## Recent findings on Flavescence dorée in Franciacorta (North Italy): prevalence of associated phytoplasma genotypes in symptomatic grapevines and in additional plant and insect hosts within and around vineyards

Fabio Quaglino<sup>1</sup>, Enea Guerrieri<sup>2</sup>, Sara Torcoli<sup>3</sup>, Camilla Barbieri<sup>1</sup>, Flavio Serina<sup>3</sup>, Piero Attilio Bianco<sup>1</sup>, Nicola Mori<sup>2</sup>

<sup>1</sup>University of Milan, Department of Agricultural and Environmental Sciences – Production, Landscape, Agroenergy, Milan, Italy <sup>2</sup>University of Verona, Department of Biotechnology, Verona, Italy

<sup>2</sup>University of Verona, Department of Biotechnology, Verona, Italy

<sup>3</sup>Franciacorta Consortium, Brescia, Italy

This study aimed to survey the spread and incidence of Flavescence dorée (FD) in Franciacorta vineyards (North Italy) and study the diffusion of the associated phytoplasmas (FDp) not only in symptomatic grapevines but also in the vineyard agroecosystem. The activities were carried out in 2021 and 2022 in 20 representative vineyards. Average grapevine yellows (GY) incidence in vineyards was around 6% in both 2021 and 2022. Molecular analyses, conducted on 1250 symptomatic vines, identified 16SrV phytoplasmas in 31% (2021) and 34% (2022) of the vines, localized in 14 out of 20 vineyards. In these vineyards, 17 (2021) and 37 (2022) species of known or potential FDp vectors were captured and grouped into 1600 pools for molecular analysis. 16SrV phytoplasmas were identified in 22% (2021) and 6% (2022) of the insect pools. Seven species (S. titanus, Allygidius spp., Dictyophara europaea, Neoaliturus fenestratus, Orientus ishidae, Phogotettix cyclops, *Psammotettix* spp.) were found to be infected both in 2021 and 2022. Moreover, molecular analyses revealed the presence of 16SrV phytoplasmas in 25 out of 45 wild plant species collected around vineyards. Sequence analyses of map gene identified (i) FDp genotype M54 in symptomatic grapevines (78% and 100% of 16SrV phytoplasma-infected grapevines in 2021 and 2022, respectively), in S. titanus, N. fenestratus, Psammotettix spp. (2021 and 2022), and *D. europaea* (2021), and in seven wild plant species; (ii) FDp genotype M51 in symptomatic grapevines (22% of 16SrV phytoplasma-infected grapevines in 2021), in D. europaea, N. fenestratus, and P. cyclops (2021 and 2022), and in 22 wild plant species; (iii) FDp genotypes M12, M50, and M122 in other insects. So far, FDp genotype M54, prevalent in northern Italy, is believed to be strictly associated with the closed "grapevine - S. titanus" pathosystem, while the spread of FDp genotype M51 includes additional host plants and vectors (D. europaea and O. ishidae). Obtained results reinforced recent evidence of an increasing FD epidemiological complexity, suggesting that also the prevalent FDp genotype M54, at least in the examined area, can be related to an opened pathosystem, involving additional plant hosts and insect vectors.

## Acknowledgements

This study was funded by Franciacorta Consortium