

Exploring the ABA signalling pathway for molecular-based phenological modelling of bud dormancy

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Abstract

Bud dormancy is a crucial stage in perennial trees and allows survival over winter and optimal subsequent flowering and fruit production. Environmental conditions, and in particular temperature, have been shown to influence bud dormancy. In the current context of climate change, it is therefore essential to better understand and predict dormancy behaviour in order to anticipate upcoming changes.

We combined physiological, transcriptional analyses and phytohormone quantification to further elucidate how key signaling pathways control dormancy progression in the flower buds of different sweet cherry (*Prunus avium* L.) cultivars. We observed that buds at different dormancy stages are characterized by the expression of genes involved in specific pathways. In particular, we found that genes related to abscisic acid (ABA) metabolism were up-regulated during dormancy, associated with high ABA levels. Based on these results, we hypothesized that ABA concentrations were correlated with dormancy depth and subsequently we successfully modelled ABA content and dormancy behavior based on the expression of a small set of genes regulating ABA levels. Such integrative approaches are extremely useful for a better comprehension of how complex processes control phenology in other perennial species and open up new perspectives for the development of future molecular-based phenology models.