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SWEET CHERRY DORMANCY: CHARACTERIZATION OF PAVDAMS ALTERNATIVE SPLICING IN GENOTYPES WITH DIFFERENT CHILLING REQUIREMENTS.

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Abstract

Sweet cherry (*Prunus avium* L.), like other species of the genus *Prunus*, undergoes a period of dormancy in which vegetative growth stops in winter and resumes in spring. The broad natural geographic range of this species, from Northern Europe to Northern Africa, implies a large variability in dormancy adaptation and chilling requirements. Although the genetic control of dormancy is not yet fully understood, it has been reported that the transcription factors DORMANCY-ASSOCIATED MADS BOX (DAMs) are involved in this process. In other Rosaceae species like European plum (*Prunus domestica* L.) and *Pyrus pyrifolia* Nakai., it has been shown that DAMs genes can be regulated by alternative splicing (AS). Flowering time in *Arabidopsis* is also regulated by a temperate-dependent AS mechanism in MADS BOX family genes. The aim of this work is to investigate the expression of *P. avium* DAM genes (*PavDAMs*) to elucidate if AS is associated with phenotypic differences in dormancy adaptation traits, like chilling requirements. For this purpose, we investigated the expression of *PavDAMs* genes by RT-PCR in cultivars with contrasting chilling requirements at different times during dormancy. Results revealed putative gene-, time- and genotype-specific AS events in these genes during this process. The AS transcripts detected are being cloned, sequenced and quantified (qPCR) to characterize AS during the dormancy period in these contrasting phenotypes. The results of this work will be presented and will provide further insight into the genetic regulation of dormancy and adaptation in sweet cherry. This information will be useful for breeding for adaptation to warmer conditions in low chilling regions or resulting from climate change.