ABSTRACT BOOK

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502 - Proteomic signatures uncover the early key players on Vitis vinifera cv. 'Regent'-Plasmopara viticola crosstalk

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The analysis of complex biological systems keeps challenging researchers. Aiming to overcome this complexity, the study of different cellular compartments, like apoplast, could allow a broader understanding of the cell dynamics. Plant apoplast, the cellular compartment external to the plasma membrane including the cell wall, is the first contact point between plant and pathogen molecules. Also, it is where the first pathogen structures develop after infection. In grapevine (Vitis vinifera L.), little is known about apoplast and the role of apoplastic proteins in cellular mechanisms, particularly in response to pathogens. Grapevine, which has a high economic importance due to its final products, is very susceptible to diseases, like to downy mildew, caused by the obligate biotrophic oomycete Plasmopara viticola. Normally, upon P. viticola infection the colonization of grapevine leaf tissues is rather fast. At 6 hours post inoculation (hpi), the pathogen penetrates through the stomatal opening and develops substomatal vesicles with primary hyphae. In tolerant cultivars, like 'Regent' (crossing line tolerant to P. viticola), the infection progress, at this early stage, is slowed down, inhibited, or completely stopped.

In this study, we have evaluated two different leaf proteomes (whole leaf and apoplast proteomes) of 'Regent' at 6hpi with P. viticola. Mock-inoculated leaves treated with water were used as control. Both proteomes were sequenced by nanoLC-MS/MS and the proteins identified by homology search in NCBIprot Vitis vinifera database. Protein differential accumulation between apoplast and total leaf proteomes, for both inoculated and mock conditions, together with functional annotation analysis, are being conducted. This analysis will allow an understanding of protein movement between the inside and outside of the cell, under non-stress conditions and after inoculation with P. viticola. Also, it will allow the identification of proteins directly involved in plant-oomycete communication and key players in the establishment of an incompatible interaction.

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