



Using Antifreeze Proteins to understand ice microstructure evolution

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Polar ice sheets are considered a unique climate archive. The chemical analysis of its impurities and the development of its microstructure with depth give insight in past climate conditions as well as in the development of the ice sheet with time and deformation. Microstructural patterns like small grain size observed in specific depths are thought to be linked to the retarding effect of impurities on ice grain growth. Clear evidence of size or chemical composition of the impurities causing this effect is missing, but in this context a major role of nanoparticles has been suggested.

In order to shed light on different mechanisms by which nanoparticles can control microstructure development we used antifreeze proteins (AFPs) as proxies for particles in ice. These proteins are small nanoparticles, approx. 5 nm in size, with the special characteristics of firmly binding to ice through several hydrogen bonds. We used AFPs from the sea-ice microalgae *Fragilariopsis cylindrus* (fcAFPs) in bubble-free, small-grained polycrystalline ice obtained by the phase-transition size refinement method.

We explain how fcAFP bind to ice by presenting the 3-D-protein structure model inferred by X-ray structure analysis, and show the importance of the chemical interaction between particles and ice in controlling normal grain growth, comparing fcAFPs to other protein nanoparticles. We used modifications of fcAFPs for particle localization through fluorescence spectroscopy. Furthermore, the effect of fcAFPs on the driving factors for ice deformation during creep, i.e. on internal dislocations due to incorporation within the lattice and on the mobility of grain boundaries due to pinning, makes these proteins particularly interesting in studying the process of ice deformation.