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▶ **To cite this version:**

Elsa Rousseau, Jérôme Coville, Frédéric Fabre, Ludovic Mailleret, Alain Palloix, et al.. Protection of the durability of major resistance genes to plant viruses through quantitative resistance, a modeling approach. ECMTB14 - 9. European Conference on Mathematical and Theoretical Biology, Jun 2014, Goteborg, Sweden. hal-02739537

HAL Id: hal-02739537
https://hal.inrae.fr/hal-02739537

Submitted on 2 Jun 2020

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Protection of the durability of major resistance genes to plant viruses through quantitative resistance, a modeling approach.

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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 plant genes conferring total, *i.e.* qualitative resistance to the virus, they are still poorly understood for plant genetic factors conferring partial, *i.e.* quantitative 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. Here, we aim at disentangling the role of these two mechanisms on the durability of plant qualitative resistances to viruses.

To investigate this, we follow by high-throughput sequencing the within-host demo-genetic dynamics of several *Potato virus Y* (PVY) variants in contrasted pepper plant genotypes, carrying a qualitative resistance and different combinations of quantitative resistances. PVY variants carry distinct mutations, each mutation conferring weak to strong adaptation to the qualitative resistance. We collect the within-host virus variants frequencies and the relative virus population size at different time points. The respective effects of genetic drift and selection are evaluated by fitting Lotka-Volterra population dynamics models to these data [4]. We estimate the fitness of the different virus variants through the evolution of the mean variants frequencies and of population size, while we evaluate the strength of genetic drift through between-host variances in variants frequencies at each time point. With this modeling approach, we will determine the mode of action by which quantitative resistance increases the durability of qualitative resistance, and provide criteria to screen host genotypes with sustainable pathogen resistance.

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Keywords : quantitative resistance, genetic drift, selection advantage, viral population dynamics, durable resistance.

ECMTB

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