

Identification of Ice-binding proteins of Arctic/Antarctic Chlorophyceae using Transcriptome Analyses

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The polar microalgae have built their own strategies to protect the cells under an environment with repeated freeze-thaw cycles of ice crystals. Among the adopted strategies, ice-binding proteins (IBPs) possibly play a key role making the microenvironment surrounding cells more habitable. IBPs seems widely spread in polar diatom and microalgae. Recent studies have identified that two types of IBPs are present in Chlorophyceae, and IBPs are more abundant in transcript and protein levels under low temperature.

To discover more IBP genes, we performed transcriptome analyses using ArF0032, one of the Arctic Chlorophyceae strains from KOPRI (Korea Polar Research Institute, Incheon, Korea) under various temperature conditions. We described up- and down-regulated gene expression focusing on IBP synthesis and secretion system. We separated up-regulated contigs under low temperature which of most include IBP homologous genes. To extend our knowledge, we choose more Arctic/Antarctic Chlorophyceae strains from KOPRI and identified characteristics of these genes and proteins. Recombinant proteins purified from *E. coli* expression system were used for thermal hysteresis analyses and ice recrystallization analyses. Biological functions and origin of these genes are discussed.