

## TOWARDS UNDERSTANDING VIRAL CROSS-PROTECTION MECHANISMS ANR JCJC ToProtectMe 2025-2027

### Abstract

Coinfection by microorganisms has been documented in almost all studied plant hosts. Yet, knowledge of their interactions remains rather limited, made more complex by the multiple microorganisms often infecting a single host. Of particular interest are the antagonistic interactions between genetically related viruses. The ability of a primary virus to block the subsequent infection of a related one, a phenomenon known as cross-protection, has led to its implementation as a biocontrol method. For instance, infecting a plant with a mild viral strain can protect the host from the damage caused by more severe related viral strains. This specific phenomenon has been described for several viruses whatever their genetic content, genomic architecture, tissue tropism and mode of transmission, as well as plant host (perennial or annual hosts). However, as for most virus-virus interactions, the mechanism(s) underlying cross-protection remain(s) unknown. This lack of knowledge hampers a broader deployment of this method that could reduce the negative economic impact of several pathogenic viruses.

Grapevine fanleaf virus (GFLV) causes the most severe viral disease of grapevine worldwide absent effective control methods in the vineyard. By using two herbaceous model hosts, *Nicotiana benthamiana* and *Arabidopsis thaliana*, we will examine cross-protection against GFLV while characterizing the intra-host spatial distribution and viral load of both primary and challenging viruses according to the time interval between their inoculations and their biological features (genetic relatedness and relative fitness). The involvement of both plant and viral factors in this phenomenon will also be examined. This research proposal is designed to decipher the mechanism(s) underlying cross-protection against GFLV.