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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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Plant Virus Ecology Network

Workshop 4

Montpellier May 30/31- June 1 2011

PLANT VIRUS ECOLOGY NETWORK

WORKSHOP 4

MONTPELLIER

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

3

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9

10 **Abstract**

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

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