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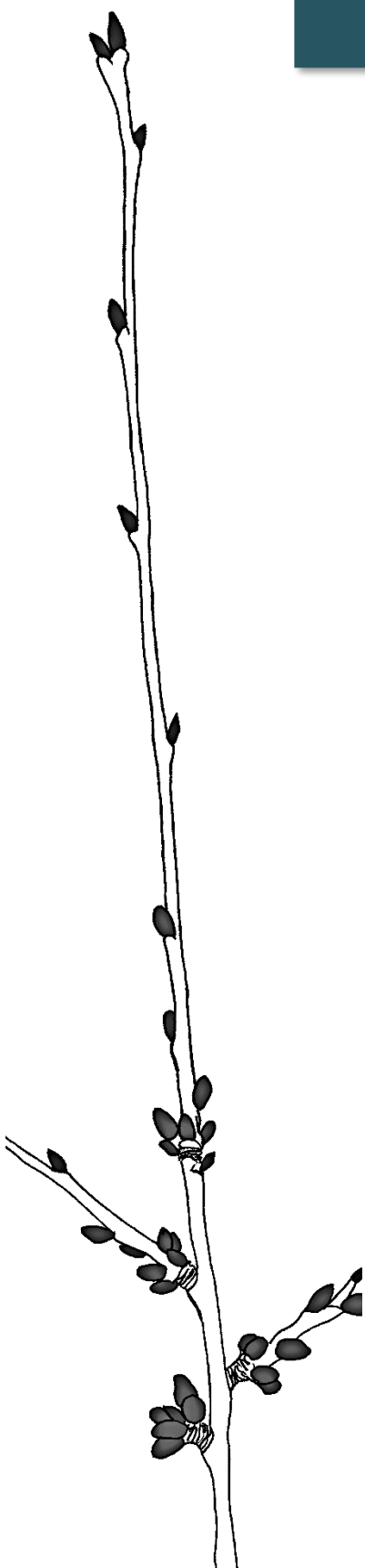
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Transcriptomic profiles highlight the role of ABA signalling in the regulation of sweet cherry flower bud dormancy

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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.

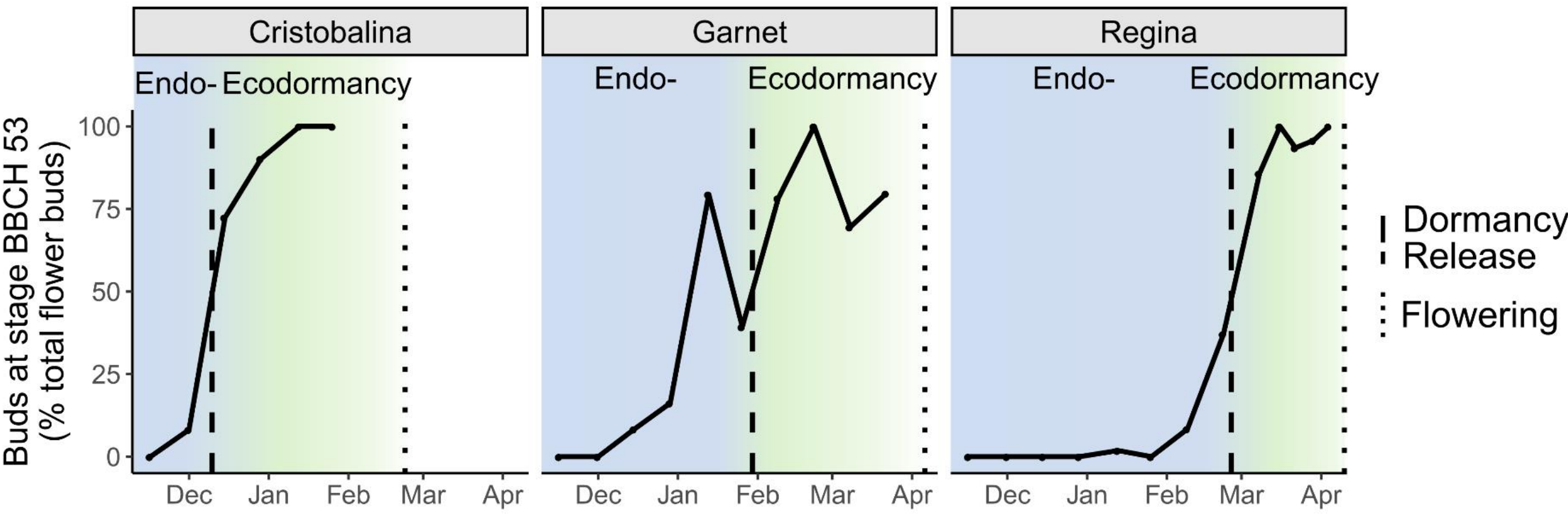
In order to further elucidate how ABA signaling pathway controls dormancy progression in the flower buds of sweet cherry cultivars, we combined:

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

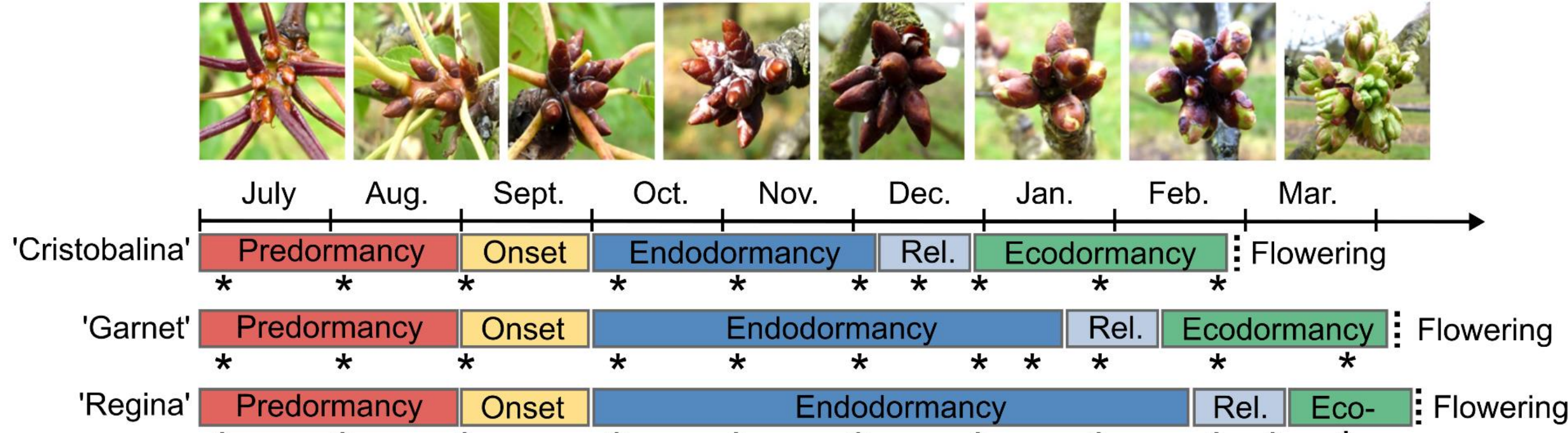
Such integrative approaches will be extremely useful for a better comprehension of complex phenological processes in other perennial species.

Experimental design

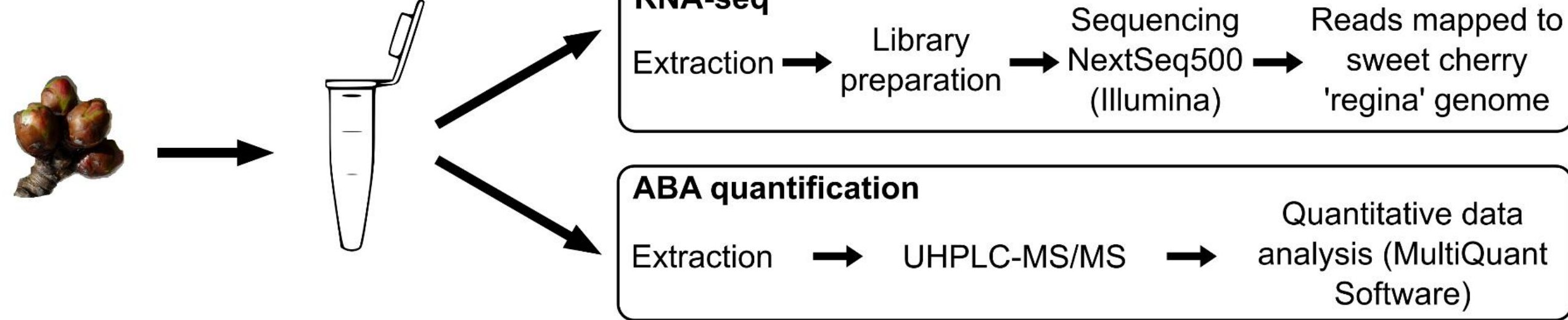
Dormancy progression in the three sweet cherry cultivars



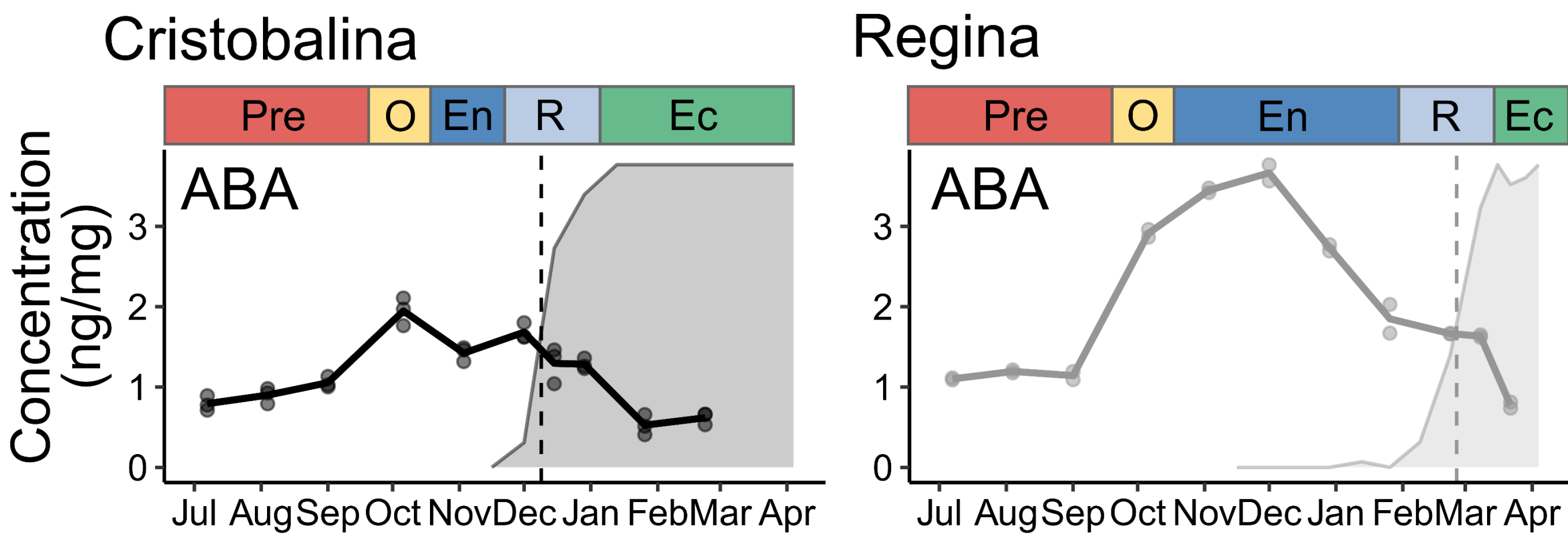
Flower bud sampling (*) throughout dormancy



Analyses



ABA levels are correlated with dormancy status

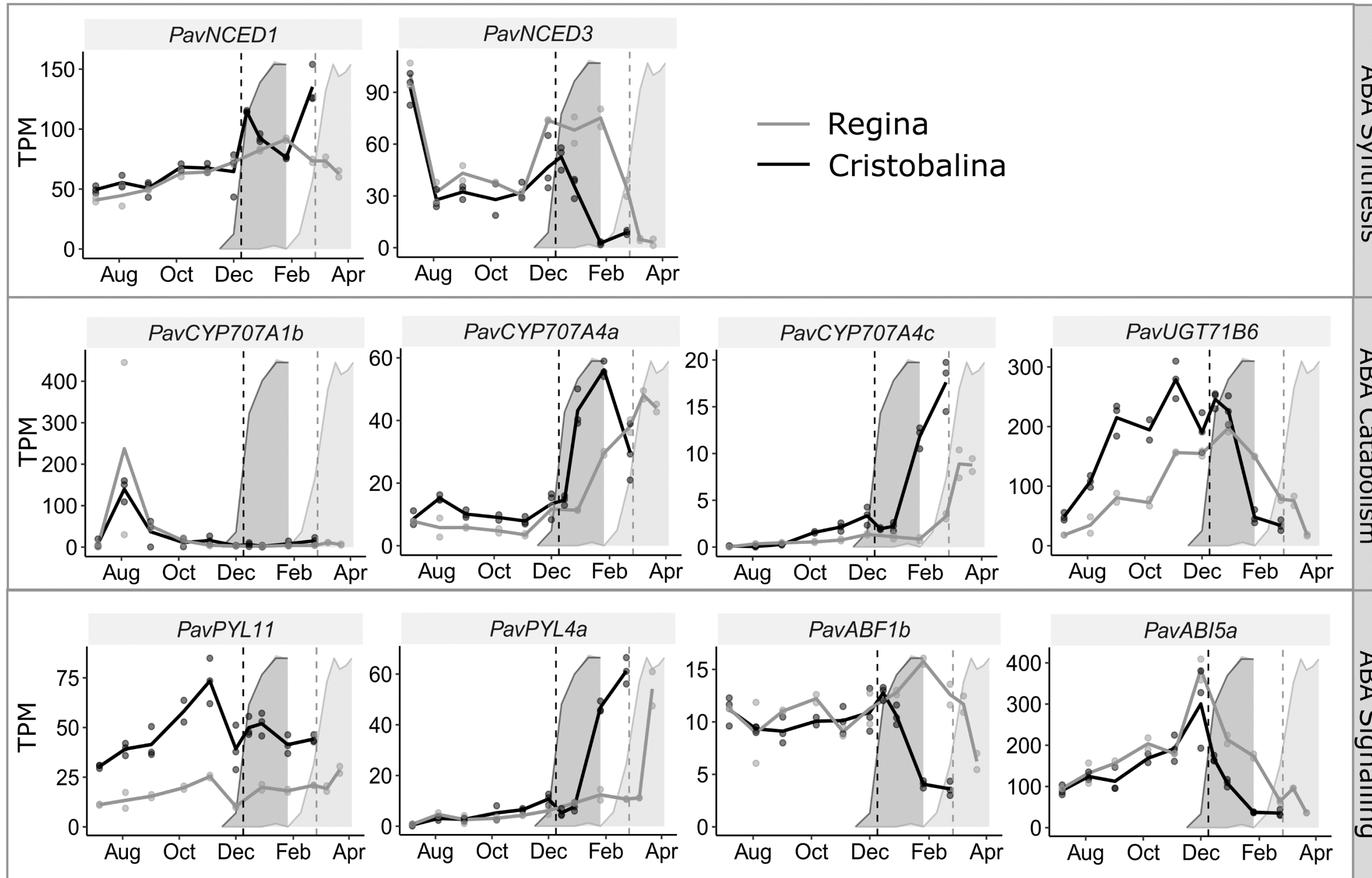


Levels of endogenous bioactive ABA in the flower buds of two sweet cherry cultivars during bud development. Background areas correspond to the dormancy depth evaluated as the percentage of bud break under forcing conditions. Dotted lines represent dormancy release. ABA: Absciscic acid; Pre: Predormancy; 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

↓ *NCED*

ABA

UGT71B6 ↙ CYP707A4 ↘

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

ABA level at different times is described by an ordinary equation

$$\frac{d ABA_i(t)}{dt} = p_{NCED1}^i * NCED1_i(t) + p_{NCED3}^i * NCED3_i(t) - (p_{CYP707A1b}^i * CYP707A1b_i(t) + p_{CYP707A4a}^i * CYP707A4a_i(t) + p_{CYP707A4c}^i * CYP707A4c_i(t) + p_{UGT71B6}^i * UGT71B6_i(t)) * ABA_i(t)$$

- 'Regina' and 'Cristobalina' data were used to calibrate the model
- 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
- 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

Vimont N, Schwarzenberg A, Domijan M, Donkpean ASL, Beauvieux R, Le Dantec L, et al. Fine Tuning of hormonal signaling is linked to dormancy status in sweet cherry flower buds. *Tree Physiol.* 2020;tpaa122.

Vimont N, Fouché M, Campoy JA, Tong M, Arkoun M, Yvin J-C, et al. From bud formation to flowering: transcriptomic state defines the cherry developmental phases of sweet cherry bud dormancy. *BMC Genomics.* 2019;20:974.