ORAL PRESENTATIONS

SESSION 1 | FLORAL TRANSITION

O8

Genetic and molecular characterization of bud dormancy in apple: deciphering candidate gene roles in dormancy regulation.

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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. At the molecular level, bud dormancy in apple is probably controlled by a group of genes encoding MADS-box transcription factors commonly known as *Dormancy-Associated MADS-box* (*DAM*) genes. However, their precise mode of action and integration in gene networks controlling dormancy progression in apple are still unknown. In this context, the present work aims to prospect and characterize the role of *DAM* 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, and several cultivars from Brazil, in order to identify allelic variation present in genes involved in bud dormancy and flowering control. For this purpose, we are developing 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 by performing yeast two-hybrid assays. Furthermore, we are carrying over chromatin immunoprecipitation followed by sequencing (ChIP-seq) experiments in order to identify their genome-wide 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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