

PROJECT TITLE

Study of the enzymatic regulation behind priming in Mycorrhiza- and Systemin- Induced Resistance

CONSORTIUM

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SUMMARY OF THE REPORT

In nature, plants have evolved complex strategies to survive to the different biotic and abiotic stresses that constantly challenge them. These strategies include the association with Arbuscular Mycorrhizal Fungi (AMF). Mycorrhizal plants show an estate of enhanced resistance against pest and pathogens called Mycorrhiza Induced Resistance (MIR), which is the matter of our study. In previous studies we found that the tomato peptide Systemin (Sys) is likely involved in the correct establishment of the symbiosis in tomato and the regulation of MIR against *B. cinerea*. Moreover, we found that exogenous treatments with Sys induce resistance against necrotrophic pathogens in tomato and *Arabidopsis*. Therefore, we are focused on the study of the molecular mechanisms behind MIR and Sys-IR and the possible link between them by using different omics technics.

Interestingly we observed very similar patterns in the proteomic and metabolomic profiles in MIR and Systemin-induced Resistance (Sys-IR), suggesting that the two resistance inducers may be related and share common defense signalling elements. In both cases we observe a high impact of the peptide treatment or the symbiosis in the proteomic profile in the absence of infection, whereas at the metabolomic level the major changes occurred after the pathogen infection, showing a typical priming profile. These observations lead the hypothesis that there must be a regulation at the enzymatic level that would explain the link between the two profiles. Besides, very interestingly we observed that a great impact of the two treatments was observed in many pathways of the primary metabolism such as carbohydrate metabolism, photosynthesis or redox reactions.

During the transnational access project, we could access the Hit-Me platform at INRAE Bordeaux in order to performed a study of the enzymatic activities of the primary metabolism. The analysis included the measurement of enzymes participating in the glycolysis, tricarboxylic acid cycle (TCA), carbohydrate metabolism, oxidative pentose phosphate pathway (OPPP), photosynthesis and amino acids metabolism, as well as the measurement of soluble sugars and some redox metabolites. These deep study of important elements of the central metabolism lead us to a better understanding of the mechanisms behind Sys-IR and MIR and the link between them.