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Activity of different proteinaceous ice nucleating particles

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A variety of microorganisms (bacteria, fungi, lichen) from land produce protein structures, which act as a template for ice nucleation [1]. Also marine sources of ice nucleating particles (INPs) came in focus in the recent years. The atmospheric spatio-temporal distribution of INPs from microorganisms is still not well known. However, it is often assumed that the observed onset of atmospheric ice nucleation (T>-20°C) is due to the existence of ice-nucleation active biological particles.
In this study we compare the ice nucleation activity of different proteinaceous particles produced by bacteria and fungi. For bacteria we investigate (i) cells and fragments of Pseudomonas syringae from commercially available SnomaxTM and (ii) the Pseudomonas syringae INA protein expressed in living Escherichia coli bacteria. We also analyzed freeze-dried leaves [2] where we assume that proteinaceous particles are responsible for the ice nucleation activity. For fungi the widespread soil fungus Mortierella alpina was investigated which had been extracted from natural soil [3].
Immersion freezing experiments are performed at the cold stage LINA (Leipzig Ice Nucleation Array). We attempt to describe the activity of a single proteinaceous ice nucleating particle [4] in order to achieve direct comparability. Further, the results are compared with complex natural systems e.g. soil dust.
The objectives of this study are to clarify potential differences in the ice nucleation potential of proteinaceous particles and to draw conclusions concerning the need to differentiate them for modelling purposes.

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