

PREDIRE

Project title: Constitutive level of basal defences in healthy apple cultivars as predictors of multi-resistance and performance of plant defence stimulators

Acronym: PREDIRE (PREDIction of RESistance in apple)

Project duration: 36 months – Start date: 1 October 2016 End date: 30 September 2019

Key-words: basal defences, constitutive expression, structural annotation, functional annotation, sequence diversity, RT-qPCR, primers, expression QTL, genome-wide association mapping, SNP, apple, scab, fire blight

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Summary:

Apple is susceptible to numerous diseases and pests that request intensive chemical controls with much concern for human health and environment. Breeding new resistant varieties and/or stimulating plant defences in commercial orchards are thus major stakes. Especially, increasing the level of basal defences against a large range of bioagressors instead of focusing on complete resistance against particular ones is a major goal to efficiently decrease the number of treatments. We hypothesize that the constitutive level of basal defences (i.e., before any induction) is driving the plant capacity to reach a sufficient resistance level to control a pathogen or pest attack, possibly with the help of Plant Defence Stimulators (PDS). In several plant models, constitutive defences have actually been associated to quantitative resistance and are highly suggested to predict the protective efficiency of PDS. Accurate assessment of the constitutive level of defence-related genes at the transcriptional level is thus a major stake, which is challenged by the genetic variability of the corresponding gene families especially when a large germplasm has to be screened. The genomic resources recently developed in apple at IRHS Angers (new genome sequence, accurate annotation, resequenced panel, SNP genotyping array), the germplasm resources present on-site, and the skill of the involved teams in bioanalysis, quantitative genetics and functional analysis of defences with or without PDS allow us to explore the genetic variability of defence gene sequences and to decipher the genetic control of constitutive defences thanks to expression QTL (eQTL) analysis.

Goals: The genetic variation of apple constitutive defences at the transcriptional level will be assessed and characterized in a large range of apple cultivars (several hundreds of old apple cultivars from various European origins). We want to perform a proof-of-concept that the constitutive expression level of some particular defence genes (i) can be accurately assessed with RT-qPCR in a very large apple germplasm, (ii) is subject to heritable genetic variation, (iii) can be subject to eQTL analysis thanks to genome-wide association studies (GWAS), and (iv) is potentially correlated to apple scab and fire blight partial resistance and to PDS protective efficiency. The major technical challenge is to define robust conserved primer pairs allowing the accurate assessment of gene expression of multigenic families in a large germplasm by RT-qPCR.

Methodology: The experimental approach is subdivided in 4 tasks, with the 5th task devoted to the

dissemination of results:

- 1- Characterizing in silico a set of max. 50 apple defence-related gene families (bioanalysis, functional annotation of subfamilies)
- 2- Designing and validating robust RT-qPCR primer sets for 15-20 families in 30 apple cultivars
- 3- Assessing the genetic variation of the constitutive expression level of 3 candidate defence-related genes and performing GWAS on 400 cultivars with the help of available high-density genotyping data (487k Axiom array)
- 4- Correlating the constitutive expression levels of defence genes to scab and fire blight resistance or to the PDS protective efficiency against these diseases on either 30 cultivars (x 15-20 genes) or 400 cultivars (x 3 genes)