

Determination of DNA methylation and histone modification kinetic in regulatory regions of Dormancy Associated MADS-box gene 6 (*DAM6*) in sweet cherry (*Prunus avium*) during bud dormancy release

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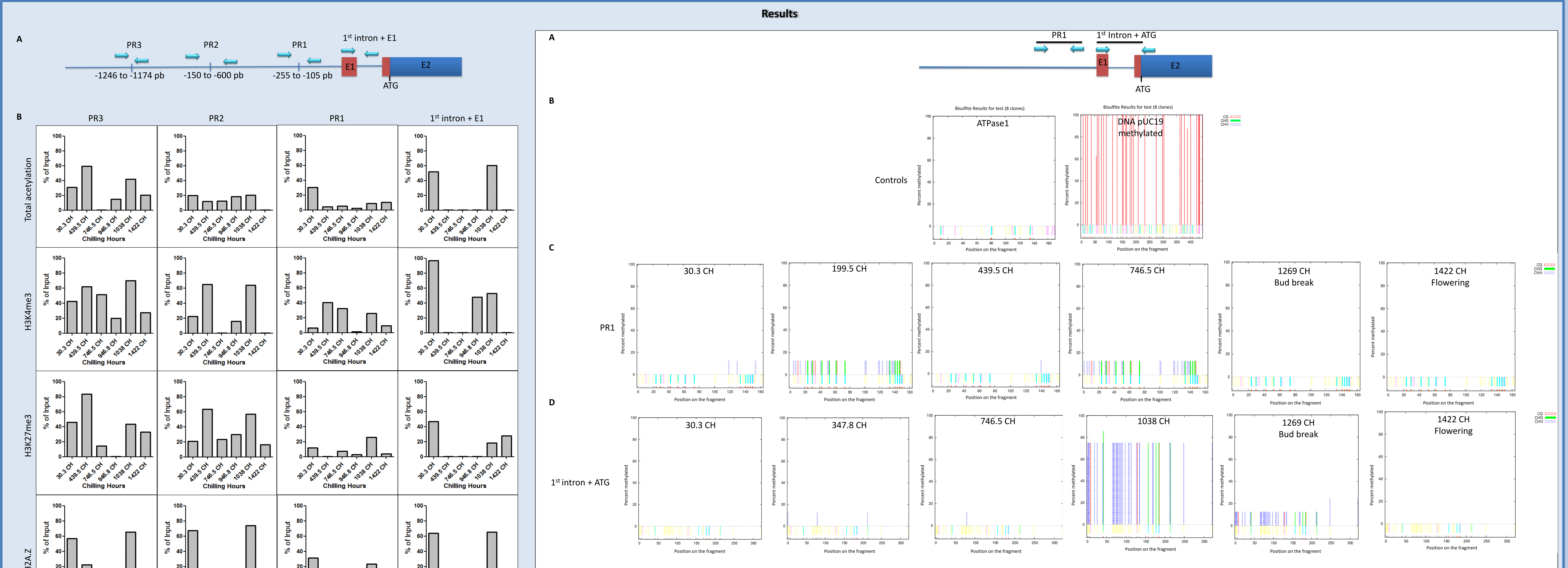
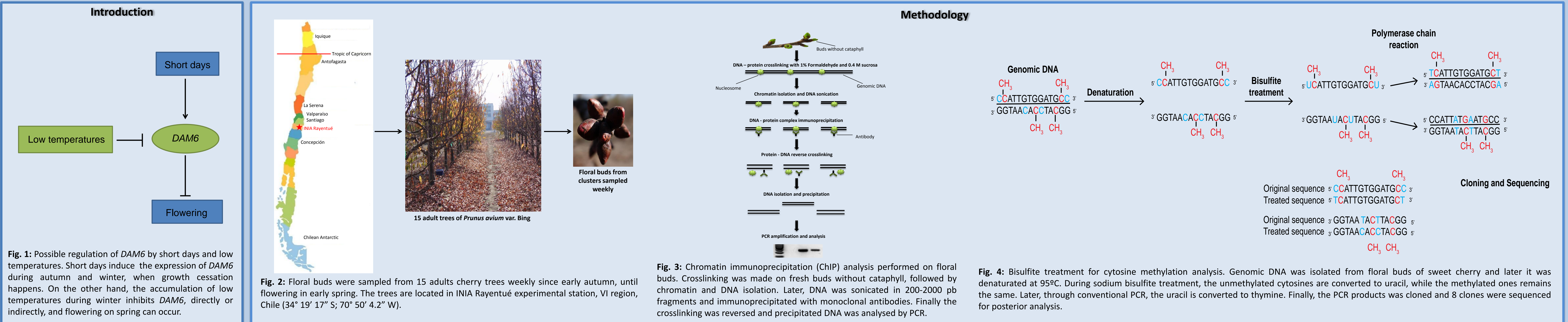
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Bud dormancy release in *Rosaceae* depends on a minimum accumulation of chilling hours. *DORMANCY ASSOCIATED MADS-BOX* (*DAM*) genes are strong candidates for the regulation of bud growth cessation, dormancy maintenance and bud break. Epigenetic mechanisms appear to control the silencing of *DAM6* in peach in a similar way to *FLC* (*FLOWERING LOCUS C*) in *Arabidopsis* during vernalization, proposing a similar regulation in dormancy. To better understand the molecular mechanism of dormancy release in sweet cherry (*Prunus avium* var. Bing); we isolated the promoter and first intron of *DAM6*. The kinetic of histone modifications and DNA methylation of this regions, in response to chilling hours (CH) accumulation, was studied in floral buds sampled weekly during the dormancy period on fall, winter, and spring.



Conclusions

- Gene silencing signals: The presence of H3K27me3 in PR1 increases at 1038 CH, while the presence of the histone variant H2A.Z increases in PR2, PR3 and first intron at the same CH. These results are complemented with the presence of DNA methylations in the first intron at 1038 CH.
- Gene activating signals: the presence of total acetylation decreases in PR1 and PR3 during chilling accumulation. While the presence of H3K4me3 decreases in PR1, it is not present in PR2 and first intron when flowering occurs at 1422 CH. These results complemented well with an absence of DNA methylations at bud break and flowering time.
- The kinetic of post-translational modifications and DNA methylations are very dynamic across the time.
- It is necessary to perform a relative expression analysis of *DAM6* to correlate the obtained results with gene expression.

Contact detail and acknowledgment

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