32-Combining experimental assays with epidemiological surveys to assess indicators of *Plum pox virus* epidemicity

Borron S.[1], Dallot S.[1], Bonnot F.[2], Jevremovic D.[3], Pichaut JP.[1], Jacquot E., Labonne G.[1]

[1] INRA, UMR 385 BGPI, Campus International de Baillarguet, Cirad TA A-54/K, F-34398 Montpellier cedex 5, France
[2] CIRAD, UMR BGPI, F-34398 Montpellier cedex 5, France
[3] Fruit Research Institute, Kralja Petra I 9, Čačak, Serbia

dallot@supagro.inra.fr
sonia.borron@supagro.inra.fr

The huge increase in sequence data those last decades has allowed defining better demarcation criteria for viral taxonomic assignments. For the epidemiologists, such demarcation based on molecular properties, especially at the strain level, is particularly meaningful if one can link the different strains to specific phenotypes (host range, pathogenicity,…) and can thus identify specific epidemic risks for a given host or for a given agro-ecological context.

Plum pox virus (PPV, genus *Potyvirus*, family *Potyviridae*) is responsible for the sharka disease, the most serious disease of stone fruit trees (*Prunus* species). In the framework of a collaborative European research program, an important effort has been made to increase the knowledge of PPV genetic diversity (www.sharco.eu). Based on molecular criteria (genetic distances and successful recombinant genomes), eight different strains have been distinguished but very little is known about their specific biological and epidemiological properties. Such a situation is due to different reasons: (i) the quarantine pest status of PPV does not allow experiments unless carried out under a strict confinement; (ii) the perennial nature of the *Prunus* hosts makes the experiments generally long and complicated; and (iii) the epidemiological behaviour of a given strain (or even isolate) can be influenced by specific agro-ecological conditions occurring at a given location.

In this study, we combined biological experiments with epidemiological surveys to gain a better knowledge on PPV epidemic properties. A first approach was thus developed for the three most prevalent PPV strains (M, D and Rec) in Europe, which have different geographical distributions. The experimental assays were designed to allow measuring indicators of the key steps of the infection cycle on three *Prunus* species (apricot, peach and plum): (i) ability for a given strain to infect the host after aphid-mediated (using a clone of *Myzus persicae*) inoculation, (ii) dynamic of infection in each *Prunus* host, and (iii) efficiency of the infected *Prunus* as virus sources (acquisition-transmission assays carried out with *M. persicae* as vector). In parallel to these experimental assays, surveys have been carried out in Serbia in order to assess (i) the relative prevalence of these three PPV strains known to spread in this country, and (ii) their *Prunus* host preference.

These two approaches bring different but complementary information. The experimental assays did not evidence strict host specificity (pathotype) but rather several cumulative advantages (shorter latency in apricot, better generalization in peach, higher overall aphid transmission rates) that should confer a higher epidemicity to the PPV-M strain. The results from surveys evidenced a strong host specificity (PPV-M on peach), frequent co-infections and independence between infections by the three PPV strains in plum.

Keywords: epidemic properties, experimental assays, epidemiological surveys, sharka