



A novel antifreeze protein from sea ice diatoms and its influence on ice microstructure

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Sea ice of the polar regions is an extreme habitat with regard to its abiotic constraints as low temperatures and high brine salinities. However, several microorganisms proliferate within the ice and on its peripheries, thus creating an ecosystem of global significance. The diatom *Fragilariopsis cylindrus* is a widespread polar species, dominating the assemblages of sea ice microorganisms. How this species has adapted to such harsh living conditions, and to what extent sea ice itself is influenced by these biota, are still open questions. Recently, attention has focused on antifreeze proteins (AFPs) that probably contribute to the success of *F. cylindrus* in sea ice. What defines these proteins is the ability to influence ice crystal growth. By binding the crystal surface they lower the freezing point of a solution below the melting point, thus causing a thermal hysteresis. Moreover, they inhibit grain boundary migration in polycrystalline ice (recrystallization), keeping the crystals small in size.

Here we present a characterization of AFPs from *F. cylindrus*, which belong to a new AFP-family. Our results help to understand how diatoms may survive in sea ice and possibly influence its microstructure. We describe the activity of a recombinant AFP that clearly showed freezing point depression and recrystallization inhibition. Moreover, we show that AFPs have a strong influence on ice microstructure, as revealed by crystallographic observations (automatic fabric analyzer) of frozen AFP solutions. Further molecular and crystallographic research will be carried on in order to improve our knowledge of physical and biological antifreeze mechanisms of this protein and their effect on sea ice.