



## Supplementary Information for

Growth suppression of ice crystal basal face in the presence of a moderate  
ice-binding protein does not confer hyperactivity

Maddalena Bayer-Giraldi, Gen Sazaki, Ken Nagashima, Sepp Kipfstuhl,  
Dmitry A. Vorontsov, Yoshinori Furukawa

Maddalena Bayer-Giraldi  
Email: maddalena.bayer@awi.de

### This PDF file includes:

Supplementary text  
Fig. S1  
Table S1  
Reference for SI reference citations

## **Supplementary Information Text**

### **S1 Activity of *fcIBP11* in pure water**

In order to analyze whether *fcIBP11* can be used in pure water, we measured the TH-activity 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  $\mu\text{M}$  *fcIBP11* 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 *fcIBP11* molecule and ice. Therefore, since our focus was on the physical aspect of ice crystal growth and its interaction with *fcIBP11*, 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 *fcIBP11*, we will include the aspect of salinity in our future work.

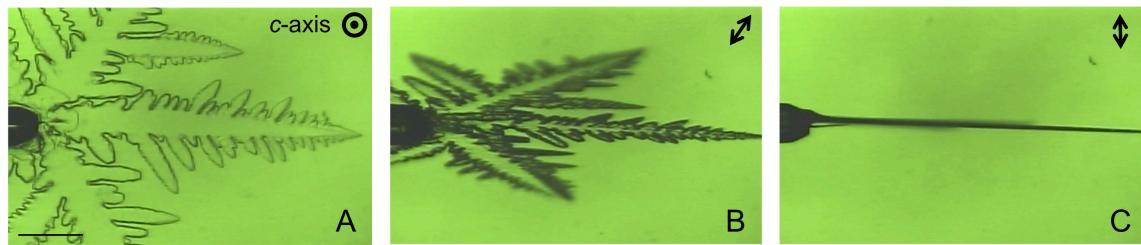
### **S2 Rotation of the ice crystal in the free growth cell**

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 shown 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.

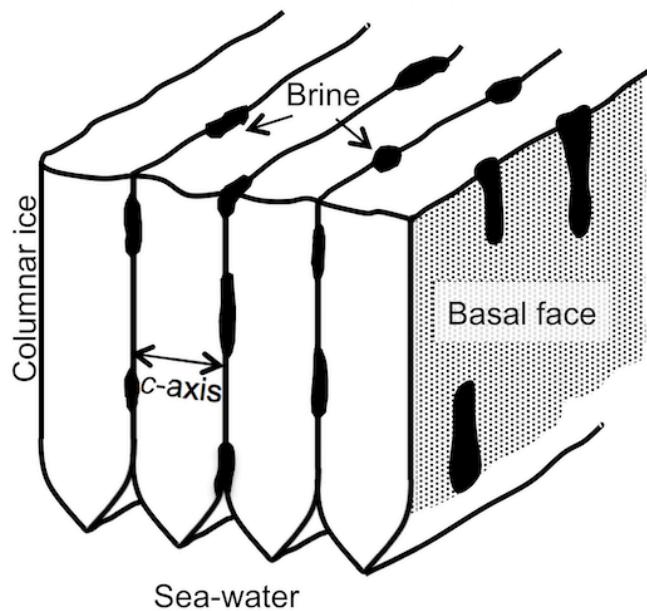
### **S3 Relevance in sea-ice**

Considering the sea-ice context of the diatoms, its structure, and potential ecological role of the *fcIBPs*, the binding of *fcIBP11* 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 *fcIBP11* 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 *fcIBP11* 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  $1.5 \mu\text{M}$  *fcIBP11* and  $\Delta T = 0.5^\circ\text{C}$ . The image shows the crystal oriented with the basal plane parallel to the observation plane (A), with the basal plane rotate by  $45^\circ$  (B) and by  $90^\circ$  (C). Size bar =  $200 \mu\text{m}$ .



**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.**

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	<i>Pseudopleuronectes americanus</i>	no	moderate	(6)
AFP II	<i>Hemitripterus americanus</i>	no	moderate	(6)
AFP III	<i>Anarhichas lupus</i>	no	moderate	(7)
AFP IV	<i>Myoxocephalus octodecemspinosis</i>	no	moderate	(8)
AFGP 7-8	<i>Gadus ogac</i>	no	moderate	(9)
<i>Mp</i> AFP	<i>Marimononas primoryensis</i>	yes	hyperactive	(10)
<i>Tm</i> AFP	<i>Tenebrio molitor</i>	yes	hyperactive	(11)
<i>Sbw</i> AFP	<i>Choristoneura fumiferana</i>	yes	hyperactive	(12)
<i>Lp</i> IBP	<i>Lolium perenne</i>	Yes	Moderate	(13)
<b>DUF3494</b>				
<i>Col</i> AFP	<i>Colwellia sp</i> SLW05	yes	hyperactive	(14)
<i>Efc</i> IBP	Antarctic bacterial metagenome	yes	moderate	(15)
<i>Fc</i> IBP11	<i>Fragilaropsis cylindrus</i>	yes	moderate	This study
<i>Cn</i> AFP	<i>Chaeotoceros neogracile</i>	yes	moderate	(16)
AFP1	<i>Glaciozyma antarctica</i> PI12	yes	moderate	(17)
<i>Tys</i> AFP8	<i>Typhula ishikariensis</i>	yes	hyperactive	(18)

## References

1. 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+Business 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 *Fragilaropsis 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 habitability 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, Ca<sup>2+</sup>-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  $\beta$ -helix antifreeze protein. *Nature* 406:322-324.
12. Graether SP, *et al.* (2000)  $\beta$ -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 ice-binding sites confer hyperactivity of an antifreeze protein from a snow mold fungus. *Biochem. J.* 473:4011-4026.