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# Identification & Characterization of Fungal Ice Nucleation Proteins

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Freezing of water at relatively warm subfreezing temperatures is dependent on ice nucleation catalysis facilitated by ice nuclei (IN). These IN can be of various origins and although extensive research was done and progress was achieved, the nature and mechanisms leading to an effective IN are to date still poorly understood.
Some of the most important processes of our geosphere like the water cycle are highly dependent on effective ice nucleation at temperatures between -2°C - -8°C, a temperature range which is almost exclusively covered by biological IN (BioIN). BioIN are usually macromolecular structures of biological polymers. Sugars as well as proteins have been reported to serve as IN and the best characterized BioIN are ice nucleation proteins (IN-P) from gram negative bacteria. Fungal strains from Fusarium spp. were described to be effective IN at subfreezing temperatures up to -2°C already 25 years ago and more and more fungal species are described to serve as efficient IN. Fungal IN are also thought to be proteins or at least contain a proteinaceous compound, but to date the fungal IN-P primary structure as well as their coding genetic elements of all IN active fungi are unknown.
The aim of this study is a.) to identify the proteins and their coding genetic elements from IN active fungi (F. acuminatum, F. avenaceum, M. alpina) and b.) to characterize the mechanisms by which fungal IN serve as effective IN. We designed an interdisciplinary approach using biological, analytical and physical methods to identify fungal IN-P and describe their biological, chemical, and physical properties.