

Microbial Diversity in Soil Cores from the Yukon River Basin, Alaska

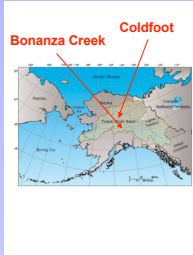
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Problem

Understanding microbial diversity in permafrost areas is an important part of assessing the impact of carbon and nutrient release from soils as permafrost melts. In controlled experiments, it has been shown that bacterial abundance and richness increase with increasing primary productivity (Horner-Devine and others, 2003). As part of a larger investigation to examine carbon cycling within the river basin, this study was designed to answer the question: What is the microbial abundance and diversity in active layer soils and permafrost soils in the Yukon River Basin?

Methods

Two soil cores within the Yukon River Basin, Alaska, were collected in summer 2005 for analysis. One site was located at the Bonanza Creek Long-Term Ecological Research Site near Fairbanks in an area of discontinuous permafrost and the other site was located 400 kilometers to the north near Coldfoot, Alaska, in an area of continuous permafrost within the Arctic Circle. Both sites are characterized as black spruce forest with permafrost depths averaging 42-55 cm below land surface.



Soil samples were collected from a range of depths above and below the permafrost and analyzed for (1) total and living bacteria by counting using DAPI stain, (2) culturable bacteria by the most probable number (MPN) method for nine metabolic types of microorganisms using methods developed by Bekins and Warren, 1999, and (3) five metabolic types of microorganisms using quantitative polymerase chain reaction (qPCR) to analyze soil DNA.

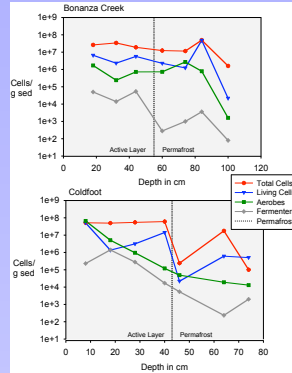
Results

Water Chemistry

	T	pH	DOC	NO ₃	NH ₄	SO ₄	PO ₄	CO ₂	CH ₄
	°C		mg/L	µeq/L	mgN/L	µeq/L	mgP/L	mmol/L	µmol/L
Bonanza Creek (42 cm bls)	9.9	5.06	108	0.3	0.18	19	0.018	9.6	8.2
Coldfoot (23 cm bls)	5.3	4.35	38	<0.2	0.019	19	0.007	2.1	0.66

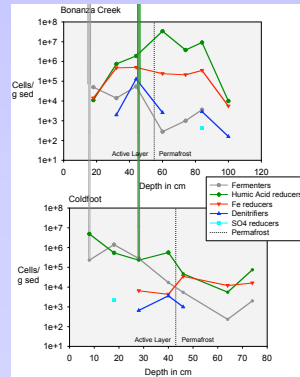
Soil pore waters in the active layer at the Bonanza Creek site had higher pH, DOC, and dissolved CH₄ and CO₂ compared to the Coldfoot site. Dissolved oxygen was measured at >1.0 mg/L in water pumped from piezometers at both sites.

Abundances of Total Bacterial Cells, Living Cells, Aerobes, & Fermenters



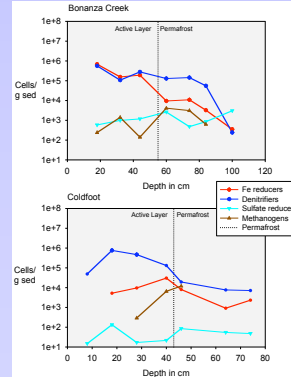
Total microbial abundances were from 1×10^5 to 6×10^7 cells/g dry weight sediment in 14 samples analyzed from the 2 cores. Living bacteria account for 1.4 to 98% of the total. An active ecosystem is indicated by the presence of dividing cells from 0.7 to 7% of total living cells in all samples except one and the presence of protozoa (data not shown). The aerobes account for a large portion of the living bacteria. Fermenters were cultured as well even though oxygen was present in water associated with the sediment.

MPN Analysis for Reducing Bacteria and Archaea



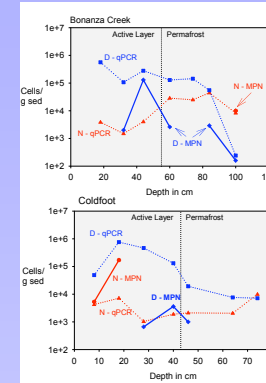
Data show a general decline with depth, although the abundances of humic acid reducing bacteria are high, particularly in the Bonanza Creek samples. It is likely that the humic acid reducers are the same bacterial types as the Fe reducers and fermenters. Denitrifiers and SO₄ reducers were found in only a few samples and no methanogens were found by this method.

qPCR Analysis for Reducing Bacteria & Archaea

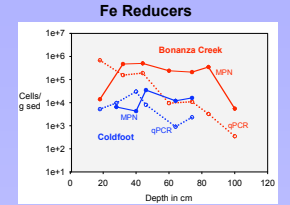


Using the qPCR method, denitrifiers and SO₄ reducers were in all samples and methanogens were in 9 out of 14 samples. The difference between the MPN and qPCR data is most likely because the qPCR method is a culture independent method for determining living and dead cells whereas the MPN method cultures living cells in a selective media.

Comparison of qPCR and MPN Data for: Nitrifiers (N) & Denitrifiers (D)



Nitrifiers and Denitrifiers were identified in all soil samples using qPCR whereas they were detected in a few samples by MPN analyses.



The abundances and trends for data from the qPCR and MPN methods were most similar for the Fe reducers. For the qPCR experiments, *Geobacter* abundances were generated to represent abundances of Fe reducers and the detection limit was about 10^1 . The abundances are higher in soils from the Bonanza Creek site and the trends for the MPN & qPCR data are consistent at each site.

Conclusions

- The active layer and upper 40 cm of the permafrost support a healthy microbial ecosystem as demonstrated by finding a diverse population of aerobic and anaerobic bacteria cultured from soils, the finding of living cells in the 10^4 to 10^7 range, and the presence of dividing cells and protozoa.
- Although the microbial abundances decreased with depth, significant abundances of bacteria were in the permafrost and, in most cases, no sharp declines were observed at the permafrost boundary, which demonstrates that these organisms are well acclimated to freezing temperatures.
- The abundances of bacteria were as high as 10^6 to 10^7 for aerobes, humic acid reducers, fermenters, and iron reducers. These are high bacterial abundances for a cold climate (<10 °C) and it may reflect the high concentration of organic carbon, which was measured as high as 47% dry weight.
- In general the microbial abundances were higher at the Bonanza Creek site compared to the more northern site at Coldfoot. The temperature, water chemistry, and microbial abundances suggest more decomposition of organic material might be occurring at the Bonanza Creek site than at the Coldfoot site.
- The microbially diverse soils in black spruce forests of the Yukon River Basin have the potential to metabolize carbon as permafrost melting increases.

Acknowledgements

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References

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