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Impact of selection, genetic drift and viral accumulation on the evolution of a plant RNA virus

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Genetic control is an efficient way to fight against crop disease, but this method is limited by the pathogen ability to evolve and break down the resistance. In the pepper-*Potato virus Y* (PVY) pathosystem, studies have demonstrated that the plant genetic background can increase the durability of a major resistance gene (Palloix et al., 2009), especially by constraining pathogen evolution (Quenouille et al., 2013). We conducted an experimental evolution to (i) measure the pathogen ability to adapt to plants combining a major resistance gene and different kinds of genetic backgrounds and (ii) identify the role of the evolutionary forces imposed on the virus population by the different genetic backgrounds.

We used six doubled-haploid (DH) lines of *Capsicum annuum* carrying the PVY resistance allele pvr23 and differing in their genetic background. All these lines were selected for their contrasted effects on viral accumulation, and on the intensities of selection and genetic drift imposed to the viral population. Three variants of PVY isolate SON41p showing different levels of adaptation to the DH lines were chosen. Each variant carried one amino acid substitution in the VPg, named 101G, 115K or 119N, allowing them to overcome the pvr23 resistance. We performed an experimental evolution by passaging serially the PVY variants on the six DH lines. The VPg gene of the viral lineages was sequenced at each evolutionary cycle and their final level of adaptation and aggressiveness was assessed.

We found that different evolutionary processes occurred in the lineages, resulting in fitness gains, extinctions of the virus population or no evidence of adaptation. The fitness gains were always observed in lineages showing at least one amino acid mutation in the VPg. Genetic drift had a significant impact on virus evolution, since all the lineages that evolved in plants inducing a strong genetic drift did not adapt or became extinct.

Using experimental evolution, we demonstrated that plant genetic backgrounds inducing strong genetic drift reduced or prevented the virus adaption to the major resistance gene.

Références :

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[2] Quenouille, J., Montarry, J., Palloix, A., and Moury, B. (2013). Farther, slower, stronger: how the plant genetic background protects a major resistance gene from breakdown: Mechanisms of polygenic resistance durability. *Molecular Plant Pathology* 14, 109–118.



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