



Conference Proceeding

Looking for the genetic traits underlying resistance to grapevine yellows

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Grapevine yellows (GY) are diseases that lead to very serious damage to the grapevine, ranging from yield reduction to plant death. They are associated with the presence of several phytoplasmas transmitted by different insect vectors. Nowadays, the only strategy to limit the spread of GY diseases is based on the removal of infected plants and insecticide treatments targeting the insect vectors. However, inter- and intra-specific differences in susceptibility to GY disease have already been observed among grapevine varieties, and this different behaviour suggests the presence of genetic traits associated with resistance in the grapevine germplasm. To strengthen more sustainable agriculture, the identification of these traits and the selection of the grapevine varieties showing partial resistance to GY is essential, therefore different approaches were developed to identify resistant traits. The first approach aims to

the identification of Quantitative Trait Loci (QTLs) in a segregant population generated by the crossing between Chardonnay and Tocai friulano, two varieties with very different susceptibility level. F1 individuals were initially analyzed with Genotyping by Sequencing (GBS) and the data obtained were then used to create a linkage map. At the same time, F1 individuals were planted in two experimental vineyards and for phenotyping. An additional approach to uncover the genetic differences involves three Chardonnay clones that showed a different susceptibility to GY. The clones were sequenced using the PacBio platform coupled with Illumina, and comparison of their genomes is ongoing. Moreover, two of them were experimentally infected in field using the insect vector, and the transcriptomic profiles in the initial phase of the GY infection showed interesting differences.