TRANSCRIPTOMIC CHARACTERIZATION OF BUD DORMANCY IN APPLE

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The knowledge of mechanisms that control quantitative traits is valuable for crop breeding efforts. Apple production depends on the fulfillment of chilling requirement for bud dormancy release. Insufficient winter chilling results in irregular and suboptimal budbreak in spring, with negative impacts on apple yield. We used apple cultivars with contrasting chilling requirements (CR) for bud break to observe the expression of the whole set of apple genes in response to chilling accumulation in the field and controlled environments. Vegetative terminal and floral buds were sampled from field grown 'Royal Gala' (600-800 h CR) and 'Castel Gala' (350 h CR) through winter 2009 in the city of Papanduva - SC. Buds collected in the field were immediately frozen in liquid nitrogen and stored at -80°C. For cold treatments, 20 cm brindles were exposed to different regimes of low temperatures and then forced in a growth-permissive environment. In parallel, apical buds from cold-treated brindles were frozen as described after the same treatments. Similar assays with plant material collected in 2010 served as biological replicates. Total RNAs were isolated from frozen samples and sent to the IRHS (INRA/AgroCampus-Ouest/Université d'Angers, France), where the RNA was analyzed on the AryANE v1.0 oligonucleotide microarrays representing 57,000 apple genes. The results are the log2 ratio of expression for each gene between two samples. Data were tested for functional enrichment by Fisher's exact tests and the program KOBAS 2.0. The largest amount of differentially expressed genes was found in samples of 'Royal Gala' exposed to cold. Cold exposure mostly repressed expression of transcripts related to photosynthesis in samples with low budbreak values. Among the differentially expressed candidates, we identified genes that have potential roles in the circadian clock, hormonal signaling, regulation of growth and flower development. Differential expression of candidate genes was reassessed by real time PCR in the same samples and independent cold-treated samples, as well as in different organs. RT-qPCR results were consistent with those of the microarray for most of the genes. Two genes, annotated as flowering locus C-like, are 10-fold more expressed in dormant buds than in other organs and are highly induced by extended cold. One of these two genes is differentially expressed between the cultivars and is located in a genomic region inside the confidence interval of a major quantitative trait locus for timing of budbreak. The results from our study provide additional support to narrow the search for genes related to the control of dormancy progression in apple.

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