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Identification of Ina proteins from Fusarium acuminatum

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Freezing of water above -36˚C is based on ice nucleation activity (INA) mediated by ice nucleators (IN) which can be of various origins. Beside mineral IN, biological particles are a potentially important source of atmospheric IN. The best-known biological IN are common plant-associated bacteria. The IN activity of these bacteria is induced by a surface protein on the outer cell membrane, which is fully characterized. In contrast, much less is known about the nature of fungal IN.

The fungal genus *Fusarium* is widely spread throughout the earth. It belongs to the Ascomycota and is one of the most severe fungal pathogens. It can affect a variety of organisms from plants to animals including humans. INA of *Fusarium* was already described about 30 years ago and INA of *Fusarium* as well as other fungal genera is assumed to be mediated by proteins or at least to contain a proteinaceous compound. Although many efforts were made the precise INA machinery of *Fusarium* and other fungal species including the proteins and their corresponding genes remain unidentified.

In this study preparations from living fungal samples of *F. acuminatum* were fractionated by liquid chromatography and IN active fractions were identified by freezing assays. SDS-page and *de novo* sequencing by mass spectrometry were used to identify the primary structure of the protein.

Preliminary results show that the INA protein of *F. acuminatum* is contained in the early size exclusion chromatography fractions indicating a high molecular size. Moreover we could identify a single protein band from IN active fractions at 130-145 kDa corresponding to sizes of IN proteins from bacterial species. To our knowledge this is for the first time an isolation of a single protein from *in vivo* samples, which can be assigned as IN active from *Fusarium*.