



DNA was extracted from F1 plants and a preliminary screening was performed to check the parental origin of the seedlings (e.g. discarding those derived from selfing) by SSR (Simple Sequence Repeats) analysis with ten molecular markers. Genotyping the selected plants is in progress by GBS (Genotyping By Sequencing) for subsequent SNPs calling. A genetic map will be produced from this data. Phenotypic and molecular information will be used to find QTLs associated with grapevine yellows resistance. Moreover, data integration with transcriptomic profiles obtained with RNAseq from low and very susceptible varieties, previously obtained (Bertazzon *et al.*, 2019) and full genome by Next Generation Sequencing (NGS) of approximately 20 grapevine varieties showing opposite behavior against the disease, will be the basis for the identification of the candidate genes associated to grapevine yellows resistance.



- Setting up of cages for insects in the single plants in the field (left), and detail of a cage (right). A cage containing 20 insect vectors was placed in every plant, in order to infect all the grapevine plants

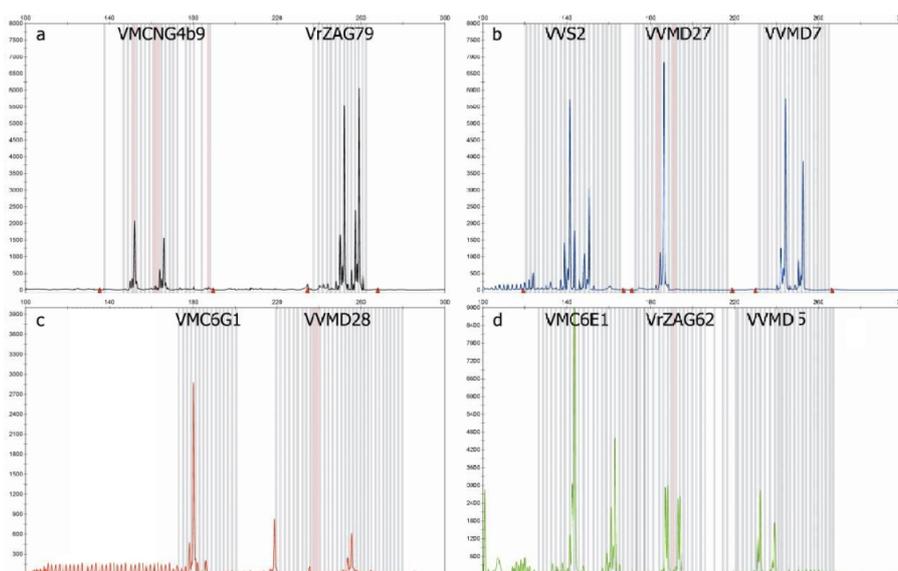
■ SCIENTIFIC DATA AND FIRST RESULTS

First results and perspectives

Obtainment of a sufficient number of progenies by breeding and their prosperous multiplication and plantation in the field was the first result. DNA was extracted from more than 300 genotypes, followed by screening with ten SSR markers to discriminate among crossed and self-crossed progeny. Results showed that approximately 20% of the progeny was self-crossed, thus these plants were discarded.

The nucleotide sequencing work started with DNA extraction from leaf samples of 208 plants, including the two parents "Tocai friulano" and "Chardonnay". After DNA extracts evaluation for quality and quantity, a total of 188 samples were sent to sequencing by GBS to obtain a high-density genetic map.

In 2019 a total of 140 plants were caged with infective insects. At the end of the work, the identification of genetic traits associated to resistance and susceptibility to grapevine yellows could be exploited to generate grapevine plants resistant to this disease and for increasing or eliciting the grapevine yellows resistance in plants.



- Genetic analyzer electrotraces. Example of 10 *loci* multiplex PCR molecular profile used to identify crossed or self-crossed progeny by SSR. The 10 primer pairs were labeled with NED(a), 6-FAM (b), PET (c), VIC (d) dyes. Grey stripes represent the home-made binset produced with reference varieties

KEY WORDS

Grapevine yellows, resistance, tolerance, “flavescence dorée”, “bois noir”, breeding, disease

FURTHER INFORMATION

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April, 2020



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 727459

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