

## Within-plant genetic drift to control virus adaptation

Tamisier, L. (1,2), Nemouchi, G. (1), Szadkowski, M. (1), Girardot, G. (2), Fabre, F. (3), Palloix, A. (1), Moury, B. (2).

(1) GAFL, INRA, 84140 Montfavet, France

(2) Pathologie Végétale, INRA, 84140 Montfavet, France

(3) UMR 1065 Santé et Agroécologie du Vignoble, INRA, Villenave d'Ornon, France

Managing adaptation of pathogenic organisms to genetically-resistant crop plants is a major challenge in agriculture. Plant breeders usually choose the plant resistance genes according to their immediate efficiency and spectrum of action against pathogens. To promote resistance durability, it would be also desirable to choose them according to their effects on pathogen evolution. In this perspective, one standing question is: which pathogen evolutionary trait (or combination of traits) should be targeted by plant resistance genes in order to minimize pathogen adaptation?

We explored this question on the pepper (*Capsicum annuum*; family Solanaceae) – *Potato virus Y* (PVY; genus *Potyvirus*, family Potyviridae) system using an experimental evolution approach. We chose six pepper genotypes possessing the same major-effect resistance gene but carrying different genetic backgrounds. At the individual plant level, these genotypes exert contrasted effects on PVY initial fitness (measured as PVY load within the plant at the beginning of experimental evolution) and on selection and genetic drift effects in PVY populations.

Seven serial passages of 64 independent PVY populations were performed in the different plant genotypes (one passage per month). The PVY evolutionary trajectories were highly contrasted and dependent on the pepper genotype. Of the 64 PVY lineages, nine went to extinction, 18 showed a significant fitness gain (within-plant load) in their respective pepper genotype compared to the initial PVY, one showed a significant fitness decrease while the others did not show any significant fitness change. In contrast, we observed little virulence changes. As virus clones were used at the beginning of the experiment, fitness changes were the result of de novo mutations appeared during the experiment. Indeed, almost all PVY fitness gains were due to the fixation of one or two amino acid substitutions in PVY VPg, the protein linked to the viral RNA, which is a ligand of the product of the plant major-effect resistance gene.

Using linear regressions, we analysed the effects of PVY initial fitness ( $F_i$ ), effective population size ( $N_e$ ) and selection coefficient ( $S$ ) during plant infection, and their pairwise interactions on the change of PVY fitness during experimental evolution. The two significant factors were  $N_e$  and the interaction  $N_e \times F_i$ , which explained 36% of the variance of PVY fitness changes. No significant effect of  $S$  was detectable. High and significant PVY fitness gains were observed mostly when  $N_e$  was high and  $F_i$  was low, which could be explained by low genetic drift and more opportunities for large-effect beneficial mutations for PVY. Extinctions of PVY lineages were observed only when  $N_e$  and  $F_i$  were low, which could be explained by the combination of high genetic drift (and subsequent Muller's ratchet processes) and low probability of de novo mutations due to low  $F_i$ .

Our study shows that it is possible for plant breeders to combine a high resistance efficiency (low  $F_i$ ) and high resistance durability (no virus adaptation), even with strong selection exerted on virus populations by a major-effect resistance gene, by using plant genotypes where viruses have a low  $N_e$  during infection.