



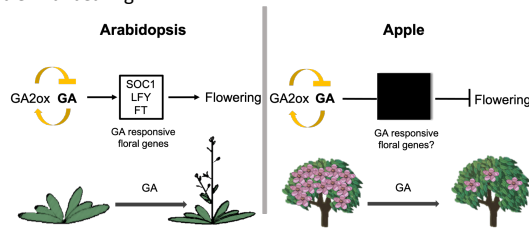
Using the Regulation of GA2ox as a Model to Understand the Role of Gibberellin in Apple Flowering

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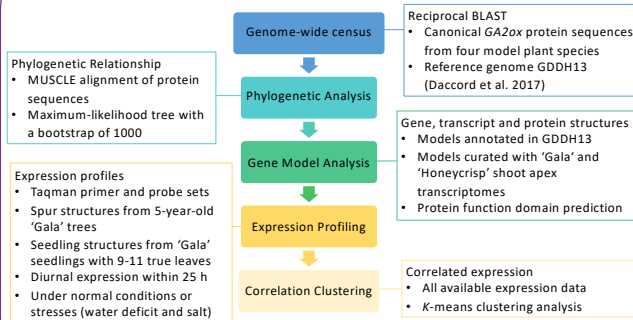
Background

- Opposite from their promotive roles in flowering in the annual model plant *Arabidopsis thaliana*, gibberellins (GAs) can repress flowering in apple (*Malus x domestica* Borkh.). The genetic and molecular mechanisms underlying the repressive role of GAs in apple flowering is not clear.
- While the downstream players in the apple GA signaling pathway seem to differ from those in Arabidopsis, the function and regulation of *MdGA2ox* by GA appears to be conserved: *MdGA2ox* genes encode GA catabolic enzymes that control GA levels; meanwhile, their expression is tightly under genetic control by GA. This tight link between *MdGA2ox* genes and GA can be leveraged to study GA activities related to apple flowering.
- GA activities in spur structures are considered to contribute to biennial bearing in several popular apple cultivars, which causes instable production and significant economic loss every year.
- Understanding GA activities in apple is an important first step to develop GA-based methods for flowering control and to tackle biennial bearing.



Intro Figure 1. The paradox of gibberellin's role in flowering and conserved regulation of *GA2ox*.

Methods



Results

1. A total of 16 canonical *GA2ox*-like genes were identified in the apple genome, representing eight homoeologous pairs.

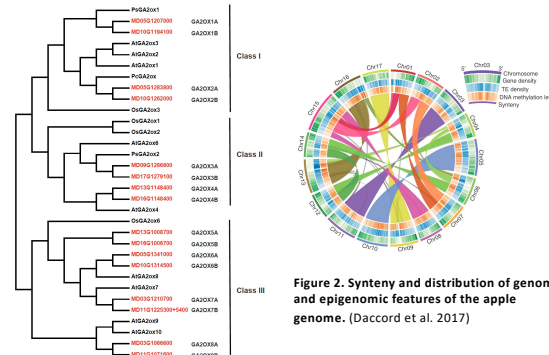


Figure 2. Synteny and distribution of genomic and epigenomic features of the apple genome. (Daccord et al. 2017)

Figure 1. Refined phylogenetic tree of *GA2ox* in apple and model plant species. Apple sequences are highlighted in red. Genes were renamed based on their phylogenetic relationships and genomic organization.

2. Gene, transcript and protein structures

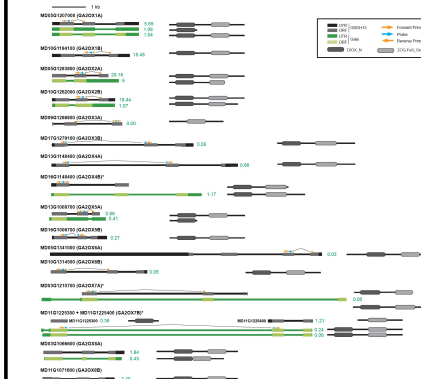


Figure 3. Curated gene, transcript and protein models of *MdGA2ox*. Values in green are expression levels (FPKM) of isoforms in the 'Gala' shoot apex. * denotes gene models that were curated based on transcriptome data.

3. Expression of *MdGA2ox* indicates ubiquitous GA activities in apple spurs.

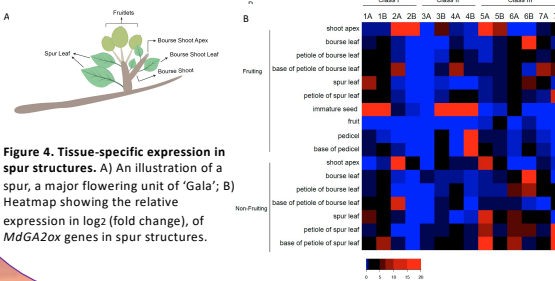


Figure 4. Tissue-specific expression in spur structures. A) An illustration of a spur, a major flowering unit of 'Gala'; B) Heatmap showing the relative expression in log₂ (fold change), of *MdGA2ox* genes in spur structures.

4. Divergence and potential functional redundancy between homoeologous pairs.

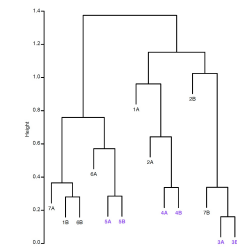


Figure 5. K-means clustering of *MdGA2ox* genes. Genes highlighted in purple are highly correlated homoeologous pairs.

Conclusion

- ❑ The apple genome has a total of 16 *GA2ox* genes, representing eight pairs of homoeologs.
- ❑ In most of the structures studied, except fruit flesh, expression of at least half of *MdGA2ox* genes was easily detectable, indicating ubiquitous GA activities in apple spurs.
- ❑ Expression profiling and correlation clustering of *MdGA2ox* suggest both gene divergence and potential functional redundancy between homoeologous pairs.
- ❑ Further characterization of function and regulation of *MdGA2ox* will enable a better understanding of GA's role in apple flowering.

Reference:

Daccord N, Celton JM, Linsmith G, Becker C, Choise N, Schijlen E, Van de Geest H, Bianco L, Micheletti D, Velasco R, Di Pierro EA. High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. *Nature genetics*. 2017;49(7):1099.

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