

ASSESSING THE IMPACT OF PROTEINS ON ICE STRUCTURE USING NUCLEAR MAGNETIC RESONANCE.

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Ice is an important form of water in the solar system. In polycrystalline ice, liquid water gathers at the interstices between ice crystals, due to freezing temperature depressions near grain boundaries, resulting in a complicated and dynamic pore structure of liquid-filled intercrystalline veins within a solid ice matrix [1]. Impurity concentrations, temperatures and pressures influence this vein network structure and impact physical, transport and rheological properties of ice. However, the nature of the internal pore structure is not fully understood, but has been suggested as a potential habitat for microbes [2]. Recent research on cryospheric systems on Earth has shown that microorganisms can remain viable within glaciated environments [3–5] and even metabolically active at sub-zero temperatures [6,7]. Life discovered in these environments expands the Earth's biosphere to include the continental ice sheets of Antarctica and Greenland and suggests a habitat for life elsewhere in our solar system, such as the polar ice caps on Mars [8] or in the ice shell of Europa [9].

Nuclear magnetic resonance (NMR) measurements of diffusion and magnetic relaxation have been applied to study the geometry and interconnectivity of the liquid-filled network in laboratory ice [10] including investigation of recrystallization inhibition [11, 12]. In this research NMR measurements were used to observe the impact on ice microstructure of an ice-binding protein (IBP) excreted by the V3519-10 organism (Flavobacteriaceae family) isolated from the Vostok ice core in Antarctica. Control ice samples containing a non-ice binding protein at equivalent concentrations were also analyzed. The experiments ran for ~ 70 days at -15°C with NMR measurements made at discrete intervals during the time course. Recrystallization inhibition was observed as a function of IBP concentration and persisted over the 70-day experimental time frame [12]. No recrystallization inhibition was observed in the control sample.

These findings indicate that microbial processes such as ice binding protein production can impact ice structure, creating a persistent small crystal structure. This presumably creates more favorable conditions for microbial habitability within the ice matrix at sub-zero temperatures. It also suggests that microbial processes could contribute to creating a persistent small crystal structure in natural ices, which could impact ice rheology. This research demonstrates the utility of advanced NMR techniques for applications to ice

microstructure and has broader implications for understanding geophysical properties of cryospheric systems. The research also has implications for biogeophysical applications examining microbial habitability in ice on Earth and elsewhere in the solar system.

References:

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