

## GO BACK FROM THE ADULT PHASE

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The juvenile state of woody plants manifests itself in various morphological and physiological phenomena, and the juvenile characters are often not highly correlated each other. Research in juvenility of woody plants was focused primarily on vegetative reproduction and induction of flowering, which are the most general aspects of aging in trees. Many of the morphological and physiological changes related to aging can be understood as consequences of the interaction among several genetic pathways controlling transition, which are integrated at the transcriptional level from *Flowering Time (FT)* and *Leafy (LFY)*. *Twin Sister of Flowering Time (TSF)* acts as a flowering pathway integrator redundantly with *FT*. Searching in the genome of peach ([www.peachgenome.org](http://www.peachgenome.org)), one locus for *FT* and for *TSF* was found. The expression of both genes have been tested to unravel their role in plant juvenility which occurs during the growth of flowering plant *in vitro* conditions. A time scale analyses has been conducted to verify the role of *Short Vegetative Phase (SVP)*, *Early Bolting (EBS)*, *Gigantea (GI)*, *Constans1 (CO1)* and *Constans2 (CO2)*, *Tempranillo1 (TEM1)* and *Tempranillo2 (TEM2)*. These gene are target of many endogenous and environmental factors, such as biological clock, ontogenetic development, growth regulators, temperature, photoperiod, vernalization and touch-related mechanic stimuli.

The mRNA level of *FT* was down-regulated, ranging from 50 to 100 times less, compared to the field grown donor plant. *TSF* was completely shut down in the plants *in vitro* grown. Biological clock and photoperiod doesn't seems to affect *FT* and *TSF*, and no modification in the level of gene expression of *GI*, *CO1* and *CO2* has been found. Noteworthy appears that the ontogenetic development program and the environmental factors are strongly related to the down-regulation of *FT* and *TSF*, as appear from the large up-regulation of the genes *SVP* *EBS* *TEM1* and *TEM2*. Bioinformatic analyses of promoters of the studied genes reveal a possible cross interaction among the representative proteins of endogenous and environmental factors since the specific recognition motifs are present on the promoters of both genes *FT* and *TSF*.

Our work revealed additional complexity and temporal aspects of the regulatory network at the pathway integration level. We propose that the core genes of changing phase are the pivot that induce the plant to go back from adult phase to juvenility.