



Different approaches to identify genetic traits responsible for susceptibility and resistance to *Flavescence dorée* in grapevine

Flavescence dorée
Vitis vinifera
Susceptibility
Resistance
Genomics
Transcriptomics

AIMS:

In this PhD thesis different approaches were used with the general aim to better understand the grapevine mechanisms underpinning resistance and susceptibility to Flavescence dorée (FD) and to pave the way to the identification of genetic and genomic traits associated to FD resistance.

APPLICATIONS:

Results obtained in the present thesis, and those that will be achieved in the future, will be useful for new breeding programs and clonal selection. Moreover, the knowledge of the molecular and metabolic mechanisms adopted by scarcely susceptible varieties and clones could help in the development, for example, of biostimulants capable to induce such defenses even in the most susceptible plants.

RESULTS:

The study performed in a highly FD-infected vineyard showed the ability of Tocai friulano (a scarcely susceptible variety) to block and avoid the spread of the symptoms and the pathogen into the whole canopy.

The second PhD work concerns the study of a population obtained by a cross between two cultivars showing different susceptibility to FD. Genotyping by sequencing analysis was performed and the resulting SNP dataset was used both to construct a linkage map and to identify polymorphisms putatively involved in gene regulation. Parallely, the observation and the analysis of different FD symptoms in infected plants belonging to the progeny led to the identification of valuable phenotypic traits that could be used during phenotype evaluation aimed to QTL identifications.

Finally, the existence of differences in FD susceptibility among three Chardonnay clones was used to find out genetic variants distinguishing the less susceptible clone from the other two.

