TRANSCRIPTOMIC PROFILING REVEALS FLOWER DEVELOPMENT GENE INDUCTION DURING ENDODORMANCY TO ECODORMANCY TRANSITION IN APRICOT AND PEACH FLORAL BUDS.

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Winter dormancy is a mechanism to protect buds on perennial trees from harsh conditions. Trees enter endodormancy, cease growth and start accumulating chilling hours at the beginning of winter. Once a set chilling requirement (CR) is fulfilled, the trees move into ecodormancy, a stage where trees remain dormant until the arrival of optimal conditions for growth. The transition between dormancy stages is strictly regulated by physiological factors and environmental cues. However, the genetic mechanisms underlying dormancy transition from endodormancy to ecodormancy are still unclear. Here we utilized the transcriptome profiles of apricot (*Prunus armeniaca*) and peach (*Prunus persica*) cultivars with different CRs (early blooming vs late blooming) to explore the genetic regulation of flower bud dormancy. Floral buds from grafted replicates of four apricot cultivars and four peach cultivars with different CRs at time points spanning from early winter to bud break were subjected to RNA-seq analysis. The transcriptome variances showed that the trees with different chill hours were moving through stages of dormancy at different rates. Thus, the samples were analyzed based on physiological stages instead of time points. Of 26,872 genes, 608 were consistently differentially expressed between endodormancy and ecodormancy in both species. Functional analysis reveals these genes are involved in lipid localization, pollen development, cell wall biosynthesis and stimuli response. 99 of them are within previously identified peach CR quantitative trait loci (QTL) regions, indicating that they are strong candidates for dormancy regulation. Co-expression analysis identified two clusters of genes, related to abiotic and biotic stress, flower and pollen development, lignin biosynthesis and lipid transportation, that were highly induced at ecodormancy in peach and apricot. Our analysis reveals that the induction of flower development genes may be an indicator of endodormancy to ecodormancy transition, providing new insights into bud activity at winter dormancy.