Uncovering mildew resistance biomarkers in grapevine: an integrated omics approach

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State of the art

Grapevine (*Vitis vinifera* L.) is one of the most important and cultivated fruit plant in the world due to its food products mainly to the wine industry. The European Union is the world's leader in wine production, with almost half of the total vine-growing area. Portugal is the fifth wine producing country and the second with the highest collection of grapevine varieties [1].
The domesticated *V. vinifera* cultivars frequently used for wine production are highly susceptible to fungal diseases, which if not controlled, presents serious negative effects for the country's economy. Downy and Powdery mildews are the most destructive vineyard diseases, affecting all the green parts of the vine (leaves, shoots and bunches), causing yield reduction with significant production losses and financial consequences [2].
An alternative strategy to fungicide applications for disease prevention is the development of new grapevine varieties through breeding programs: combining the high degree of resistance of wild *Vitis* species (resistant to pathogens) with good berry quality for wine production of the domesticated *V. vinifera* (susceptible). Hence, to understand the innate resistance mechanism of *Vitis*, the metabolic characterization of grapevine leaves is of upmost importance, not only because plants contain a unique metabolome that change with the environment, development and upon fungal infections, but also to find resistance-associated biomarkers.

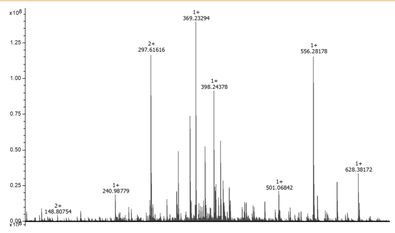
Major goal

Identification of grapevine metabolic and protein biomarkers associated with resistance or susceptibility to fungal diseases that can be used as molecular screening traits in grapevine breeding programs

V. Vinifera leaves
Susceptible

Vitis leaves
Resistant

Metabolic Analysis

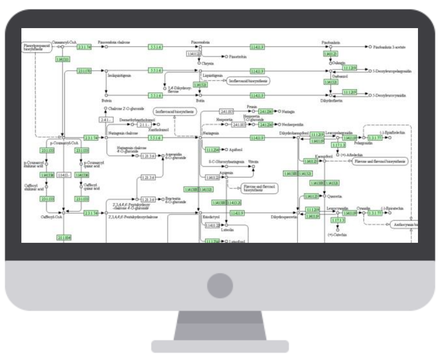


Extraction of grapevine leaf metabolome with our optimized protocol [3]

Metabolic Comparison

Metabolite identification and statistical analysis

Pathway Analysis



Pathway analysis to identify major proteins/metabolites differentiating resistant and susceptible plants

Targeted Proteomics

Proteins of interest, associated with fungal resistance or susceptibility, will be selected and quantified by a targeted proteomics approach

Targeted Transcriptomics

qPCR for evaluation of enzyme expression

Biomarker Validation

Validation of the identified biomarkers in new grapevine bred cultivars in collaboration with the Portuguese and German ampeleographic collections

Acknowledgments

This work was supported by projects UID/MULTI/00612/2013, PEst-OE/QUI/UI0612/2013, PEst-OE/BIA/UI4046/2014, by the investigator FCT program IF/00819/2015 and grant SFRH/BD/116900/2016 from Fundação para a Ciência e Tecnologia (Portugal). We also had support from the Portuguese Mass Spectrometry Network (LISBOA-01-0145-FEDER-022125) and the Project EU_FT-ICR_MS, funded by the Europeand Union´s Horizon 2020 research and innovation programme under grant agreement nr. 731077.

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