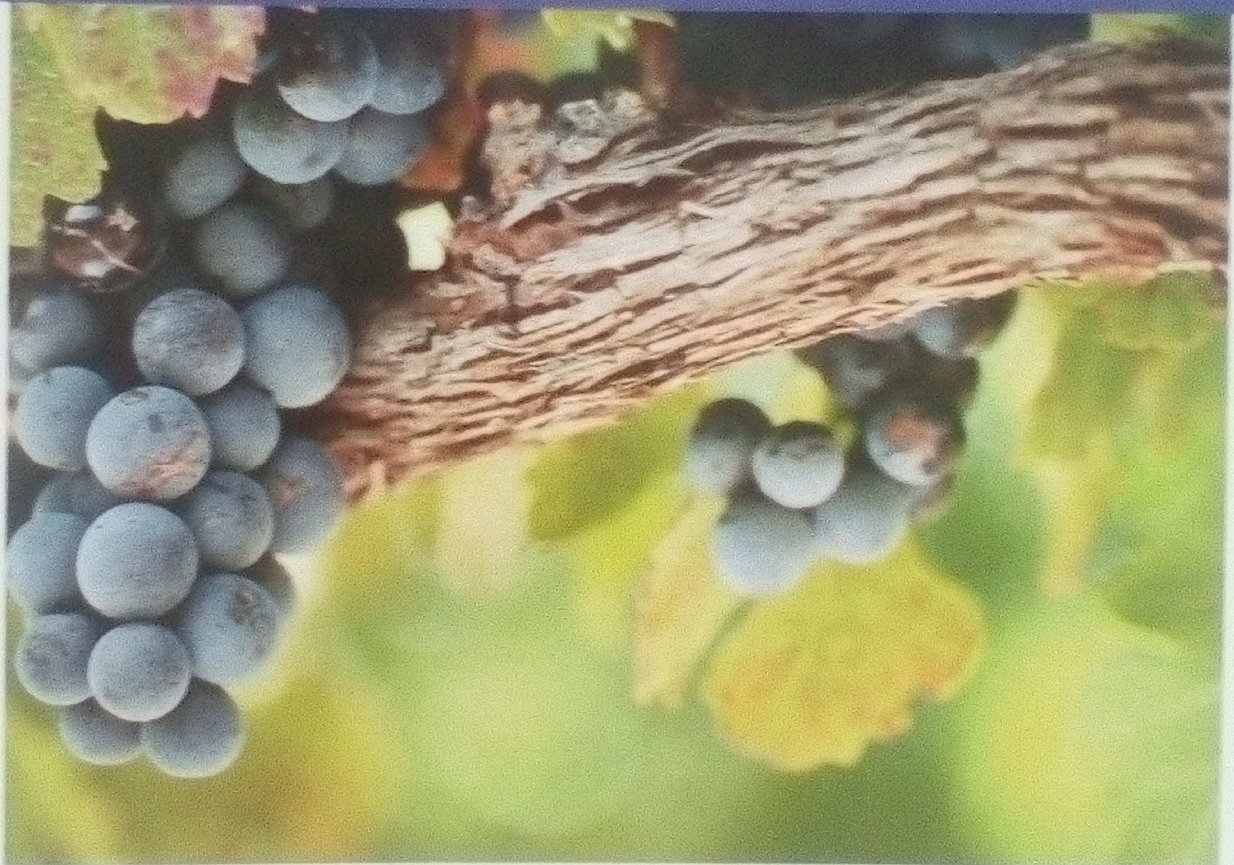


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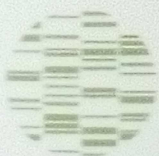
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## Metabolomic study to evaluate the resistance against *Plasmopara viticola*

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Downy mildew is a destructive disease of grapevine caused by the biotrophic oomycete *Plasmopara viticola*; it is responsible for extreme damages to vineyards in humid regions for the cultivated species *Vitis vinifera*. The introduction of resistant or tolerant varieties can be the solution to avoid or reduce the massive use of fungicides. Metabolomics can help in exploring the interaction between grapevine and *Plasmopara viticola* and in extending the current knowledge about the perturbations occurring in the plant system after biotic stresses. In our study, we evaluated the metabolic changes in 4 resistant or tolerant genotypes containing different sources of resistance (Bianca, Jasmine, BC4 and Solaris) and one susceptible genotype (Pinot noir). We investigated primary and secondary metabolism identifying and quantifying lipids (LC-MS/MS), phenols (LC-MS/MS), primary compounds (GC-MS), and semi-quantifying volatile compounds (GC-MS) at 0, 12, 48 and 96 h post infection. Jasmine and Bianca show the smallest number of altered metabolites (47 and 48 respectively), while Pinot noir has the greatest number of altered metabolites (82). BC4 and Solaris show less extreme behaviour with 56 and 63 altered metabolites respectively. Finally, we applied a network-based visualization approach to integrate the outcomes of different metabolomics assays and to explore the differences between the varieties.

**Keywords:** biotic stress, downy mildew, metabolomics, *Plasmopara viticola* resistance