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Interfacial Water Ordering Is Insufficient to Explain Ice-Nucleating Protein Activity

Max Lukas,* Ralph Schwidetzky, Anna T. Kunert, Ellen H.G. Backus, Ulrich Pöschl, Janine Fröhlich-Nowoisky, Mischa Bonn, and Konrad Meister*

ABSTRACT: Ice-nucleating proteins (INPs) found in bacteria are the most effective ice nucleators known, enabling the crystallization of water at temperatures close to 0 °C. Although their function has been known for decades, the underlying mechanism is still under debate. Here, we show that INPs from Pseudomonas syringae in aqueous solution exhibit a defined solution structure and show no significant conformational changes upon cooling. In contrast, irreversible structural changes are observed upon heating to temperatures exceeding ~55 °C, leading to a loss of the ice-nucleating activity. Sum-frequency generation (SFG) spectroscopy reveals that active and heat-inactivated INPs impose similar structural ordering of interfacial water molecules upon cooling. Our results demonstrate that increased water ordering is not sufficient to explain INPs’ high ice-nucleating activity and confirm that intact three-dimensional protein structures are critical for bacterial ice nucleation, supporting a mechanism that depends on the INPs’ supramolecular interactions.
The curve of *P. syringae* shows two substantial increases in the cumulative number of IN per unit mass, $N_m(T)$ (Figure 1C) around $-3.0$ and $-7.5$ °C with plateaus between $-4.5$ and $-7.0$ °C and below $-9.5$ °C. At the plateaus, at temperatures below each increase of $N_m(T)$, fewer IN are active. The two rises in the curve reveal that the ice-nucleation activity stems from two distinct classes of IN with different activation temperatures. We attribute the observed rise at $-3.0$ °C to large assemblies of INPs (class A IN) and the rise at $-7.5$ °C to smaller assemblies of INPs (class C IN) in accordance with previous studies. The freezing curve of the purified INPs looks similar to the nonpurified INP solution, with a change in the ratio of the INP number in the two classes at $-3.0$ and $-7.5$ °C (see also Figure S2). Clearly, the purification process was successful and yielded active INPs. The reduction of class A IN activity for the purified sample indicates that the purification reduced the number of the larger INP aggregates compared to the nonpurified solution. This observation is in line with the hypothesis that the bacterial membranes are involved in the formation of larger functional INP aggregates, and we expect bacterial membrane fragments to have no ice affinity.

Heat-treated INP solutions (see the SI for details on heat treatment) behave fundamentally differently. As apparent from comparing the droplet freezing statistics of the highest dilution concentrations shown in Figure 1B, the rises at $-3.0$ and $-7.5$ °C are completely absent. Instead, we observe activity only around $-25$ °C, which corresponds to background freezing of pure water in our system. Evidently, the heat treatment of the purified INPs completely inactivates their ice-nucleation abilities.

Using SFG spectroscopy, Pandey et al. reported that fragmented *P. syringae* bacteria (Snomax) show an increased capability to order water in their vicinity when cooled to temperatures close to the melting point of deuterated water. Control experiments using misfolded and denatured INP fragments, lipids, and the protein lysozyme did not show this effect. The alignment of water into an ordered structure was concluded to be a condition that will promote interfacial ice nucleation.

Here, we conducted further SFG experiments with active and heat-inactivated INPs to determine whether there is a direct causal correlation between enhanced SFG water signals at low temperatures and bacterial ice-nucleation activity. In SFG, a broadband infrared pulse resonant with the probed molecular vibrations and a visible pulse are combined at a surface to generate light at the sum frequency of the two incident fields. The SFG process is bulk-forbidden in isotropic media, and only ensembles of molecules with a net orientation, e.g., at an interface, can generate a detectable signal.

Figure 2A shows the temperature-dependent SFG spectra of aqueous solutions of purified INPs. The broad response from the O–D stretching bands of interfacial water molecules appears at frequencies below 2700 cm$^{-1}$ and is affected by their interactions with the INPs adsorbed to the air–liquid interface. In the frequency region of 2800–3000 cm$^{-1}$, the SFG spectra show strong signals that we attribute to C–H stretching vibrations.

The SFG intensity of the O–D bands strongly increases upon lowering the temperature close to the melting temperature (3.82 °C for D$_2$O), indicating an increase in the structural order of the interfacial water molecules. This effect is completely reversible, as evident from the integrals of the water (O–D) bands for two cycles shown in the insets. The observed effect is also significantly larger than the effect observed for pure water (insets in Figure 2 and Figure S4). In contrast, the signal intensity of the C–H stretching vibrations remains constant upon lowering the temperature.
proteins. The amide I SFG spectra at room temperature are sensitive to the secondary structure and orientation of the INPs. These changes indicate that there is a substantial change in the protein structure after inactivation. The lipid signal presumably originates from membrane lipids and is in agreement with the current theoretical model of the INP structure of structurally similar proteins. We propose that the observed irreversible conformational changes cause a loss of the proteins’ native functional structure and are the origin of the complete elimination of the INP’s ice-nucleation activity after heat treatment.

The CD spectrum of the purified INPs (Figure 3A) looks unusual, and its deconvolution using the structural database does not allow a clear distinction into the common secondary structures of α-helix, β-turn, β-strand, or random coil. The spectral shape, however, shows similarities with those of AFPs derived from Marinomonas primoryensis (MpAFP) and Rhagium inquisitor (RiAFP) with slightly shifted peak positions. Both AFPs have β-helical folds, which is in agreement with the current theoretical model of the INP as shown in Figure 1A and the inset of Figure 4A. The negligible changes in CD spectra at low temperatures are further consistent with temperature-dependent measurements of structurally similar β-helical AFPs.

In summary, we purified INPs from P. syringae using ice-affinity methods and report experimental evidence that the purified INPs are ice-nucleation active and that they adopt defined solution structures, which show resemblance with β-helical AFP spectra. We further show that enhanced interfacial water ordering at temperatures close to the melting point of ice is found not only for active but also for completely inactivated INPs. While protein-induced enhanced interfacial water ordering likely constitutes an essential part of INPs’...
working mechanism, our results reveal that increased water ordering observed with SFG spectroscopy is, by itself, not a sufficient condition for INP activity. Instead, our results highlight that the intact three-dimensional fold is essential for the ice-nucleation activity of INPs. This observation, combined with the similarity of the protein structure of the INPs from *P. syringae* and other ice-binding proteins, suggests that supramolecular interactions and ordering are key to the exceptional ice-nucleation activity of bacterial INPs. We hypothesize that the completely intact native structure of the INP is required for the formation of the functional aggregates that allow the formation of ice nuclei or embryos large enough to enable freezing at −2 °C (∼104 kDa). Specifically, if the observed water ordering effect plays a role in bacterial ice nucleation, we can surmise that some secondary structures of the INPs remain at least partially intact, inducing a similar degree of order. However, the breakdown of higher-order structures (tertiary, quaternary) leads to the loss of the collective alignment of INP units that explains the substantial loss in effectiveness. This hypothesis would predict a freezing behavior of the inactivated INPs comparable to structurally similar antifreeze proteins and will be tested in future studies.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acs.jpcllett.0c03163.

Experimental details, experimental methods, and supporting Figures S1–S7: Coomassie blue-stained SDS PAGE analysis of ice-affinity purifications of the INPs; freezing experiments of aqueous solutions of *P. syringae* (A) and purified INPs (B); fraction of frozen droplets for *P. syringae* and purified INP solutions corresponding to data shown in Figure 1; temperature-dependent sum-frequency generation measurements of pure D2O at 22 and 5 °C; SFG spectra in the amide I region; SFG spectra of Snomax (gray) and purified INPs (black) as well as inactive INPs (red); CD spectra of purified INPs derived from *P. syringae* at temperatures from 25 to 75 °C in water as well as an autoclaved sample (121 °C) (A), and the melting curve of the protein obtained from the circular dichroism values at 222 nm (B); and CD spectra of purified INPs and fragmented *P. syringae* (Snomax), normalized to the highest local maximum, respectively (PDF).

AUTHOR INFORMATION

Corresponding Authors

Max Lukas − Max Planck Institute for Polymer Research, SS128 Mainz, Germany; orcid.org/0000-0001-6949-8423; Email: lukas@mpip-mainz.mpg.de

Konrad Meister − Max Planck Institute for Polymer Research, SS128 Mainz, Germany; University of Alaska Southeast, Juneau, Alaska 99801, United States; orcid.org/0000-0002-6853-6325; Email: meisterk@mpip-mainz.mpg.de

Authors

Ralph Schwidetzky − Max Planck Institute for Polymer Research, SS128 Mainz, Germany

Anna T. Kunert − Max Planck Institute for Chemistry, SS128 Mainz, Germany

Ellen H.G. Backus − Max Planck Institute for Polymer Research, SS128 Mainz, Germany; Department of Physical Chemistry, University of Vienna, 1090 Vienna, Austria; orcid.org/0000-0002-6202-0280

Ulrich Pöschl − Max Planck Institute for Chemistry, SS128 Mainz, Germany; orcid.org/0000-0003-1412-3557

Janine Frohlich-Nowoisky − Max Planck Institute for Chemistry, SS128 Mainz, Germany; orcid.org/0000-0002-1278-0054

Figure 4. Circular dichroism spectrum of purified INPs compared to the spectra of two AFPs. (A) CD spectra of purified INPs derived from fragmented *P. syringae* at 25 °C in water [circular dichroism (mdeg)]. (B) CD spectrum of an AFP derived from *Marinomonas primoryensis* (MpAFP) [ellipticity (mdeg)]. Data obtained from Garnham et al. (C) CD spectrum of an AFP derived from *Rhagium inquisitor* (RiAFP) [mean residue ellipticity (deg cm−1/dmol × 10−3)]. Data obtained from Hakim et al. Dashed lines indicate zero in all panels. The insets show cross sections of the proteins with the β-sheets highlighted in purple.
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Misch Bonn – Max Planck Institute for Polymer Research, 55128 Mainz, Germany. orcid.org/0000-0001-6851-8453

Complete contact information is available at: https://pubs.acs.org/10.1021/acs.jpcllett.0c03163

Author Contributions

These authors contributed equally.

Notes

The authors declare no competing financial interest.

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