



Joint estimation of effective population sizes and selection coefficients from time-sampled data: a case study on virus populations exposed to plant resistance

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Joint estimation of effective population sizes and selection coefficients from time-sampled data: a case study on virus populations exposed to plant resistance.

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Recent results indicate that quantitative trait loci (QTL) of the host genetic background modulate the durability of major resistance genes to plant viruses (Quenouille *et al.* 2013, 2014). This is particularly interesting for plant breeders. Two biological mechanisms can explain such observations: (i) QTLs increase the genetic drift acting on virus population and (ii) QTLs decrease the selective advantage of the adapted virus variants. Up to date, if several methods have been proposed to estimate the intensity of drift when neutral genetic markers are available, few allow to estimate jointly effective population sizes (N_e), a measure of the intensity of genetic drift, and selection coefficients (s) when no neutral markers are available.

In this study, taking advantage of time-sampled data, we propose a modeling approach to jointly estimate the N_e of a viral population and the selection coefficients of several loci involved in pathogenicity properties. Experiments were set up to follow the within-host dynamics of 5 *Potato virus Y* (PVY) variants in 15 pepper plant genotypes carrying the major resistance gene *pvr2³* and several QTL combinations. The 5 PVY variants carry distinct mutations, each one conferring weak to strong adaptation to *pvr2³*. We determined the within-host virus variants frequencies at 6 time points, from 6 to 34 days after inoculation, using high-throughput sequencing. Estimates of N_e and of the coefficients s of each variant were inferred for each pepper genotype by fitting mechanistic-statistical models relying on Lotka-Volterra equations and Dirichlet-multinomial distributions (Fabre *et al.*, 2012). Results indicated that N_e was varying from 40 to 510 (mean 229) depending on pepper genotypes. Whether such plant genetic factors increasing the genetic drift acting on virus populations can be used to slow down virus adaptation at larger scales (field, landscape) still remains to be investigated. More generally, the proposed methodology is of wide interest to disentangle the relative role of genetic drift and selection during within-host virus evolution.

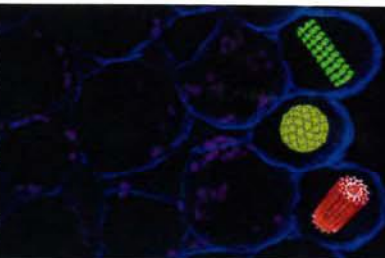
References: Fabre *et al.* 2012, PloS Path., 8(4), e1002654 ; Quenouille *et al.* 2013, Mol. Plant

Pathol, 14, 109-118 ; Quenouille *et al.* 2014, Heredity, 112, 579-587.



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