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

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ABSTRACT

Dormancy is an adaptive mechanism that enables plants to survive unfavorable climatic conditions and allows flowering to occur only when the conditions are more permissive. 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. Dormancy in apple is triggered by exposure to low temperatures and therefore, the predicted impact of the ongoing climate change will result in difficulties for apple production.

Year : 2015
Project number : 1503-008
Type of funding : AAP EMBRAPA
Project type : AAP
Research units in the network :
Start date : 2016-11-01
End date : 2018-10-31
Flagship project : no

Project leader : Evelyne Costes
Project leader's institution : INRA-INRAE
Project leader's RU : AGAP

Budget allocated : 49842 €
Total budget allocated (including co-financing) : 99684 €
Funding : Labex

GOAL

This project aims to identify and characterize genes playing a regulatory role in the bud dormancy process in apple tree through the combination of genetic and molecular strategies. For this purpose, (1) we will make use of target enrichment and sequencing of candidate genes (CGs) for determining the allelic variation present in a French core collection in all genes known to be involved in flowering in Arabidopsis. Next, a GWAS will be done to associate allelic variability on apple flowering time genes to bud break date. (2) We will characterize at the molecular level the function of Dormancy-Associated MADS-box (DAM) and other MADS-box proteins related to the dormancy process regulation. For this end, we will identify their molecular partners by yeast-two-hybrid assays and their transcriptional target genes by ChIP-seq.

RESULTS

WP1. Exploring the allelic variability of flowering genes in an apple core collection In this WP, we aim to explore the allelic variability of an INRA apple core collection (generated by INRA IRSH, Angers) and implanted in Montpellier experimental stations. WP1.1 Phenotyping. The phenotyping for bud break date and dormancy release has started in spring 2015 at Montpellier, and will continue until the end of the

project. WP1.2 Target enrichment and sequencing of candidate genes. A sequencing by capture will be carried out focusing on ~726 apple genes orthologues of ~333 Arabidopsis flowering-related genes. WP1.3 Association mapping. Sequencing data will be used to perform a GWAS that allow to precise the list of CGs associated to bud break and dormancy. WP2. Molecular characterization of MADS-Box proteins associated to bud dormancy control in apple. For the molecular experiments, 'Gala' trees are already being grown simultaneously at experimental sites in Brazil and Montpellier. WP2.1 Sampling of the plant material and expression analysis. We will characterize the transcriptional expression profiles of MdFLC, MdDAM1 and MdAGL24 in buds from dormancy.
WP2.2 Identification of interacting proteins of MdFLC, MdDAM1 and MdAGL24 and re-construction of transcription complexes regulating bud dormancy in apple. The formation of combinatorial complexes between MdFLC, MdDAM1, MdAGL24, MdDAM2, MdDAM3, MdDAM4, MdMAF2 and other candidate MADS-box proteins will be tested. WP2.3 Genome-wide identification of target genes of MdDAM1, MdFLC and MdAGL24. ChIP-seq experiments for MdDAM1, MdFLC and MdAGL24 will be done and validation of the target genes will be performed on material harvested at Brazil and France by ChIP-PCR.
WP2.4 Data integration. All the data produced in this project will be integrated with the transcriptomic-based data created by Brazilian partner and dedicated to bud dormancy characterization in the Apple BDDB. Together, these analyzes will allow a better characterization of key points in dormancy molecular control, as well as identify possible biotechnological resources for application
in breeding programs.