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INFLUENCE OF CITRUS ROOT EXTRACTS ON *Phytophthora parasitica* METABOLOME ANALYZED BY MASS SPECTROMETRY TECHNIQUES. ; R.J.D. DALIO¹; H.J. MÁXIMO¹;

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Phytophthora parasitica is an oomycete pathogen that infects a broad range of crops of worldwide economic interest. Currently an effective control method for this pathogen is not available, therefore, understanding the mechanisms involved in its virulence is crucial. In this work, *P. parasitica* secondary metabolite production was studied by matrix laser-assisted desorption ionization mass spectrometry imaging (MALDI-MSI) and ultrahigh-performance liquid chromatography coupled with electrospray ionization quadrupole time-of-flight tandem mass spectrometry (UHPLC/ESI-Q-TOF-MS) combined to the chemometric tools, and its metabolic profile was evaluated under the influence of *C. sunki* (natural host) and *P. trifloriata* (resistant plant) extracts. The spatial distribution of several metabolites was revealed in *P. parasitica* colonies by MALDI-MSI, and the metabolite ion of m/z 246 was identified as the protonated molecule of Arg-Ala. The MALDI-MSI showed the variations in surface metabolite profile of *P. parasitica* under the influence of *P. trifloriata* extract. The *P. parasitica* metabolome analysis by UHPLC-ESI-Q-TOF-MS resulted in the detection of Arg-Gln (m/z 303), as well as L-arginina (m/z 175), and other unidentified metabolites. Significant variations in such metabolome was detected under the influence of the plant extracts when evaluated by UHPLC-ESI-Q-TOF-MS. The two techniques showed to be complementary providing important informations at the molecular level when applied for the *in vitro* evaluation of plant extract influences on microbial growth.

Key words: *Phytophthora parasitica*; MALDI-MSI; UHPLC-ESI-Q-TOF; SCiLS; Metabolomics.