

Unravelling the transcriptomics of winter dormancy in raspberry

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Abstract

Climate change is progressively decoupling the environmental cues of dormancy, temperature, and photoperiod. The subsequent shifts in the phenology threaten natural ecosystems and the viability of perennial crops. A deeper understanding of the mechanisms and genetics underlying this process is key for the development of climate-resilient cultivars. This study aims to provide an insight into the mechanisms underlying dormancy in red raspberries (*Rubus idaeus*).

We present the transcriptomic profile of dormancy in two genotypes with contrasting responses. Glen Ample shows a typical perennial response while Glen Dee retains the ability to break bud during the winter. We used RNA-seq and weighted co-expression network analysis (WGCNA) to obtain a time-resolved model of dormancy in both cultivars. K-means clustering was applied to compare the networks and identify candidate genes not expressed or altered in Glen Dee.

Our results provide a month-by-month overview of dormancy, as well as markers for every stage. The data highlights the regulatory role of epigenetic mechanisms in the silencing of gene expression leading to dormancy induction. The transcription factor *RiVRN1*, homologous of *VERNALIZATION 1*, was identified as candidate for the dysregulation of dormancy induction in Glen Dee.