# Towards an understanding of cross-protection mechanisms against grapevine fanleaf virus

## Abstract

Cross-protection is a biocontrol method used to protect plants (both annual and perennial species) from damage caused by viral diseases. It has been successfully used to control pepino mosaic virus on tomatoes, zucchini yellow mosaic virus on squash, papaya ringspot virus on papaya and citrus tristeza virus on citrus in several countries, among others. Promising results have also been obtained against grapevine fanleaf virus. This strategy, which consists in primary infecting a plant with an attenuated viral variant (cross-protecting virus) to prevent subsequent infection by severe related ones (challenging virus), was first proposed in 1929 by McKinney.

Although cross-protection was demonstrated almost a century ago, the underlying mechanisms remain poorly understood. In particular, although the genetic relatedness between cross-protecting and challenging variants has been highlighted in numerous articles, the degree of sequence identity required for cross-protection to occur is still unknown. This lack of data has led to a long, tedious and sometimes unsuccessful empirical search for variants that protect against certain viral strains. The first objective of this project is to determine the degree of sequence identity required between cross-protecting and challenging variant(s) for the establishment of cross-protection against grapevine fanleaf virus (GFLV). GFLV is the main agent responsible for fanleaf disease, a disease for which no solution can be deployed in the medium term. This question is of crucial importance, as it will enable us to identify the protection range conferred by a cross-protecting variant, information that is necessary to establish appropriate cross-protection. In addition to genetic relatedness, two other parameters have been shown to impact cross-protection success against other viral species, and will therefore be examined: (i) the relative fitness of the cross-protecting and challenging variants (defined here as their relative ability to infect and colonize the host) and (ii) the time interval between their inoculations.

These objectives represent key steps (i) in the development of a project to study the mechanisms underlying cross-protection, (ii) in the implementation of cross-protection trials in vineyards and, more generally, (iii) in the development of decision making tools for the identification of cross-protecting variants.