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Poster Communication Abstract – PH.51

TRANSCRIPTOMIC REPROGRAMMING OF ROUGH LEMON (*CITRUS JAMBHIRI* LUSH) INFECTED BY *PLENODOMUS TRACHEIPHILUS* REVEALS THE ACTIVATION OF SYSTEMIC ACQUIRED RESISTANCE (SAR)

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"Mal Secco" Disease (MSD) is a severe vascular disease of citrus caused by the mitosporic fungus *Plenodomus tracheiphilus*. The current geographical distribution of MSD comprises mainly all citrus-growing countries of the Mediterranean basin. Here, we describe the results of RNA sequencing and de novo transcript assembly in rough lemon leaves subjected to artificial inoculation by P. tracheiphilus, used as model of compatible host-pathogen interaction. The analysis of the transcriptomic data unequivocally indicated that the entire gene set encoding the components of systemic acquired resistance (SAR), from salicylic acid biosynthesis on, was strongly up-regulated. Many WRKY transcription factors have been found up-regulated in infected plants, indicating a strong activation of the defensive mechanism. The strong induction of WRKY40, WRKY18 and WRKY70 transcription factors accounts for a defense response specifically addressed towards fungi as they respond to chitin, a well-established elicitor of plant defense responses to fungal pathogens. In addition, *P. tracheiphilus* is able to overcome the basal immunity of rough lemon plants (PTI) as the essential regulator of plant defense (RPM1 interacting protein 4) was down-regulated, and the expression of BIR2, which is negative regulator of basal level of immunity was up-regulated in the diseased plants. *P. tracheiphilus* infection induced also the expression of oxidative burst peroxidases (RBOHs), involved in generating reactive oxygen species (ROS) with antimicrobial activity, and a subset of ROS-scavenging genes. Interestingly, a wide number of glutathione transferases were also up-regulated by the infection in accordance with early studies on the role of GSTs in plant biotic stress response. As the main scope of the work was the identification of putative target genes for genome editing experiments, a wide range of genes belonging to structural and transcription factor families have been identified and they could be taken in consideration for targeted mutagenesis, RPM1 and BIR2 being only two of them.