

## Constitutive expression of DREB/CBF-like genes from an Antarctic vascular plant *Deschampsia antarctica*, resulted in improved cold tolerance in transgenic rice plants

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*Deschampsia antarctica* is an Antarctic hairgrass that grows on the west coast of the Antarctic peninsula. In this report, we have identified and characterized two transcription factor, *D. antarctica* C-repeat binding factor 4 and 7 (DaCBF4 and DaCBF7) as transcription factors functioning in process of cold resistance. Both proteins contain a single AP2 domain and were predominantly localized to nuclei showing traditional feature of AP2 transcription factor. The interaction of DaCBF7 with the C-repeat/dehydration responsive element (CRT/DRE) core sequence (ACCGAC) was also confirmed in vitro. DaCBF4 and DaCBF7 were induced by abiotic stresses, including drought and cold, but salinity induced only DaCBF7. To investigate its possible cellular role in cold tolerance, a transgenic rice system was employed. Both transgenic rice plants overexpressing DaCBF4 (Ubi:DaCBF4) and DaCBF7 (Ubi:DaCBF7) exhibited markedly increased tolerance to cold stress. Their survival ratio under cold treatment were higher than wild type rice plants within range of 3.5 and 5 fold without growth defects; however, overexpression of these genes exerted little effect on tolerance to drought or salt stress. Transcriptome analysis of a Ubi:DaCBF7 transgenic line revealed 13 genes that were up-regulated in DaCBF7-overexpressing plants compared to wild-type plants in the absence of cold stress and in short- or long-term cold stress. Five of these genes, dehydrin, remorin, Os03g63870, Os11g34790, and Os10g22630, contained putative CRT/DRE or low-temperature responsive elements in their promoter regions. Transcriptome analysis of a Ubi:DaCBF4 transgenic line revealed 22 genes that were up-regulated in DaCBF4-overexpressing plants compared to wild-type plants with or without cold stress. Among them, 9 genes were induced significantly in both transgenic lines in common, which encoding PR protein, protease inhibitor, glutathione peroxidase, malate dehydrogenase, ribonuclease family protein, and several unknown proteins. These results suggest that overexpression of CBF transcription factor genes of *D. antarctica* directly and indirectly induces diverse genes in transgenic rice plants and confers enhanced tolerance to cold stress across different taxa.