Proceedings of the SIGA Young Web Meeting
7 July, 2020
ISBN **978-88-944843-0-4**

Abstract – SY33

TRANSCRIPTOME ANALYSIS OF ROUGH LEMON (*CITRUS JAMBHIRI* LUSH.) LEAVES INFECTED BY *PLENODOMUS TRACHEIPHILUS*, THE PATHOGEN OF "MAL SECCO" DISEASE

RUSSO R.*, SICILIA A.**, CARUSO M.*, ARLOTTA C.*, DI SILVESTRO S.*, NICOLOSI E.**, LO PIERO A.R.**

*) CREA-OFA, Corso Savoia 190, 95024 Acireale (Italy)
**) Department of Agriculture, Food and Environment, University of Catania, Via Santa Sofia 98, 95123 Catania (Italy)

Mal secco is one of the most severe diseases of citrus, caused by the mitosporic fungus *Plenodomus tracheiphilus* that is widespread in different Mediterranean countries. The damage caused by the disease can lead to high yield losses, related to the reduction of canopy volume, and finally to the death of tree. The disease has a relevant economic impact on different citrus species, such as lemon (*C. limon*), citron *(C. medica*), lime (*C. aurantifolia*), bergamot (*C. bergamia*), sour orange (*C. aurantium*), volkamer lemon (*C. volkameriana*) and rough lemon (*C. jambhiri*). With the main aim of identifying candidate genes involved in the response of citrus plants to mal secco, we performed a transcriptome analysis of rough lemon seedlings, particularly sensitive to the disease, subjected to artificial inoculations in comparison with plants inoculated with water. Leaves of 6-months old seedlings were inoculated (0.1 ml of inoculum containing 106 conidia ml-1 prepared according to Gentile et al., Acta Horticolturae 535: 259-263, 2000) with P. tracheiphilus Pt10 strain (kindly provided by Prof. Vittora Catara). Total RNA was extracted from inoculated and control leaves using the RNA easy kit (Qiagen) according to the manufacturer's instructions 14 days after the inoculum at which symptoms of chlorosis started to become evident. The extracted RNA was quantified and qualified by using a NanoDrop2000 Spectrophotometer and an Agilent 2100 Bioanalyzer, respectively. The average RIN was of 8.2 suggesting that the quality of RNA samples was very high and appropriated for libraries construction. The RNASeq library preparation was performed according to our previous method described by Sicilia et al. (BMC Plant Biol., 19, article number: 355, 2019) and it included three replicates for each treatment. The amplified fragments were sequenced using an Illumina HiSeqTM 2000 obtaining a total of 228 million clean reads, with a Q30 of 93%, that were assembled into 117538 unique sequences (unigenes), 87% of which were successfully annotated in at least one database. The *de novo* transcriptome was mapped back in order to validate the assembly and quantify the expression level, obtaining 83% of coverage. The analysis of Differential Expressed Genes (DEGs) between control and inoculated samples highlighted a sharp response triggered by the pathogen since a total of 8358 significant DEGs have been discovered. Among them, 4930 genes were up-regulated and 3428 were down-regulated in the inoculated samples. The analysis of the most significantly enriched KEGG pathways indicated that a crucial role in the plant response to the fungus is played by genes involved in "carbon metabolism", "biosynthesis of amino acids", "ribosome" and "phenylpropanoid compounds" suggesting that a rearrangement of protein and secondary metabolite biosynthesis occurred as defense mechanism against the threat. This study provides novel information to clarify the interaction between plant and pathogen, highlighting the molecular and biochemical mechanisms involved in the response of *C. jambhiri* against *P. tracheiphilus*.