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# Transcript, lipid and metabolite changes contribute to low temperature memory in Arabidopsis

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Cold priming, also called cold acclimation, the adaptation of plants to low, non-freezing temperatures, is an important aspect of winter survival of plants. In addition, a tightly regulated deacclimation process, i.e. the subsequent loss of freezing tolerance in spring, is necessary to combine the transition to reproductive growth with the need for maintained freezing tolerance to be prepared for recurring cold periods. The molecular and metabolic basis of cold priming has been investigated in detail, but hardly anything is known about memory of a cold event during a subsequent warm spell. We show that cold priming at 4°C followed by an intervening lag phase at 20°C improves the freezing tolerance of the Arabidopsis accessions Col-0 and N14 after the occurrence of a second cold trigger compared to the primed plants. For the identification of possible molecular determinants of this improved freezing tolerance transcripts, metabolites and lipids were investigated after priming, memory phase and triggering by Illumina-based RNA-Seq, GC-MS metabolite profiling and UPLC FT-MS-based lipidomics. Both accessions showed differences in transcript, lipid and metabolite content when comparing triggered with primed plants. Unique changes after triggering included 93 and 128 differentially expressed genes in Col-0 and N14, respectively, with an overrepresentation in functional categories such as lipid and secondary metabolism, stress, redox and cell wall related reactions in Col-0. Furthermore, in Col-0 and N14 three and six lipids showed significant differences in content. They included three arabidopsides as unique triggering responses in N14. In addition, one metabolite in N14 was identified as a unique triggering response. Possible functions of these candidates will be discussed. This is to our knowledge the first report on molecular and metabolic changes accompanying cold stress memory and triggering by a second cold stress.