

STONE FRUIT TREES AND THE ROLE OF ENVIRONMENTAL CUES DURING WINTER DEVELOPMENT: THE PEACH PERSPECTIVE

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Deciduous trees are one of the most resilient plants on the planet due to their adaptability based on the location where they grow. They are constantly cycling between a period of growth during spring and summer followed by a period of dormancy during autumn and winter. Some of the most nutritive fruits are produced by deciduous trees and their productivity depends on the proper progression of these trees from one phase to the other. Predicting how deciduous trees will respond to climate change requires a comprehensive understanding of the environmental cues and genetic factors involved in dormancy. Within the peach context it has been observed that while a prolonged period of cold is indeed essential for bud-development during endodormancy, there are other environmental cues that control the differentiation of the flower bud organs and the maturation of the pollen. Our work in this regard is the culmination of research conducted on both floral and vegetative buds in multiple varieties of peach with different chilling requirements and observations based on the influences of genomic variations which influence the different phenotypes. Preliminary transcriptomic data hinted towards a more active involvement of vegetative buds during the period of dormancy within the context of gene regulation and development. However, in the grander scheme of things how this activity is involved with the response of the tree to environmental cues remains elusive. To better understand the dynamics of differentially expressed genes and the effects of climatic variations, a detailed transcriptomic study was conducted spanning across the period of chilling accumulation as well as timepoints before and after this period. This data

was supplemented with observational data recording average daily temperatures and length of day for the sampling period to identify gene clusters that correlate with specific environmental cues. Specifically within this regard we explore the role of the peach SVP homolog as well as other DAM genes and their potential interactions with a set of homologous genes involved in the signal transduction of environmental cues. Furthermore, combining the transcriptomic data with quantitative data regarding hormonal and nitrogen content enabled the identification of specific regulatory functions and gene pathways that could help identify targets for further research.