Structural basis for the Antifreeze activity of an Ice Binding Protein (*Le*IBP) from Arctic yeast

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ABSTRACT

Psychrophilic Arctic yeast, Leucosporidium sp. produces a glyco-ice binding protein (*Le*IBP) with a molecular mass of about 25 kDa that has a unique ability to lower the freezing point below the melting point once it binds to ice. Antifreeze proteins (AFPs) and ice binding proteins (IBPs) are found in many polar organisms and inhibit the growth of ice crystals to protect themselves from freezing. *Le*IBP exhibits the least protein sequence similarity with other previous known antifreeze protein structures. To better understand the ice binding mechanism of *Le*IBP, we have expressed full-length recombinant *Le*IBP in large amounts in *Escherichia coli* and purified the proteins. Here, we report the crystal structure of *Le*IBP at 1.57 Å resolution. Structural analysis of *Le*IBP revealed a dimeric right-handed β-helix fold, which is composed of three parts: a large coiled structural domain, a long helix region (Residues 96–115 form a long α-helix which packs along one face of the β-helix) and a C-terminal hydrophobic loop region (243-PFVPAPEVV-251). Unexpectedly, the C-terminal hydrophobic loop region has an extended conformation pointing away from the body of the coiled structural domain and forms an intertwined dimer interactions. From this structure we propose an ice binding sites, which is flat and contains a regular pattern of aligned Thr, Ala and Ser residues. Furthermore, we supplemented the crystal structure with site-directed mutagenesis to link the structural information of the *Le*IBP with the ice binding properties. The data support the existence of differences in the ice binding modes of *Le*IBP compared with other known AFPs and IBPs.

References

1. Lee, J.K., Park, K.S., Park, S., Park, H., Song, Y.H., Kang, S.H., and Kim. H.J. (2010) An extracellular ice-binding glycoprotein from an Arctic psychrophilic yeast. Cryobiology, 60, 222-228.