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Cold acclimation, deacclimation and memory in Arabidopsis

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Plants from temperate regions can be cold acclimated by exposure to low, but non-freezing temperatures resulting in improved freezing tolerance. Whereas the molecular and metabolic basis of cold acclimation has been investigated in detail, little is known about the molecular regulation of deacclimation of cold acclimated plants under warm conditions. Transcript profiling identified genes encoding transcription factors that were transiently induced during the first 24 h of deacclimation, constituting potential regulators determining the rate of loss of freezing tolerance under these conditions. We are currently characterizing the mode of action of the first candidates. In addition, after cold acclimation at 4°C and a deacclimation phase at 20°C, a second treatment at 4°C improved the freezing tolerance of Arabidopsis compared to plants that had only received one cold treatment. This indicates that the plants remembered the first cold treatment and reacted more efficiently to the second cold acclimation. To identify transcripts, lipids and metabolites related to this cold memory, we used Illumina-based RNA-Seq, LC-MS-based lipidomics and GC-MS-based metabolite profiling. We are currently analyzing candidate genes with the aim to identify regulators of cold memory in Arabidopsis.