

Welcome to the Fourth Conference of the International Plant Proteomics Organization

Hosted from Winnipeg, Canada

March 9th – 11th 2021

PROGRAMME

On behalf of the Scientific and Organizing Committees, I would like to welcome you to INPPO2020 – being held virtually, and in 2021. I hope you have a productive and meaningful experience!

Christof Rampitsch, Conference Chair.

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fungicides. In addition, we explore opportunities to enhance fungicide efficacy and reduce costs to the growers. This information will support the reduction of selective pressure against antifungal-resistant strains and provide new tools to oppose emerging resistant pathogens.

TALK#3.2

Modulation of apoplast proteome by downy mildew in susceptible and tolerant grapevine cultivars

Joana Figueiredo^{1,2,3}, Cavaco AR¹, Guerra-Guimarães L^{4,5}, Leclercq CC⁶, Santos RB¹, do Céu Silva M^{4,5}, Renaut J⁶, Sousa Silva M^{2,3}, Figueiredo A¹

¹Biosystems & Integrative Sciences Institute (BioISI), University of Lisboa, Portugal

²Laboratório de FTICR e Espectrometria de Massa Estrutural, Universidade de Lisboa, Portugal

³Departamento de Química e Bioquímica, Faculdade de Ciências da Universidade de Lisboa, Portugal

⁴Centro de Investigação das Ferrugens do Cafeeiro, Universidade de Lisboa, Portugal

⁵Instituto Superior de Agronomia, Universidade de Lisboa, Portugal

⁶Luxembourg Institute of Science and Technology, Luxembourg

Grapevine (*Vitis vinifera* L.) is among the most important fruit crops worldwide, with an enormous economic impact due to its final products. Downy mildew, caused by the obligate biotrophic oomycete *Plasmopara viticola*, is one of the most destructive grapevine diseases. Plant apoplast is the cellular compartment external to the plasma membrane including the cell wall and the free space between cells. It is where the first reactions take place between plant and pathogen molecules and, in case of oomycetes, is where the first pathogenic structures develop. However, plant apoplast is particularly demanding to analyse. Despite our knowledge on its involvement on several biological processes, its composition and dynamics is still poorly known. In a first approach to characterize the grapevine apoplast, we have optimized a vacuum-infiltration-centrifugation method that allows a simultaneous extraction of apoplastic proteins and metabolites. This methodology was applied to study two grapevine cultivars, *V. vinifera* cv. 'Trincadeira' (highly susceptible) and 'Regent' (tolerant) during a time course of infection with *P. viticola*. Apoplast samples (mock and inoculated) were collected at 6h, 24h, 48h, 72h and 96h after inoculation for proteomic analysis. The same time-points were used to evaluate the pathogen growth and plant responses by light and epifluorescence microscopy. The nanoLC-MS/MS analysis followed by homology search in NCBIprot *Vitis vinifera* database allowed the identification of a total of 1547 proteins. A principal component analysis was performed and revealed a good separation between grapevine cultivars and between mock and inoculated samples, for each time-point. Further functional annotation is being conducted in order to determine which biological processes/molecular functions are modulated along the infection process. This study will allow a deeper understanding of the apoplast dynamics and grapevine defences to *P. viticola*.

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