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ABSTRACT BOOK

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P26. MULTI-OMIC APPROACH TO UNDERSTAND RESISTANCE IN GRAPEVINE AGAINST *PLASMOPARA VITICOLA*

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Grapevine (Vitis vinifera L.), a major fruit crop worldwide, is susceptible to many microbial infections. Downy mildew is one of the most severe disease caused by the obligate biotrophic oomycete Plasmopara viticola (Berk. et Curt.) Berl. et de Toni. The current strategy for grapevine disease control is based on the extensive and expensive use of pesticides with negative impact on the environment and human health. To reduce sprayings, V. vinifera cultivars were crossed in the past with resistant Vitis spp to select resistant hybrids. Given that plant resistance and plant-pathogen interactions are complex biological processes and are up to now poorly understood, a multi 'omic' approach is most suited for this kind of studies.

The aim of the work was to correlate differentially expressed genes with the metabolites which significantly differ between the infected and non infected leaf disks at different time points. Among metabolites at present some polyphenols and lipids seems to be involved in plant-pathogen interaction and alterations in their biosynthetic pathways may be responsible for resistance phenotype against Plasmopara viticola.

In this study we focused our work on the perturbation of different classes of metabolites in leaf disks of resistant variety 'Jasmine' induced by the infection with Plasmopara viticola pathogen after 0, 12, 24, 48 and 96 hours. In targeted metabolomics approaches phenolics and lipids were determined using a LC-MS/MS methods. In order to better understand the changes in lipid profile untargeted lipidomic approach was also applied.

For these analysis LC-MS was coupled to high resolution Exactive Orbitrap mass spectrometer (Thermo Fisher). HCD fragmentation was performed with three different energies 30, 60 and 100 eV. On the same set of samples the transcript profiling (RNAsequencing) was done using the Illumina Next Generation Sequencing (NGS) technology.

The results of this study will allow us to identify signaling metabolic pathways and provide new knowledge in plant-pathogen interaction.