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## EXPLOITING VIRAL GENETIC DIVERSITY TO UNCOVER SHARKA DISPERSAL AT REGIONAL AND LOCAL SCALES

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### BACKGROUND and OBJECTIVES

A good understanding of disease spatiotemporal dynamics is essential for the definition of optimal strategies of surveillance and management. Plant RNA viruses are fast-evolving pathogens for which molecular evolution and dispersal occur at a similar time scale. Thus, spatial epidemiological processes leave measurable imprints on viral genomes that can be used to gain insights into, for example, the origin and dissemination pathways of emerging viruses at global or regional scales (Lefeuvre et al., 2010). More locally, viral genetic polymorphism combined with epidemiological data can help differentiating introduction events and reconstructing transmission chains within a given outbreak (Morelli et al., 2012; Ypma et al., 2012).

The aim of this study is to improve our knowledge of the spatial dynamics of sharka, one of the most devastating viral diseases of stone fruit trees. Its causal agent, *Plum pox virus* (PPV, genus *Potyvirus*), is disseminated by the plantation of contaminated material and by many aphid species in a non-persistent manner. We investigated if PPV genetic diversity could be used (i) to reconstruct dissemination routes at a regional scale and (ii) to assess the relative influence of introduction events and secondary aphid dispersal in a local outbreak.

### MATERIAL and METHODS

This study focused on a peach production region of southern France where epidemics related to PPV strain M have been documented since the early 1990's. A recently discovered outbreak encompassing 215 susceptible peach orchards was intensively surveyed and 843 geo-referenced PPV isolates were genotyped by CE-SSCP and/or partially sequenced. We obtained whole genome sequences for 16 isolates representative of the PPV diversity in this area, as well as for 43 isolates collected over 17 years in 10 other PPV outbreaks distant from 1.5 to 40 km. Phylogeographic analyses were carried out under a Bayesian framework (BEAST package).

### RESULTS and CONCLUSIONS

Our data set displayed a strong temporal signal allowing the reconstruction of the evolutionary history and dispersal of PPV in the study region. Distinct clades were found spreading in northern and southern areas separated by a series of hills that may have prevented further PPV dispersal by aphids. In both areas, gene flow was evidenced between nearby outbreaks. The PPV diversity spreading in the intensively surveyed outbreak was found to stem from multiple introductions events from nearby inoculum sources as well as from more distant ones, suggesting that both aphid dispersal and plantation of contaminated material may have contributed to the epidemic. The next step will be to formally reconstruct the transmission chains and to get direct estimates of the dispersal function within and between orchards.

### REFERENCES

- Lefeuvre, P., et al., 2010. The spread of Tomato yellow leaf curl virus from the Middle East to the world. *PLoS Pathogens* 6(10): e1001164.
- Morelli, M.J. et al., 2012. A Bayesian inference framework to reconstruct transmission trees using epidemiological and genetic data. *PLoS Computational Biology* 8: e1002768.
- Ypma R.J.F. et al., 2012. Unravelling transmission trees of infectious diseases by combining genetic and epidemiological data. *Proceedings of the Royal Society B* 279: 444–450.