Proceedings of the LXV SIGA Annual Congress
Piacenza, 6/9 September, 2022
ISBN: **978-88-944843-3-5**

Oral Communication Abstract – 7.06

THE STUDY OF THREE GRAPEVINE CLONES TO UNCOVER THE GENETIC TRAITS RESPONSIBLE FOR THE LOW SUSCEPTIBILITY TO FLAVESCENCE DORéE

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Flavescence dorée, grapevine clones, genome sequencing, transcriptomic profiles

Flavescence dorée (FD) is one of the most destructive grapevine yellows diseases and a quarantine pest in the European Community. It is caused by phytoplasmas, which are transmitted in vineyard by the leafhopper *Scaphoideus titanus*. Inter and intraspecific differences in susceptibility to FD have already been observed among grapevine varieties and clones of the same variety. Grapevine varieties and clones completely resistant to FD have not been uncovered yet, however these differences suggest the presence of genetic traits in grapevine related to high or low susceptibility to FD.

Cultivated grapevines are clonally propagated and the genome of each cultivar is preserved, except for the accumulation of mutations over time that can generate distinguishable clones with several notable phenotypes. The differences between the genome of clones of the same variety are less than those between different varieties; thus, in order to highlight the genetic features responsible for the different phenotypes, the study of the genomes of clones with different susceptibility to FD can be a valid technique to achieve the goal.

The aim of this work is to find out the genetic traits responsible for the different susceptibility to FD among three Chardonnay clones, analyzing the diversity in their genomes and transcriptomic profiles. The clones were sequenced by accurate whole genome techniques, Hi-Fi reads sequencing on PacBio platform coupled with Illumina, and then the genomes were *de novo* assembled. Moreover, two of them were experimentally infected in field by

means of the insect vector and the transcriptomic profiles in the early stage of FD infection were analyzed. In particular, the clones were compared in absence of the disease and the vector, in presence of the healthy vector and with the FD infective vector.

The results obtained from the preliminary genome comparison showed higher similarity between the three clones than compared with the reference genome from variety Pinot noir, while the analysis to identify the genomic differences among clones are still in progress. The transcriptomic profiles showed interesting differences in some pathways expressed in presence of healthy vectors, while the clones shared a similar expression profile before being in contact with the vectors as well as after the challenge with the FD infective vectors. These findings might suggest the involvement of antibiosis mechanisms in the partial resistance of the specific Chardonnay clone to FD.

The results obtained, and those that will be achieved in future, are useful for new breeding programs and clonal selection. Grapevine plants more resistant to FD will permit to decrease the insecticides used to control the disease in vineyards. Moreover, the knowledge of the molecular and metabolic mechanisms involved in scarcely susceptible clones could pave the way for the development, for example, of biostimulants capable to induce such defenses even in the most susceptible plants.