



Exploring diversity of grapevine responses to Flavescence dorée infection

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Abstract

Flavescence dorée, a serious threat to grapevine cultivation in several European Countries, is caused by phytoplasmas in the 16Sr-V ribosomal group, classified as quarantine organisms in the EU and transmitted mainly by the insect vector *Scaphoideus titanus*. The disease is controlled only by indirect and preventive measures, with important economic and environmental concerns. Genetic resources from the great variety of *Vitis vinifera* germplasm together with application of new genomic techniques could be applied to produce resistant/tolerant plants, once the genetic bases of susceptibility are elucidated. In a current Italian project (BIORES*) we are evaluating different international and local grapevine cvs. as well as microvine plants for their response to FD transmission and multiplication in controlled conditions. Infective vectors were caged onto potted plants of 8 varieties for 5 weeks. Insect survival and infectivity were monitored and plant infections were quantitatively tested 11 weeks post inoculation.

In parallel, previous data and materials generated by the Project Consortium are being mined to select putative resistance- or susceptibility-related genes, to be further validated in functional analyses, either on already produced transgenic plants or in future genome editing experiments to introduce precise targeted mutations in candidate genes of the highly susceptible cv. Chardonnay, with the final goal of reducing FD susceptibility without compromising other productive traits.

*Funded by the European Union – NextGenerationEU.

Keywords: Phytoplasma, Germplasm, Breeding, Genome editing, Sustainable viticulture.