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**Modelling the evolutionary dynamics of viruses within their hosts: a case study using  
*Potato virus Y* and high-throughput sequencing.**

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**Abstract**

Uncovering how natural selection and genetic drift shape the evolutionary dynamics of viral populations within their hosts can pave the way to a better understand of virus emergence. Mathematical models play a central role in these studies and are also needed to predict the likelihood of future emergence. In this work, we analysed the within-host population dynamics of 4 *Potato virus Y* (PVY) variants with different pathogenicity properties using high-throughput sequencing. Data were then confronted with several dynamical models to infer simultaneously the competitiveness of the virus variants and the intensity of genetic drift experienced by viruses during the colonization of host plants.

Regarding selection, results indicate that the frequencies of the 4 PVY variants are appropriately described using Lotka-Volterra models where the competition coefficients,  $\beta_{ij}$ , that account for the competition exerted by variant  $j$  on variant  $i$  are equal to the ratio of their individual fitness,  $r_i/r_j$ . Regarding genetic drift, results indicates that the between host variances of the frequencies of the variants are appropriately described using Dirichlet-multinomial distributions whose scale parameters vary with time and mean parameters are the solutions the Lotka-Volterra models. These scale parameters, closely related to the fixation index  $F_{ST}$ , revealed that the genetic differentiation of virus populations among plants increased from 0 to 10 days after inoculation (dai) and then decreased until 35 dai. This suggests that the genetic drift experienced by viruses during plant colonization varies according to the host growth or phenology. Overall, this study evidences that simple mathematical models can accurately describe both the selection and genetic drift processes shaping the evolutionary dynamics of viruses within their hosts.