

[GM27]

### Overexpression of Antarctic *CBF* genes increased the stress tolerance in rice plants

Jungeun Lee<sup>1</sup>, Mi Young Byun<sup>2</sup>, Yoonjee Kang<sup>1</sup>, Woo Taek Kim<sup>\*2</sup>, Hyungseok Lee<sup>\*1</sup>

<sup>1</sup>Division of Life Sciences, Korea Polar Research Institute, Incheon, 406-840, Korea,

<sup>2</sup>Department of Systems Biology, College of Life Science and Biotechnology, Yonsei University, Seoul 120-749, Korea

C-repeat/dehydration-responsive element binding factors (CBF/DREBs) are a family of transcription factors that play a key role in regulating freezing tolerance, binding to the DRE/CRT *cis*-acting element commonly present in stress responsive genes in plant species. As a step towards understanding the stress response of antarctic vascular plants, we have researched *CBF* genes in *Deschampsia antarctica*, the only natural grass species colonized in the Maritime Antarctic, isolated *CBF* orthologs and developed the stress tolerant transgenic crop by overexpression of *Deschampsia CBF* genes (*DaCBFs*) in rice. For example, Transgenic over-expression of *DaCBF7* in rice (*pUBI::CBF7*) resulted in a dramatic increase in tolerance to low-temperature stress, while the response high salinity or dehydration was not changed, suggesting that *DaCBF7* gene is specifically related to cold tolerance response. To describe the cold-tolerance phenotype of the transgenic rice, we compared the transcriptome response between wild type rice and transgenic rices and identified a set of genes regulated by overexpression of *DaCBFs* in response to cold stress.

\*Corresponding Author email : soulaid@kopri.re.kr

[GM28]

### Over-expression of Arabidopsis UPF3 forms P bodies recruited by deadenylation complex

Ki Hun Shin<sup>1</sup>, Gagan Kumar Panigrahi, Sang Hyon Kim<sup>\*</sup>

<sup>1</sup>Division of Bioinformatics and Biosciences, Myongji University, Yongin 449-728, Korea

UP-FRAMESHIFT 1, 2 and 3 (UPF1, 2 and 3) are key factors in nonsense-mediated mRNA decay (NMD), in which erroneous mRNAs containing premature termination codons (PTCs) are decayed in eukaryotic cells. According to our previous studies, UPF3 mainly localizes to the nucleolus, and UPF1 and UPF2, to the cytoplasm, and to the nucleolus and the cytoplasm, respectively. Unlike UPF1 and UPF2, over-expression of fluorescent protein-tagged UPF3 forms cytoplasmic foci. Transcription and translation inhibitors, actinomycin D and cycloheximide significantly reduced the number and the size of the foci, and over-expression of UPF3 in the *ein5-1* mutant increased them compared with wild type Col-0, suggesting the foci are P bodies. Co-expression with deadenylation complex components CAF1a or CCR4a completely co-localizes with UPF3 to the P bodies, while that with decapping components DCP1, 2 or 5 partly merged with UPF3. Finally, by mutant studies of known UPF3 domains involved in interaction with other protein components of exon-junction complex (ECJ) and UPF3, we suggest UPF3 forms P bodies by direct binding to mRNA through the N-terminal RRM domain.

\*Corresponding Author email : kim6189@mju.ac.kr