Molecular and genetic characterization of dormancy-associated and flowering-time related MADS-box transcription factors in apple

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The production of temperate fruits such as apple (*Malus* x *domestica* Borkh.) is closely related to the dormancy process, an adaptive plant survival mechanism to unfavorable climatic conditions. This process is highly heritable, suggesting a strong genetic control of the trait. It has been suggested that genes encoding Dormancy-Associated (DAM) and flowering-time related MADS-box transcription factors control dormancy, although their mode of action and integration to the process are still unknown. The present work aims to characterize apple DAM and flowering-time related MADS-box transcription factors through complementary genetic and molecular approaches. At the genetic level, a target capture sequencing assay is being employed on a French apple core collection in order to identify allelic variations present on genes involved in dormancy and flowering control. Preliminary GWAS analysis allowed refining a QTL linked to budbreak previously identified on chromosome 9. At the molecular level, we identified several *MADS-box* genes being co-expressed during dormancy, and we are currently investigating the formation of transcriptional complexes between their protein products. This possibility is being explored by yeast two-hybrid and ChIP-seq experiments. Together, these studies will better characterize key processes in dormancy molecular control, as well as identify possible resources for breeding programs.