



## Transcriptomic comparison between deflowered and overloaded apple trees: toward the understanding of biennial bearing in apple

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# Transcriptomic comparison between deflowered and overloaded apple trees: toward the understanding of biennial bearing in apple

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Under the assumption that flower induction is inhibited in the trees carrying heavy fruit load or induced by the absence of fruit, we artificially placed in situation of alternation adult apple trees of the Gala variety to study the differentially expressed genes in their apical meristems, from the period of floral induction to floral differentiation. Analysis of these genes by qRT-PCR and microarray enabled to identify the key biological processes involved. Indeed, classes of differentially expressed genes suggest that the meristems are in contrasting physiological states resulting from various metabolic, hormonal and redox states. In addition, several genes known to be involved in the control of floral induction, such as *TEMPRANILLO* (*TEM1*), *FLORAL TRANSITION AT MERISTEM* (*FTM1*) and *SQUAMOSA PROMOTER BINDING PROTEIN-LIKE* (*SPL*) were differentially expressed.

These results represent a foundation toward the understanding of molecular processes leading to the inhibition vs. promotion of floral induction in fruiting trees.