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Control of bud dormancy in Apple

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Dormancy is an adaptive mechanism that enables plants to survive unfavorable climatic conditions, for example during winter, and allows flowering to occur only when the conditions are more permissive, typically in spring. The production of temperate fruits, such as apple (*Malus x domestica Borkh.*), is closely related to bud dormancy, given that a well-adjusted dormancy cycle is crucial for the achievement of their full genetic potential. Unlike other temperate fruit crops, dormancy in apple is assumed to be triggered by exposure to low temperatures and not photoperiodic changes. Therefore, the predicted impact of the ongoing climate change will result in difficulties for apple production. The mechanisms that regulate dormancy are highly heritable, suggesting a strong genetic control of this trait. However, the genetic networks controlling dormancy progression in apple are still unknown. In this context, the present work aims to prospect and characterize the role of Dormancy-Associated MADS-box (DAM), a group of genes encoding MADS-box transcription factors, and other flowering-time related genes in the dormancy process of apple through complementary genetic and molecular approaches. At the genetic level, we are exploring an apple core collection established in France to identify allelic variation present in genes involved in bud dormancy and flowering control. For this purpose, we have developed a target capture sequencing approach on key gene families involved in dormancy and flowering regulation. At the molecular level, we are studying how DAM proteins are organized in transcriptional complexes and searching for their transcriptional targets. Together, these studies will allow a better characterization of key processes in dormancy molecular control, as well as to identify possible biotechnological resources for application in breeding programs.

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