

Supplementary Information for

Ice crystal growth in the presence of a moderate ice-binding protein: Basal face growth suppression does not confer hyperactivity

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Supplementary Information Text

S1 Activity of *fc*IBP11 in pure water

In order to analyze whether *fc*IBP11 can be used in pure water, we measured the THactivity using the nanoliter osmometer as described in Bayer-Giraldi et al. (1). Table S1 shows the data for solutions with protein concentration of $1.5 \ \mu M \ fc$ IBP11 and different salinities. We used protein dissolved in pure water (salinity 0 in the PSU system), in a phosphate buffered saline solution (PBS, salinity 9) and in a NaCl brine (salinity 60). We can see that the TH, defined as the difference between the freezing point and the equilibrium melting point, was not sensibly affected by salinity, although a slight increase in TH can be observed at higher salinities. This slight increase is probably due to a salting-out effect, as discussed in Bayer-Giraldi et al. (2), and we do not expect changes in the mechanisms of interaction between the *fc*IBP11 molecule and ice. Therefore, since our focus was on the physical aspect of ice crystal growth and its interaction with *fc*IBP11, we chose to work with pure water, in order to exclude cooperative effects of the protein and salts affecting crystal growth. Due to the fact that highly saline sea-ice brine corresponds to the natural environment of *fc*IBP11, we will include the aspect of salinity in our future work.

S2 Rotation of the ice crystal in the free growth cell

In the free growth cell, the rotation of the capillary allows the free rotation of ice single crystals. This gives us the possibility to observe ice single crystals from different directions. In addition to the details observed when the basal face of the crystal was parallel to the observation plane, as sown in Figure 3, we could observe the crystal with the basal face perpendicular to the observation plane. An example is shown in Figure S1. It becomes clear from these images that the crystals grew in a flat dendritic shape, with strong suppression of growth along the *c*-axis.

S3 <u>Relevance in sea-ice</u>

Considering the sea-ice context of the diatoms, its structure, and potential ecological role of the *fc*IBPs, the binding of *fc*IBP11 to the basal faces seems to be of crucial importance. Microbial assemblages are found mostly in the bottom part of sea-ice. Whereas the upper part of the sea-ice layer, in contact with the cold atmosphere, consists of isotropic granular ice crystals, the lower part gradually grows into the sea-water as parallel lamellae (3). As a result of the geometrical selection of the growing ice crystals, these grains have their *c*-axis oriented horizontally, as schematically depicted in Figure S2. Salts and other sea-water components are segregated from the growing ice lattice and accumulate within brine channels, which are elongated parallel to the lamellae and often terminate into the ocean. Brine channels constitute the living space for organisms, and most IBPs from sea-ice organisms are released from the cells into the brine where they interact with the icy walls of the channels. Looking at the structures of brine spaces, we see that the basal faces of the ice lamellae, which enclose the brine space in the vertical orientation, are the dominant crystallographic faces in the channels. Therefore, it is naturally of great advantage for *fc*IBP11 to bind to the basal face, in addition to their interaction with the other crystallographic faces. It has been shown that IBPs can influence brine retention in sea-ice (4). Brine retention over longer periods increases local ice porosity and therefore provides a living space for sea-ice microorganisms. Bayer-Giraldi et al. (2) suggested that *fc*IBP11 will accumulate in a matrix of extracellular polymeric substances and actively shape the structure of the brine space, thereby increasing its habitability. A change in ice porosity can possibly alter the geochemical imprint of sea-ice, which may be of relevance in a changing climate (5).



Fig. S1. An ice single crystal observed by bright field microscopy from different directions. The crystal was grown in the presence of 1.5 μ M *fc*IBP11 and $\Delta T = 0.5^{\circ}$ C. The image shows the crystal oriented with the basal plane parallel to the observation plane (A), with the basal plane rotate by 45° (B) and by 90° (C). Size bar = 200 μ m.



Fig. S2. Schematic drawing of the structure of columnar sea-ice. The crystals constitute parallel lamellae with horizontal *c*-axis. The brine is retained within inclusions, often elongated in the vertical direction along the basal faces of the ice crystals.

Table S1.	TH	of ice in	1.5	μM	fcIBP11	solutions	with	different	salinities.
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Solution (Salinity)	TH (°C)
Pure water (0)	0.05
PBS (9)	0.06
NaCl brine (60)	0.13

Table S2. The effect of selected moderate and hyperactive IBPs on the growth of the basal face at small supercooling temperature.

Protein name	Origin	Basal face growth suppression	TH activity	Reference
AFP I	Pseudopleuronectes americanus	no	moderate	(6)
AFP II	Hemitripterus americanus	no	moderate	(6)
AFP III	Anarhichas lupus	no	moderate	(7)
AFP IV	Myoxocephalus octodecimspinosis	по	moderate	(8)
AFGP 7-8	Gadus ogac	по	moderate	(9)
<i>Mp</i> AFP	Marimononas primoryensis	yes	hyperactive	(10)
<i>Tm</i> AFP	Tenebrio molitor	yes	hyperactive	(11)
SbwAFP	Choristoneura fumiferana	yes	hyperactive	(12)
<i>Lp</i> IBP	Lolium perenne	Yes	Moderate	(13)
DUF3494				
<i>Col</i> AFP	Colwellia sp SLW05	yes	hyperactive	(14)
EfcIBP	Antarctic bacterial metagenome	yes	moderate	(15)
FcIBP11	Fragilariopsis cylindrus	yes	moderate	This study
CnAFP	Chaeotoceros neogracile	yes	moderate	(16)
AFP1	Glaciozyma antarctica PI12	yes	moderate	(17)
TysAFP8	Typhula ishikariensis	yes	hyperactive	(18)

References

- Bayer-Giraldi M, Jin E, & Wilson P (2014) Characterization of Ice Binding Proteins from Sea Ice Algae. *Plant Cold Acclimation: Methods and Protocols*, eds Hincha DK & Zuther E (Springer Science+Bussiness Media, New York), Vol 1166, pp 241-253.
- 2. Bayer-Giraldi M, Weikusat I, Besir H, & Dieckmann G (2011) Characterization of an antifreeze protein from the polar diatom *Fragilariopsis cylindrus* and its relevance in sea ice. *Cryobiology* 63:2010-2019.
- 3. Thomas DN & Dieckmann GS (2010) Sea Ice (Wiley-Blackwell) 2nd Ed.
- 4. Raymond JA (2011) Algal ice-binding proteins change the structure of sea ice. *Proc. Natl. Acad. Sci. USA* 108(24):E 198.
- 5. Krembs C (2011) Exopolymer alteration of physical properties of sea ice and implications for ice hybitability and biogeochemistry in a warmer Arctic. *Proc. Natl. Acad. Sci. USA* 108(9):3653-3658.
- 6. Heman C, DeLuca CI, & Davies PL (1995) Mixing antifreeze protein types changes ice crystal morphology without affecting antifreeze activity. *FEBS Lett.* 357(2):183-186.
- 7. Vorontsov DA, *et al.* (2018) Growth of Ice Crystals in the Presence of Type III Antifreeze Protein. *Cryst. Growth Des.* 18:2563-2571.
- 8. Gauthier SY, *et al.* (2008) A re-evaluation of the role of type IV antifreeze protein. *Cryobiology* 57(3):292-296.
- 9. Furukawa Y, *et al.* (2017) Oscillations and accelerations of ice crystal growth rates in microgravity in presence of antifreeze glycoprotein impurity in supercooled water. *Scientific Reports* 7(43157).
- 10. Gilbert JA, Davies PL, & Laybourn-Parry J (2005) A hyperactive, Ca2+dependent antifreeze protein in an Antarctic bacterium. *FEMS Microbiol. Lett.* 245(1):67-72.
- 11. Liou YC, Tocilj A, Davies PL, & Jia Z (2000) Mimicry of ice structure by surface hydroxyls and water of a β-helix antifreeze protein. *Nature* 406:322-324.
- 12. Graether SP, *et al.* (2000) b-Helix structure and ice-binding properties of a hyperactive antifreeze protein from an insect. *Nature* 406(6793).
- 13. Middleton AJ, *et al.* (2012) Antifreeze Protein from Freeze-Tolerant Grass Has a Beta-Roll Fold with an Irregularly Structured Ice-Binding Site. *Journal of Molecular Biology* 416:713-724.
- 14. Hanada Y, Nishimiya Y, Miura A, Tsuda S, & Kondo H (2014) Hyperactive antifreeze protein from an Antarctic sea ice bacterium *Colwellia* sp. has a compound ice-binding site without repetitive sequences. *FEBS J.* 281:3576-3590.
- 15. Mangiagalli M, *et al.* (2017) Cryo-protective effect of an ice-binding protein derived from Antarctic bacteria. *FEBS J.* 284:163-177.
- 16. Kim M, Gwak Y, Jung W, & Jin E (2017) Identification and Characterization of an Isoform Antifreeze Protein from the Antarctic Marine Diatom, *Chaetoceros neogracile* and Suggestion of the Core Region. *Mar. Drugs* 15(318).
- 17. Hashim NHF, *et al.* (2013) Characterization of Afp1, an antifreeze protein from the psychrophilic yeast *Glaciozyma antarctica* PI12. *Extremophiles* 17:63-73.

18. Cheng J, Hanada Y, Miura A, Tsuda S, & Kondo H (2016) Hydrophobic icebinding sites confer hyperactivity of an antifreeze protein from a snow mold fungus. *Biochem. J.* 473:4011-4026.