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Unravelling the genetic architecture of virus quantitative pathogenicity

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The use of plant varieties carrying major resistance genes has been for a long time a privileged solution to fight against plant disease. However, the ability of the targeted pathogens to adapt quickly to these varieties makes it necessary to search for more durable genetic resistances. Plant quantitative resistance and tolerance are assumed to be more durable than major-effect resistance genes, but experimental evidence is still scarce. To explore the potential of these genetic resources, our goal is to measure the ability of plant viruses to adapt to plant quantitative resistance and tolerance.

To identify viral genes and mutations involved in virus adaptation to plant quantitative immunity, we performed a genome-wide association study (GWAS) on a collection of 18 Potato virus Y (PVY) isolates representative of the PVY genetic diversity. Each PVY isolate was mechanically inoculated to 5 pepper (*Capsicum annuum*) doubled haploid lines contrasted for their levels of quantitative resistance and tolerance toward the virus. Two quantitative pathogenicity traits were measured : the virulence (i.e. the level of damage caused by the virus to the plant health) and the intra-plant viral load. For the latter, a SYBR Green RT-qPCR protocol was developed in order to accurately quantify the level of nucleic acids of each PVY strain in each pepper line. Recent methods developed to perform GWAS on microbes will be used to detect viral single-nucleotide polymorphisms responsible for quantitative pathogenicity.

These experiments are in progress and should allow us to increase our knowledge of the genetic architecture of virus quantitative pathogenicity traits in interaction with plant resistance and tolerance genes, important knowledge to better understand virus evolution and emergence.