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Noémie Vimont, Mathieu Fouché, José Antonio Campoy, Adrián Schwarzenberg, Mirela Domijan, et al.. Transcriptomic profiles highlight the role of ABA signalling in the regulation of sweet cherry flower bud dormancy. 10th International Rosaceae Genomics Conference (RGC 10), Dec 2020, Barcelone, Spain. hal-03318896

HAL Id: hal-03318896

https://hal.science/hal-03318896

Submitted on 11 Aug 2021

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Transcriptomic profiles highlight the role of ABA signalling in the regulation of sweet cherry flower bud dormancy

N. Vimont, M. Fouché, J.A. Campoy, A. Schwarzenberg, M. Domijan, F. Jamois, M. Arkoun, J.-C. Yvin, P.A. Wigge, E. Dirlewanger, S. Cortijo, B. Wenden (benedicte.wenden@inrae.fr)

Univ. Bordeaux, INRAE, Biologie du Fruit et Pathologie, UMR 1332, 33140 Villenave d'Ornon, France; Agro Innovation - Groupe Roullier, 35400 St Malo, France; The Sainsbury Laboratory, University of Cambridge, Cambridge CB2 1LR, United Kingdom; Dept. of Mathematical Sciences, University of Liverpool, Cermany

Introduction

Bud dormancy is a crucial stage in perennial trees and allows survival over winter and optimal subsequent flowering and fruit production.

Recent work highlighted physiological and molecular events occurring during bud dormancy in trees, including a key role for ABA signalling in the control of dormancy onset and release in several temperate tree species.

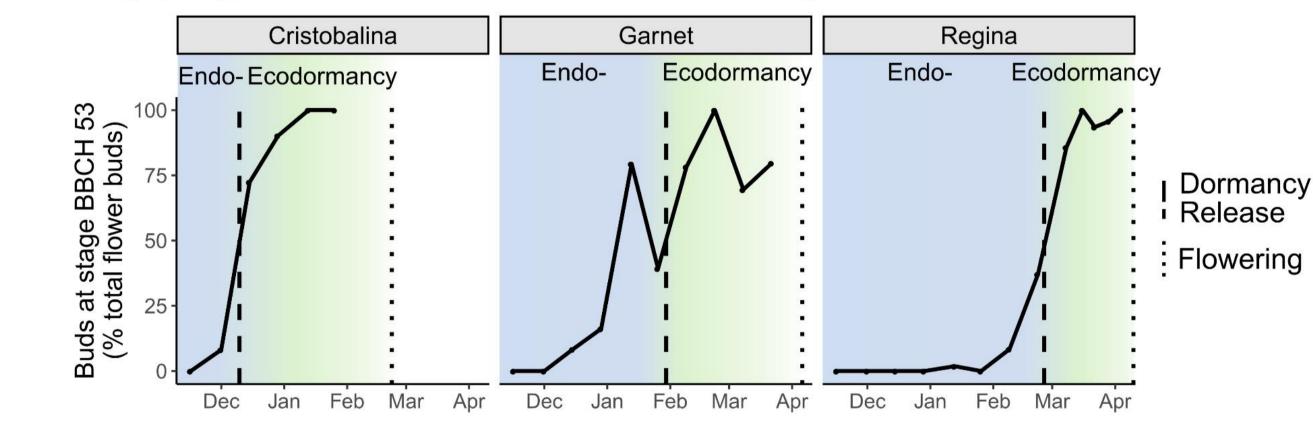
In order to further elucidate how ABA signaling pathway controls dormancy progression in the flower buds of sweet cherry cultivars, we combined:

- Physiological observations
- Transcriptional analyses
- Abscisic acid (ABA) quantification
- Predictive modelling approaches

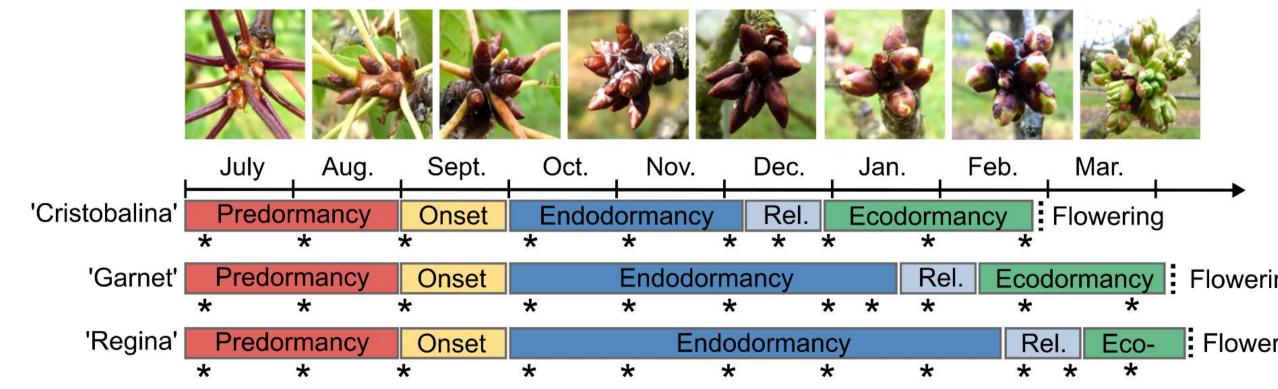
Such integrative approaches will be extremely useful for a better comprehension of complex phenological processes in other perennial

Experimental design

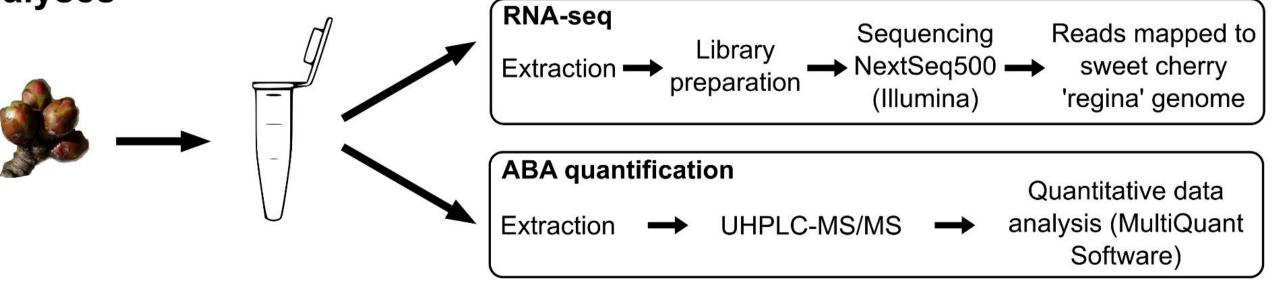




Flower bud sampling (*) throughout dormancy





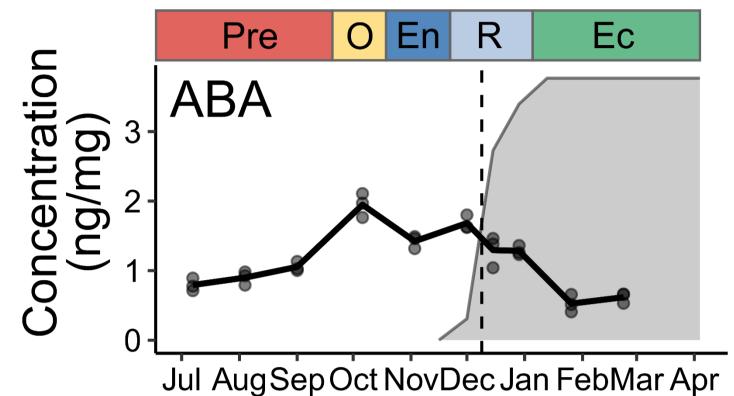


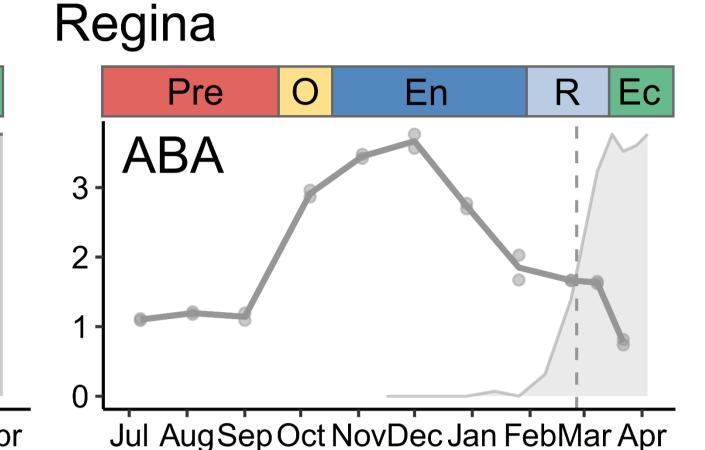


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ABA levels are correlated with dormancy status

Cristobalina



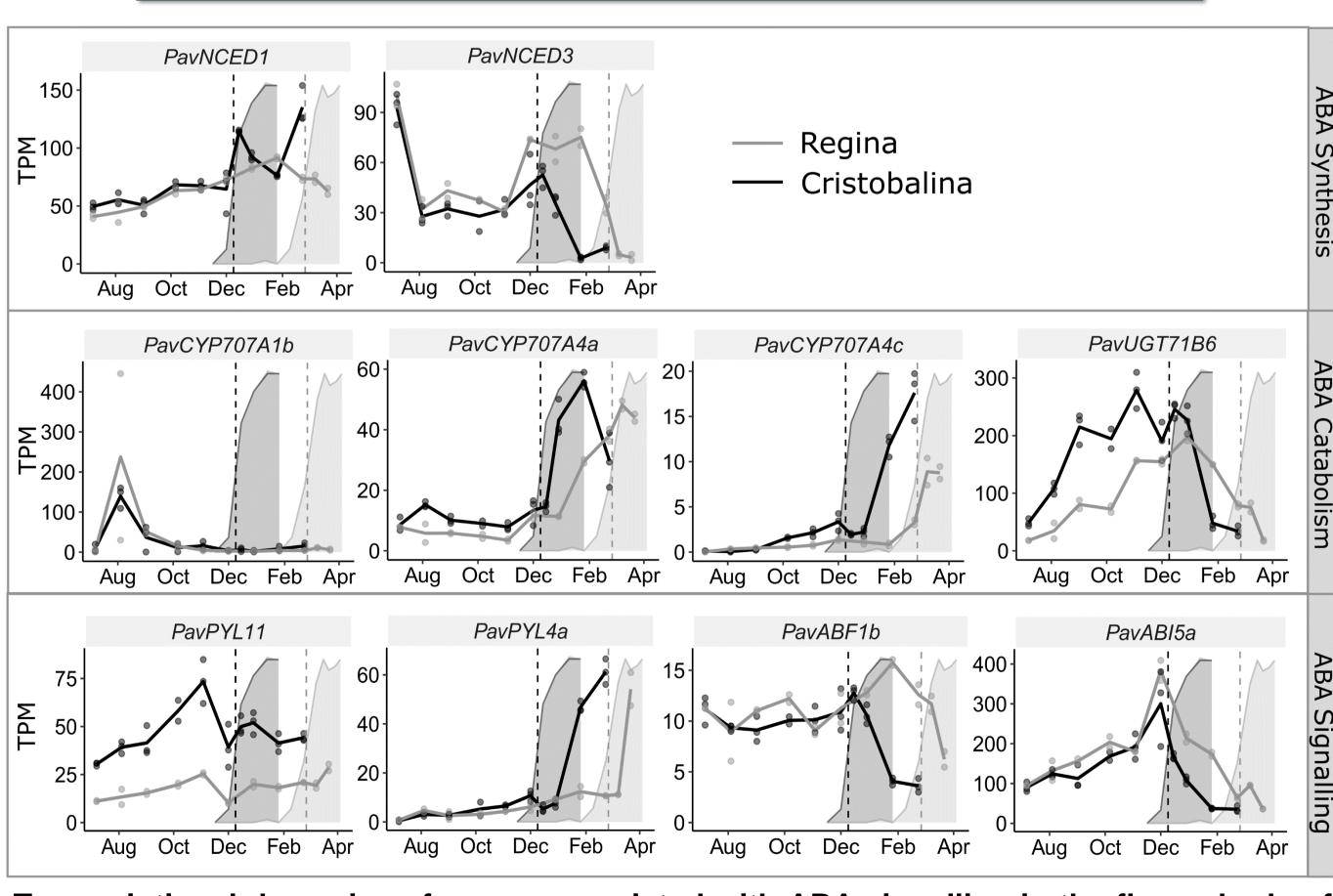


Levels of endogenous bioactive ABA in the flower buds of two sweet cherry cultivars during bud development. Background areas correspond to the dormancy depth evaluated as the percentage of bud break under forcing conditions. Dotted lines represent dormancy release. ABA: Abscisic acid; Pre: Predormancy; O: dormancy onset; En: Endodormancy; R: Dormancy release; Ec: Ecodormancy.

KEY RESULTS

- Higher levels of ABA during endodormancy
- Decrease in ABA content before dormancy release
- Higher ABA levels in the cultivar with a late dormancy release date

Expression pattern of ABA signaling genes

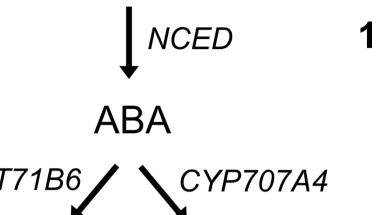


Transcriptional dynamics of genes associated with ABA signalling in the flower buds of two sweet cherry cultivars during bud development. Background areas correspond to the dormancy depth evaluated as the percentage of bud break under forcing conditions. Dotted lines represent dormancy release. TPM: Transcripts per million reads.

KEY RESULTS

- Higher expression of PavNCED3 in the late cultivar
- Early expression peak of ABA catabolism genes in the early cultivar
- Higher expression of PavUGT71B6 in the early cultivar

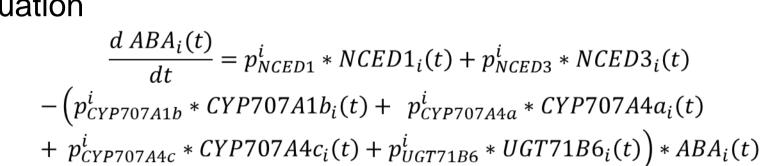
Modelling ABA levels and dormancy release



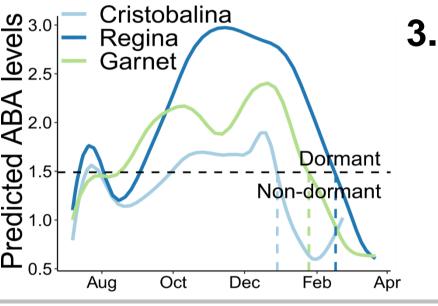
1. Model hypotheses

- ABA content can be simulated using a small set of genes involved in synthesis and degradation
- Dormancy release is triggered below an ABA threshold

2. Model construction and parameter calibration o ABA level at different times is described by an ordinary



- 'Regina' and 'Cristobalina' data were used to calibrate
- We selected the parameter set with the lowest sum of the least square



3. Testing the model on a third cultivar

- The model accurately simulates variations in ABA levels
- We simulated an ABA threshold for dormancy release
- o The model accurately predicted a dormancy release date for 'Garnet' between the dates for the early and late cultivars

KEY RESULTS

ABA levels could be simulated using a small set of genes

The model was validated for dormancy release in a third cultivar

Conclusion

- Following our observations that ABA levels were correlated with dormancy status and that dynamics of expression for ABA synthesis and catabolism may explain the differences observed between cultivars, we have successfully modeled ABA content and dormancy behavior in three cultivars exhibiting contrasted dormancy release dates.
- However, although we could verify the model on dormancy release dates in one independent cultivar, additional experiments with precise ABA levels evaluation will be necessary to validate the actual prediction of ABA levels based on gene expression associated with the dormancy status in 'Garnet'.
- The next steps will be to provide information on temperature-mediated control of the regulatory cascades.

References

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