

Towards a better understanding of dormancy in sweet cherry flower buds using molecular and epigenetic approaches

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Abstract

In perennial species, dormancy is a period of repressed growth that acts to protect sensitive tissues during unfavourable climatic conditions. Dormancy and bud burst are strongly affected by temperature. The mean surface temperature of the earth is increasing and this climatic change may have serious negative consequences on the dormancy release, potentially resulting in lower cherry production. Despite this strong effect of temperature on dormancy, the molecular events regulating dormancy and the effect of temperature on dormancy are still not very well understood. It has been shown that *DORMANCY-ASSOCIATED MADS-box (DAM)*-related genes are up-regulated in dormant buds in a certain number of plants (peach, raspberry, leafy spurge, poplar). Recent studies also highlighted the presence of epigenetic mechanisms in the regulation of bud dormancy. To better understand the mechanisms underlying the effect of temperature on dormancy we are assessing genome-wide dynamics of several chromatin marks and expression during dormancy in floral buds of sweet cherry (*Prunus avium* L.) varieties with contrasted bud burst dates. We detected transcriptional and histone methylation dynamics of dormancy-related genes during the dormancy cycle and we are currently analysing their interplay. According to the high level of synteny between *Prunus*, results obtained in sweet cherry may be transferred to other *Prunus* species in order to create new varieties that will be adapted to future climatic conditions.