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Microbial Community and Diversity Changes After a Hydrocarbon Spill on a Pristine Antarctic Lake

Abstract:

In January of 2003 a Bell Helicopter crashed on a pristine lake in Antarctica, which serves as a site of long-term ecological research, and resulted in a mixed hydrocarbon spill comprised mostly of diesel fuel (Alexander and Stockton 2003).

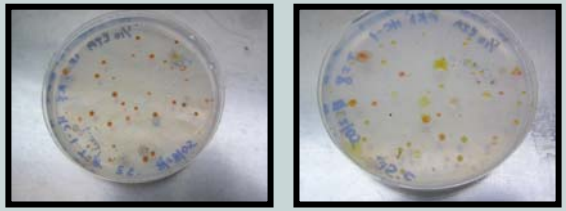
Experimental studies of hydrocarbon contamination in sea ice have shown inhibitory effects on the growth and activity of microorganisms. Diesel fuel has been shown to be very toxic, stopping growth immediately and inhibiting growth throughout the season (Fiala and Delille 1999).

Little is known about the effects and toxicity of hydrocarbons on microorganisms in cold-adapted environments, therefore it is important to assess the impacts of the spill to determine its influence on biological activity and diversity.

The diesel fuel will eventually migrate through cracks and grain boundaries in the ice until it reaches the liquid portion of the lake. Since Lake Fryxell is a hydrologically terminal lake (lacking an outflow) the hydrocarbons could exist within the lake for extended periods of time inhibiting microbial processes and growth in the water column. Indigenous microflora in the lake ice may have biodegradation capabilities, therefore the hydrocarbons may have the potential to be degraded before reaching the water column.

Figure 1. Lake Fryxell ice cover showing the location of the fuel spill

Materials and Methods:



Before fuel addition — After fuel addition

Figure 2. Uncontaminated and contaminated ice core was melted and plated onto solid 1/10 R2A agar. While many of the same colony types exhisted on both plates, several different colony types were observed on the contaminated plate.

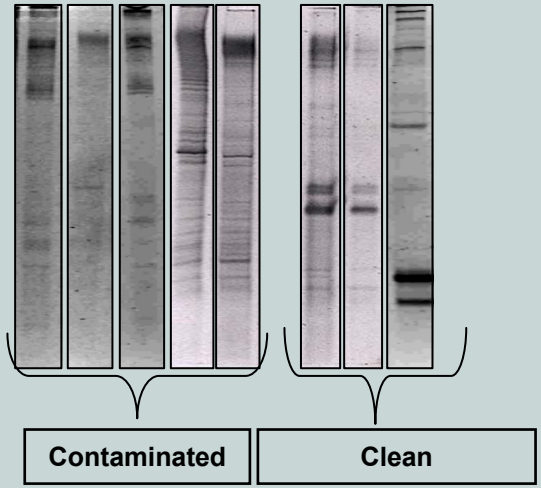


Figure 3. TTGE analysis of 16S rDNA (*E.coli* # 341F- 534R) from clean and contaminated Lake Fryxell lake ice sediment.

Results:

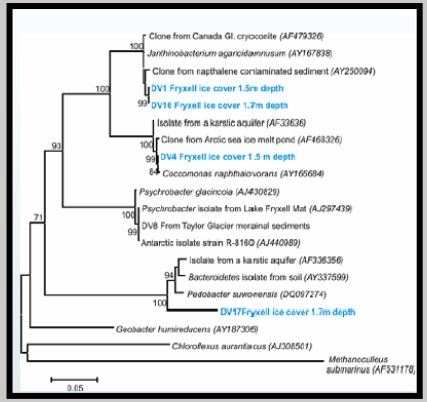


Figure 4. Isolates were obtained from ice cores prior to the fuel spill in 2001. A neighbor-joining tree was constructed based on evolutionary distance between sequences. Genomic DNA was extracted from isolates and partial sequence for the 16S rRNA was obtained. Isolatesfrom Lake Fryxell ice cover are shown highlighted in blue. Isolates from the *Beta-Proteobacteria* are closely related to known naphthalene degraders suggesting the ability to degrade complex hydrocarbons is present in the natural ice community assemblage.

Conclusions:

Little is known about the effects and toxicity of hydrocarbons on microorganisms in cold-adapted environments.

Changes in community and diversity was observed in both the TTGE analysis and culturing methods.

The identification of several hydrocarbon degrading organisms present before the spill suggests the potential for bioremediation in *situ* before the hydrocarbons contaminate the water column.

Acknowledgments:

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