



**HAL**  
open science

## Unravelling the genetic architecture of virus quantitative pathogenicity

Lucie Tamisier, Thomas Oudin, Marion Szadkowski, Pierre Mustin, Judith  
Hirsch, Loup Rimbaud, Benoît Moury

► **To cite this version:**

Lucie Tamisier, Thomas Oudin, Marion Szadkowski, Pierre Mustin, Judith Hirsch, et al.. Unravelling the genetic architecture of virus quantitative pathogenicity. 19. Rencontres de virologie végétale (RVV 2023), Jan 2023, Aussois (FR), France. hal-04195732

**HAL Id: hal-04195732**

**<https://hal.inrae.fr/hal-04195732>**

Submitted on 4 Sep 2023

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## Unravelling the genetic architecture of virus quantitative pathogenicity

**Lucie Tamisier**, Thomas Oudin, Marion Szadkowski, Pierre Mustin, Judith Hirsch, Loup Rimbaud, Benoit Moury

LT, TO, MS, PM, JH, LR, BM : INRAE, Pathologie Végétale, F-84140 Montfavet, France; LT : INRAE, GAFL, 84143 Montfavet, France

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.