

ValoRGPomme

Project title: Effective use of genetic resources in the apple elite breeding population with genomic selection

Acronym: ValoRGPomme

Project duration: Project duration: 36 months – Start date: 01/11/2018 End date: 31/10/2021

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Summary:

Context:

Apple is the second most important worldwide cultivated fruit crop and the first in France. In apple breeding programs, phenotyping for horticultural traits is lengthy and costly and marker assisted breeding, more precisely genomic selection for traits with complex genetic control, is a promising and innovative strategy. This strategy relies on the building of a genome-wide prediction (GWP) model thanks to a genotyped and phenotyped training population and the application of the model to genotyped candidates when their phenotypes are not yet available. Worldwide, elite breeding populations are most often derived from the most used cultivars and thus contain a reduced diversity. To reduce the vulnerability induced by this situation, it is necessary to enlarge the genetic diversity used in the breeding programs by an efficient use of genetic resources.

Goals:

The overall goal of the PhD project is to study how to efficiently use genomic selection to introgress favorable alleles from genetic resources into elite germplasm. More specifically, the PhD student will address the following research questions: i) how to combine data on elite and genetic resource material to apply genomic prediction to hybrids between these two gene pools? ii) What is the best genetic make-up of the training population and the best GWP model to transfer favorable alleles from genetic resources into elite germplasm? iii) would first, second or later generation hybrids between elite and genetic resource material, or hybrids from pseudo-backcross, provide more accurate GWP models?

Methodology:

Two complementary approaches will be followed to study genotype imputation accuracy and genomic prediction accuracy:

- available datasets from the apple INRA breeding program and from European genetic resources will be used with various resampling strategies and/or various statistical models
- simulations will enable to explore layouts not covered by already available data, more specifically those concerning advanced backcross or intercross generations.