

## DEEP DIVING

Project title: DoEs host domestication Promote effectors DIVERSIFICATION IN pathogens?

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### Summary:

Since the beginning of agriculture, wild plant species have been hybridized to generate new crops with higher agronomic and economic added values. However, little is known about **how host domestication may influence the evolution of pathogens and how it may even favour the emergence of new diseases**. Dessert apple *Malus x domestica* is a hybrid between several wild *Malus* species. The principal contributor is *M. sieversii*, which is endemic in Central Asia. *M. sylvestris* and *M. orientalis*, which are endemic in Europe and Caucasus, respectively, are secondary contributors. The main pathogen of *M. x domestica*, the fungus *Venturia inaequalis*, also originates from Central Asia. Although *V. inaequalis* can infect all these *Malus* species, isolates obtained from the different hosts differ in their pathogenic behaviour. Indeed, previous studies showed that virulence and aggressiveness have probably been gained during host domestication.

Here, we want to understand how successive hybridization events between *Malus* species, i.e. host domestication, have modified the pathogenicity determinants of *V. inaequalis*. We will focus on the polymorphism of protein effectors, which are known to be key determinants of the virulence of fungal pathogens.

830 putative protein effectors are predicted in the genome of *V. inaequalis*. However, in order to work on genes that are actually expressed during infection of the host and therefore might play a role in the interaction, we will take advantage of transcriptomic data obtained during the infection already available in the team. Polymorphism of the effector candidates in *V. inaequalis* populations will be measured thanks to the genome sequence available for 42 isolates that were sampled on the different *Malus* species (*M. x domestica*, *M. sylvestris*, *M. orientalis* and *M. sieversii*). Using coalescence analyses, we will determine the origin of effector candidate alleles that are segregating in strains that infect domestic apple trees. Using several tests like ABBA-BABA, **we will evaluate if new alleles were either introgressed from a local population of *V. inaequalis* preexisting on wild *Malus* trees or originated from de novo adaptation.**