

TERRESTRIAL PERMAFROST AS A MODEL ENVIRONMENT FOR BIOASTRONOMY

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The longevity of (micro)organisms in cold environments is of great interest to astrobiology since cryospheres are common phenomena in the solar system, particularly on satellites, comets and asteroids, and on some of the planets. Recent data from the Mars Global Surveyor mission suggest the possibility of permafrost or perhaps even liquid water under the Martian surface (Malin and Edgett, 2000). The probability of finding life on Mars, if it exists, is certainly higher in such environments. In addition, the evaluation of the possibility of transfer of living organisms between planets via impact ejecta (e.g., Mileikowsky et al., 2000b) requires more information on the maximum time over which microorganisms in cold environments can remain dormant and subsequently revive and reproduce.

Our strategy for the search for extraterrestrial life or its remnants is based on studying the most probable environments in which life (extant or extinct) may be found, and determining the maximum period of time over which such life could be preserved. The terrestrial permafrost, inhabited by cold adapted microbes, can be considered an extraterrestrial analog environment. Permafrost trapped cells and their metabolic end-products can teach us about possible ecosystems and potential inhabitants on extraterrestrial cryogenic bodies (Gilichinsky et al., 1993). And cells (or their remnants) that have been buried for millions of years also provide us with a unique opportunity to study the long-term viability of (micro)organisms.

Permafrost occupies a significant part of North America and Eurasia, and accounts for a total of 20% of the Earth's surface. These areas provide a temperature stable environment that allows for the prolonged survival of microbial lineages at subzero temperatures. The first reports of the existence of bacteria in permafrost appeared at the beginning of the 20th century, in relation to the discovery of mammoths and to studies of soils in Siberia, and then in the Canadian Arctic, Alaska and Antarctica. Viable bacteria have been isolated and cultured from Siberian permafrost core sections dated by stratigraphy at up to a few million years old (Gilichinsky et al., 1992) and microorganisms from ancient permafrost have been revived and isolated in pure culture (Vishnivetskaya et al., 2000). Preliminary 16S rRNA analysis of microbial communities from permafrost of different ages (Shi et al., 1997) has also been reported.

We have analyzed the degree of racemization of aspartic acid in permafrost samples from Northern Siberia, an area from which microorganisms of apparent ages up to a few million years have previously been isolated and cultured. We find that the extent of

aspartic acid racemization in permafrost cores increases very slowly up to an age of approximately 25,000 years (around 5 m depth). The apparent temperature of racemization over the age range 0-25,000 years, determined using measured aspartic acid racemization rate constants, is -19°C. This apparent racemization temperature is significantly lower than the measured environmental temperature (-11 to -13°C), and suggests active recycling of D-aspartic acid in Siberian permafrost up to an age of around 25,000 years. This indicates that permafrost organisms are capable of repairing some molecular damage incurred while they are in a “dormant” state over geologic time, and may therefore survive for much longer periods of time than we thought possible.

Permafrost, alone among cold environments, offers a sedimentary column in which we can observe the preserved genetic material of the history of biological evolution during the last several hundred thousand or maybe even a few million years. A thorough study of the phylogenetic relationships of organisms at each depth, as well as comparisons between different depths, using molecular evolution techniques, will give us a unique window into the process of the evolution of microbial communities over geologic time. Permafrost presents a golden niche for future biotechnology, and is also a unique environment for studying longevity and survivability microorganisms (pro- and eukaryotes).

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