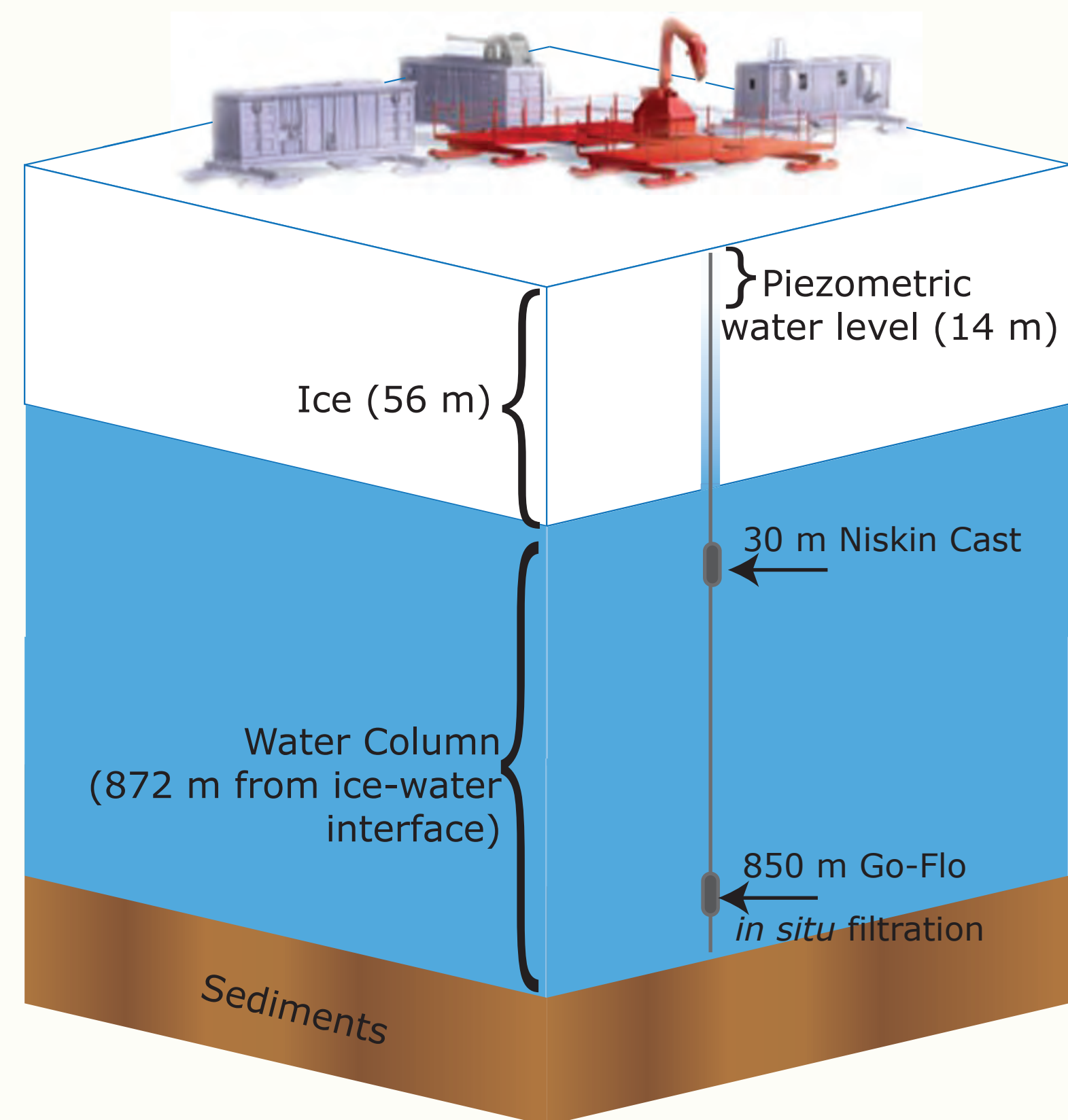


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Abstract

The McMurdo Ice Shelf lies off of the Victoria Coast of Antarctica, and comprises the northwest corner of the Ross Ice Shelf (Figure 1). The underlying water is mainly sourced from McMurdo Sound via a channel to the Ross Sea. In December 2012, we penetrated the McMurdo Ice Shelf with a hot water drill. Water samples were collected with Niskin bottles deployed to 30 m and 850 m below the ice water interface and an *in situ* water filtration unit deployed to 850 m was used to collect samples for DNA extraction. Physical characteristics of the water column (depth=917 mbsl) were profiled with a CTD. Samples from both depths contained $\sim 10^5$ cells mL⁻¹ and 2 – 3 mg chl-a L⁻¹. DNA was successfully extracted from the 850 m sample for microbial community characterization. DOC concentrations were greater at 30 m than at 850 m, but heterotrophic activity was higher at 850 m than at 30 m, while dark incorporation of ¹⁴C-bicarbonate was similar at both depths. Fluorescence analysis of dissolved organic matter revealed DOM of mainly microbial origin, consistent with expected limited allochthonous inputs to the ice-shelf cavity. These data provide new insights into an under-sampled oceanic environment.

Sample collection



The WISSARD hot water drill was used to melt a hole through the ~ 56 m thick McMurdo Ice Shelf (77°53'25"S and 167°0'30"E) in December 2012. Water samples were collected using 10 L Niskin and 5 L Go-Flo bottles (General Oceanics), and an *in situ* filtration sampler (McLane). CTD profiles were collected with a Seabird 19PlusV2 CTD. Water samples and filters were transported to the lab at McMurdo Station in insulated containers and processed within 8 hours of collection.

Figure 2. Schematic view of the sample site and sample collection (drill platform drawing modified from one by the U.S. Department of State).

Microbial community activity and structure

Microbial activity measured by ³H-leucine and ³H-thymidine uptake was significantly greater in the deep than in the shallow water samples ($P = 0.048$ and $P = 0.002$), but rates of carbon fixation (measured as uptake of ¹⁴C-bicarbonate in the dark) were similar at both depths (Figure 5). Sequence data based on the v4 region of the 16S rRNA gene indicate microbial communities dominated by Proteobacteria. Within the Proteobacteria, 42% of sequences belonged to members of the ubiquitous SAR11 clade, many of which are well adapted to oligotrophic or otherwise energy limited environments. The most abundant archaeal group, the *Thaumarchaeota* are known to include ammonia oxidizers.

Figure 5. Microbial activity measured as uptake of ³H-leucine (Leu), ³H-thymidine (TdR), and ¹⁴C-bicarbonate (Bicarb) and converted to units of carbon production. All incubations were done in the dark. Shallow=30m, Deep=850m.

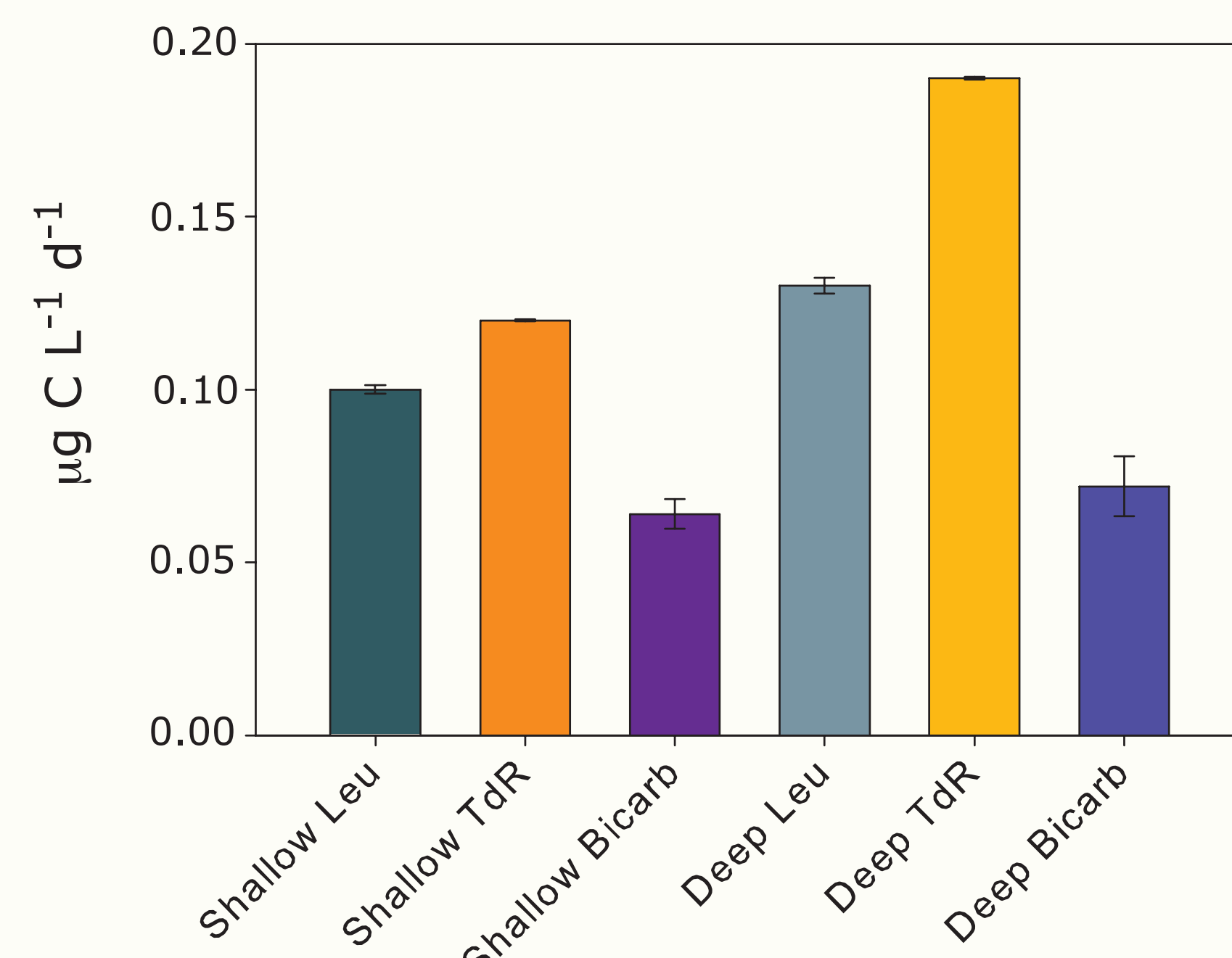


Figure 6. Phylum level taxonomic classification of microbial diversity ~ 850 m beneath the Ross Ice Shelf. Approximately 300 L of water was filtered *in situ*. Sequences were obtained by amplification of the v4 region of the 16S rRNA gene with universal primers 515F and 806R. Italicized names are archaeal; others are bacterial.

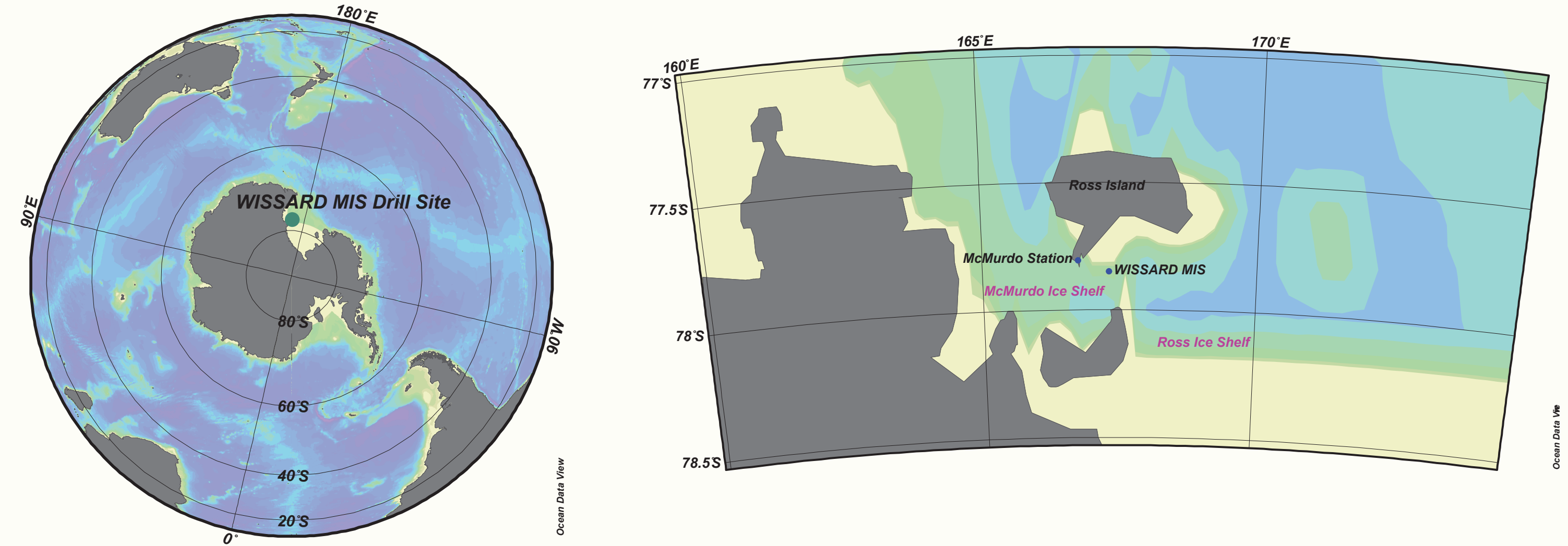
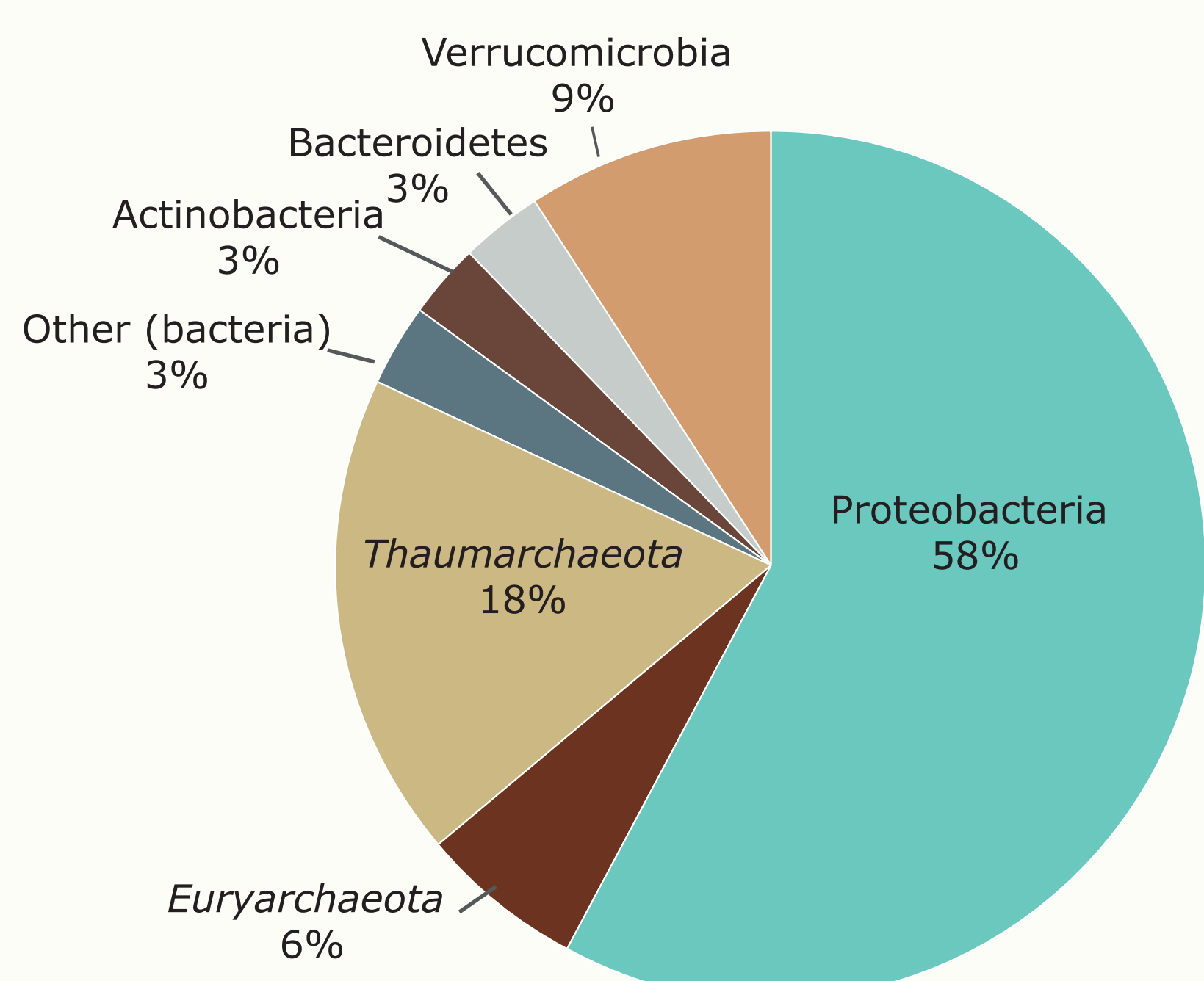


Figure 1. Map showing the location of the sample site, approximately 10 km from McMurdo Station. The site was chosen partially because of its proximity to McMurdo Station, and partly because of the depth of the water column.

Physical, chemical, and biological characteristics

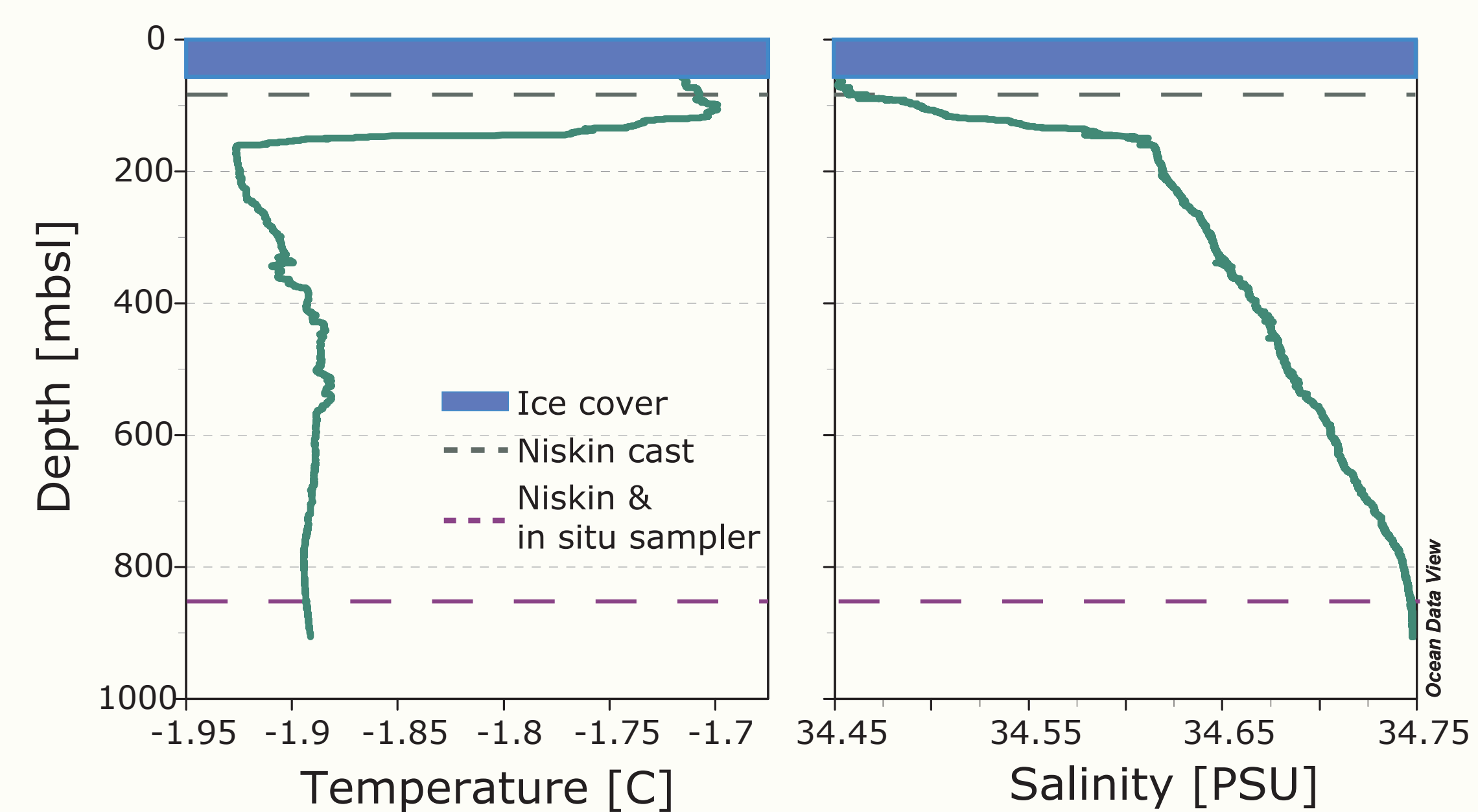


Figure 3. CTD profiles taken prior to the first sample collection. The shallow temperature anomaly matches that recorded by Robinson *et al*, 2010.

Table 1. Chemical and biological parameters

Analyte	Sample	
	Shallow	Deep
POC (µM)	28.4	26.1
PON (µM)	2.2	1.9
C:N (atomic)	11.3	12.0
DOC (µM)	42.1	31.8
Chl-a (µg L ⁻¹)	2.4	2.9
Cells mL ⁻¹ × 10 ⁵	3.4	5.7
Total ions (meq L ⁻¹)	1220	1225
DO (µg O ₂ L ⁻¹)	10.7	11.8

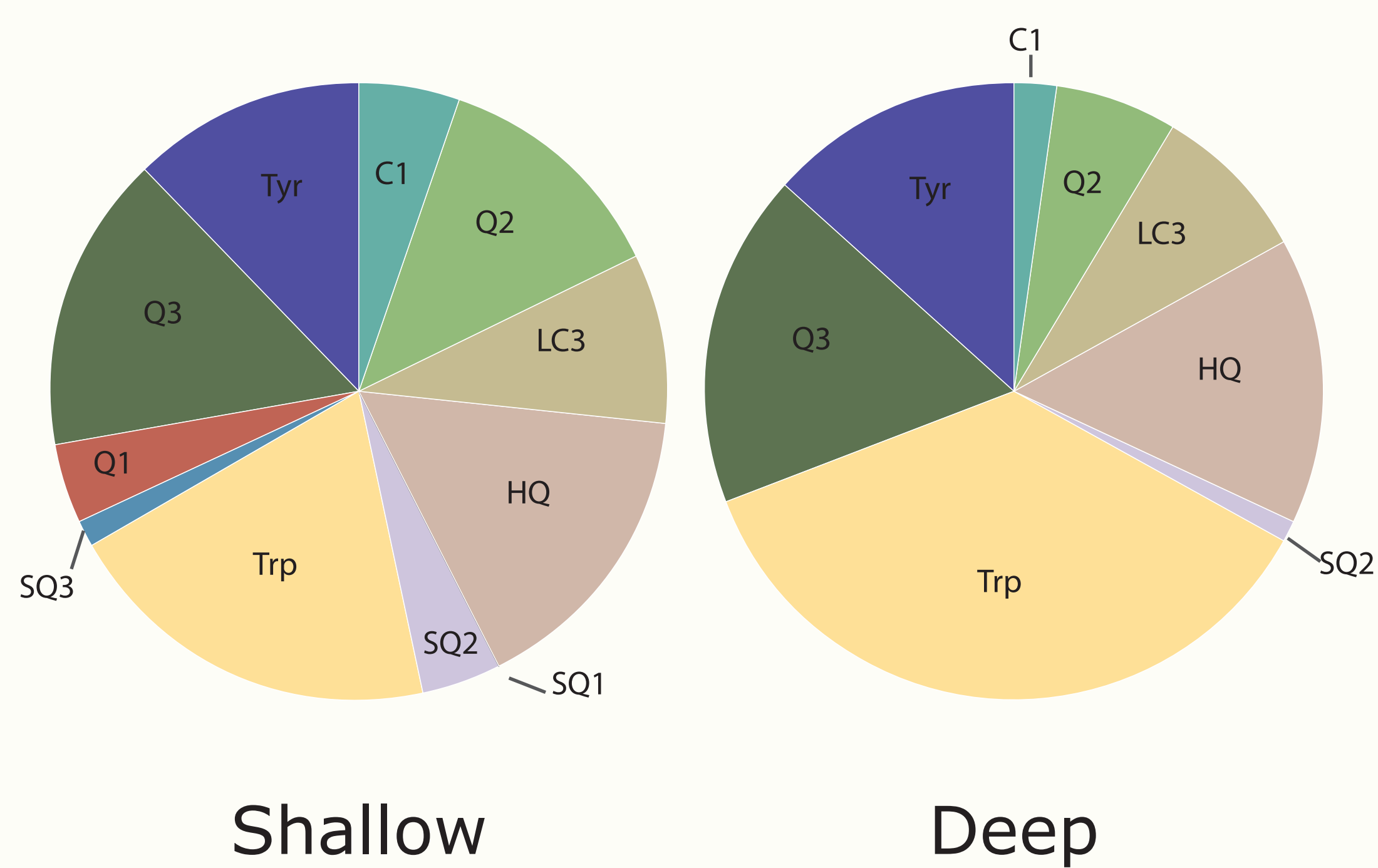


Figure 4. Components of fluorescent dissolved organic matter (DOM) resulting from PARAFAC²-modelled excitation emission matrix spectroscopy output. C1 and LC3 are unknown components. Q1, Q2, and Q3 are oxidized quinone-like components; SQ1, SQ2, SQ3, and HQ are reduced quinone-like components; Trp and Tyr are amino acid like components.

Conclusions

Sub-Ross Ice Shelf waters near McMurdo Sound are relatively well-mixed and contain relatively high concentrations of Chl-a, indicating advection from open-water, which is probably sourced from McMurdo Sound¹. Particulate organic matter was slightly richer in carbon relative to nitrogen at depth, while the bulk concentration of dissolved organic matter (DOM) decreased. The fluorescent component of the DOM lacked some quinone-like components, and was richer in amino-acid like components at depth, indicating possible microbial processing of DOM in the water column and/or transport of microbially processed DOM to depth. Rates of heterotrophic microbial activity were higher at depth, while dark carbon dioxide fixation rates were similar in the shallow and deep sample. The presence of *Thaumarchaeota* in the sequence data suggests ammonia oxidation as a potential chemoautotrophic carbon fixation mechanism, however, rates of dark carbon dioxide fixation were exceeded by rates of heterotrophic carbon production at both depths. Thus, the waters beneath the Ross Ice Shelf contain active microbial consortia whose activity is probably fueled mainly by carbon and nutrients advected from open water.