



HAL
open science

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

Elsa Rousseau, Frédéric Fabre, Jérôme Coville, Ludovic Mailleret, Alain Palloix, Rachid R. Senoussi, Frédéric Grogard, Benoît Moury

► To cite this version:

Elsa Rousseau, Frédéric Fabre, Jérôme Coville, Ludovic Mailleret, Alain Palloix, et al.. Joint estimation of effective population sizes and selection coefficients from time-sampled data: a case study on virus populations exposed to plant resistance. 15. Rencontres de Virologie Végétale (RVV), Jan 2015, Aussois, France. hal-02738942

HAL Id: hal-02738942

<https://hal.inrae.fr/hal-02738942>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Oral presentation at Rencontres de Virologie Végétale (RVV), Aussois, FRA (2015-01-18-22).

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

Elsa Rousseau^{1,2,3}, Frédéric Fabre^{4*}, Jérôme Coville⁵, Ludovic Mailleret^{1,2}, Alain Palloix⁶, Rachid Senoussi⁵, Frédéric Grogard¹, Benoît Moury³

¹ INRIA, Biocore Team, F-06902 Sophia Antipolis, France, ² INRA, UMR 1355 ISA, 400 route des Chappes, BP 167, F-06903 Sophia Antipolis, France, ³ INRA, UR407 Unité de Pathologie Végétale, F-84140 Montfavet, France, ⁴ INRA, UMR 1065 Unité Santé et Agroécologie du Vignoble, BP 81, 33883 Villenave d'Ornon cedex, ⁵ INRA, Unité BioSp, Domaine Saint Paul, Site Agroparc, 84914 Avignon cedex 9, ⁶ INRA, UR1052 Unité de Génétique et Amélioration des Fruits et Légumes, F-84140 Montfavet, France, *frederic.fabre@bordeaux.inra.fr

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.

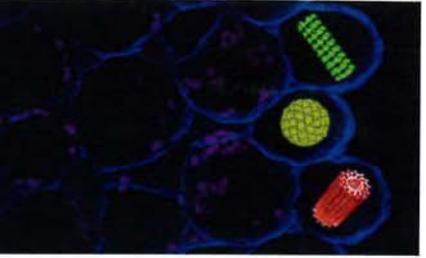
References: Fabre *et al.* 2012, PloS Path., 8(4), e1002654 ; Quenouille *et al.* 2013, Mol. Plant

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



15^{èmes} Rencontres de Virologie Végétale

18 - 22 JANVIER 2015 • AUSSOIS - FRANCE



Programme et Résumés