

# Adaptation of plant viruses to quantitative resistances

Elsa Rousseau<sup>1,2,3</sup>, Frédéric Fabre<sup>4</sup>, Ludovic Mailleret<sup>1,2</sup>, Alain Palloix<sup>5</sup>, Benoît Moury<sup>3</sup>, Frédéric Gognard<sup>1</sup>

<sup>1</sup> INRIA, Biocore Team, F-06902 Sophia Antipolis, France, <sup>2</sup> INRA, UMR 1355 ISA, 400 route des Chappes, BP 167, F-06903 Sophia Antipolis, France, <sup>3</sup> INRA, UR407 Unité de Pathologie Végétale, F-84140 Montfavet, France, <sup>4</sup> INRA, UMR 1065 Unité Santé et Agroécologie du Vignoble, BP 81, 33883 Villenave d'Ornon cedex, <sup>5</sup> INRA, UR1052 Unité de Génétique et Amélioration des Fruits et Légumes, F-84140 Montfavet, France

The deployment of virus-resistant crops often leads to the emergence of resistance-breaking (RB) pathogens that suppress the yield benefit provided by the resistance [1]. Although breakdowns are well known for qualitative resistances conferring total resistance to the virus, they are still poorly understood for quantitative resistances conferring partial resistance. Furthermore, it has been proved for several pathosystems that combining qualitative and quantitative resistances can increase the durability of the qualitative resistance [2, 3]. Two mechanisms can explain this result : either (i) an increase of genetic drift in the virus population, or (ii) a decrease of the selection advantage of the RB mutant. The purpose of the ongoing work presented here is to disentangle the role of these two mechanisms on the durability of plant qualitative resistances to viruses.

To investigate this, we concentrated on a pepper / *Potato virus Y* (PVY) pathosystem on which we report consistent variability in bottlenecks undergone by viral populations at inoculation and in viral accumulation, both determined by the host genotype. We follow by high-throughput sequencing the within-host demo-genetic dynamics of several virus variants in contrasted plant genotypes, carrying a qualitative resistance and different combinations of quantitative resistances. The respective effects of genetic drift and selection are evaluated by fitting models to these data [4]. We further aim at predicting the potential of combining qualitative and quantitative plant resistances to achieve sustainable plant resistance management at the epidemic scale.

## References

- [1] F. Fabre, E. Rousseau, L. Mailleret, and B. Moury. Durable strategies to deploy plant resistance in agricultural landscapes. *New Phytologist*, 193:1064–1075, 2012.
- [2] A. Palloix, V. Ayme, and B. Moury. Durability of plant major resistance genes to pathogens depends on the genetic background, experimental evidence and consequences for breeding strategies. *New Phytol.*, 183:190–199, 2009.
- [3] J. Quenouille, J. Montarry, A. Palloix, and B. Moury. Farther, slower, stronger: how the plant genetic background protects a major resistance gene from breakdown. *Molecular Plant Pathology*, 14:109–118, 2013.
- [4] F. Fabre, J. Montarry, J. Coville, R. Senoussi, V. Simon, and B. Moury. Modelling the evolutionary dynamics of viruses within their hosts : a case study using high-throughput sequencing. *PLoS Pathogens*, 8:1–9, 2012.

**Keywords :** quantitative resistance, genetic drift, viral evolution, durable resistance, landscape epidemiology.



Rechercher

ok

[Le CNRS](#)[Annuaire](#)[Mots-Clefs CNRS](#)[Autres sites](#)**Conférences Jacques Monod**

Centre national de la recherche scientifique

## Conférences Jacques Monod

[Appels d'offres](#)[Programme des  
conférences](#)[Présentation des  
conférences](#)[Charte des conférences](#)[Bilans des conférences](#)[Call for proposals](#)[Program](#)[Organization](#)[Conferences specifications](#)[Progress reports](#)

## Archives

## Paiement en ligne/On line payment

[Home](#) > [2014 Conference series](#) > [From emerging to pandemic viruses: interplay between host ecology and viral evolution](#)

## From emerging to pandemic viruses: interplay between host ecology and viral evolution

[French version](#) ►

**Roscoff (Brittany), France, April 2-6, 2014**

**Deadline for application: February 25, 2014**

Chairperson: **Roland R. REGOES**

ETH Zentrum, CHN H76.2, Universitaetsstr. 16, CH-8092 Zurich, Switzerland

Phone: +41 44 632 6935 - Fax +41 44 632 1271

Email: [roland.regoes@env.ethz.ch](mailto:roland.regoes@env.ethz.ch)

Vice-chairperson: **Samuel ALIZON**

Laboratoire MIVEGEC, CNRS UMR 5290, IRD, 911 Avenue Agropolis, BP 64501, 34394 Montpellier Cedex 5, France

Phone: +33 (0) 4 67 41 64 36 – Fax: +33 (0) 4 67 41 63 30

Email : [samuel.alizon@cnrs.fr](mailto:samuel.alizon@cnrs.fr)

Emerging viruses are recognized to be a threat not only to human health but also to activities, such as crop or cattle farming, and even to endangered species. This conference will study virus evolution and emergence through an original perspective by focusing on where viruses thrive. A first series of lectures will present virus outbreaks in the wild, ranging from "classical" topics (ebola in humans) to more unusual viruses (viruses infecting Archae or viruses infecting... viruses). A second series of lectures will present experimental results on outbreaks, with a particular focus on bacteriophages, which are particularly amenable to experimental evolution approaches. Finally, the third series of lectures will focus on deciphering the dynamical processes that can lead to outbreaks of new viruses. Overall, this conference stands out as one of the few that gathers researchers, who use different approaches (molecular biology, experimental evolution, mathematical modeling) and work on viruses infecting a wide variety of hosts (animals, plants, bacteria, Archae, viruses) but who are all interested in virus emergence.