

IDENTIFICATION AND CHARACTERIZATION OF *DAM* GENES MUTATIONS ASSOCIATED WITH LOW-CHILLING AND EARLY BLOOMING IN SWEET CHERRY

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Abstract:

Dormancy release and bloom time on sweet cherry (*Prunus avium* L.) cultivars depend on the environment and the genotype. The knowledge of these traits is essential for cultivar adaptation to different growing areas, and to ensure fruit set in the current climate change scenario. In this work, a major sweet cherry bloom time QTL (*qP-BT1.1^m*) spanning 327 Kbps at bottom of chromosome 1 (Calle et al. 2020) was scanned for candidate genes using the 'Regina' sweet cherry reference genome. Six *MADS-box* genes, orthologs to *DAM* (*Dormancy associated MADS-box*) genes of other *Prunus* species, were identified as candidate genes for bloom time regulation (*PavDAMs*). To investigate intra-specific variation of *PavDAMs*, 13 sweet cherry genome sequence reads (Ono et al. 2018) from cultivars with contrasting chilling requirements and bloom times were then mapped to the sweet cherry reference genome. A high level of protein sequence conservation was observed (98.8-100%). Additionally, a higher variability and several structural mutations were identified in the low-chilling and extra-early blooming cv. 'Cristobalina'. Specifically, a large deletion (694 bp) upstream of *PavDAM1*, and various INDELS and SNPs in contiguous *PavDAM4* and -5 UTRs were identified in this cultivar. *PavDAM1* upstream deletion include several cis-acting motifs, potentially involved in *PavDAM* expression. Also, the structure of a non-coding gene expressed in late-blooming cultivars seems truncated in 'Cristobalina'. Additionally, *PavDAM4* and -5 UTRs mutations revealed different splicing variants in *PavDAM5*. The results indicate that the regulation of *PavDAMs* expression and post-transcriptional regulation in 'Cristobalina' may be altered due to structural mutations in regulatory regions. Previous transcriptomic studies showed differential expression of *PavDAM* genes during dormancy in this cultivar. Together, the results indicate that

‘Cristobalina’ shows significant amino acid and structural mutations in *PavDAMs*, which correlate with low-chilling and early bloom phenotype, but the direct implication of these mutations remains to be determined. The presence of these mutations and their association with low-chilling and early-blooming was confirmed in a segregating population and in a cultivar collection, and markers were designed for selection breeding.

Key words: *Prunus avium*, dormancy, low-chilling, bloom time, *DAM*, mutation, expression.

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References: please follow the examples below

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