

Proceedings of the LX SIGA Annual Congress
Catania, Italy – 13/16 September, 2016
ISBN 978-88-904570-6-7

Oral Communication Abstract – 1.06

NATURAL SOILS MORE THAN GENOTYPES ELICIT DEFENSE PRIMING IN TOMATO PLANT

CHIALVA M.*, SALVIOLI A.*, DAGHINO S.*, BAGNARESI P.***, NERI F.***,
NOVERO M.*, SPADARO D.****, PEROTTO S.*, BONFANTE P.*

*) Department of Life Sciences and System Biology, University of Torino, Viale P.A. Mattioli 25, I-10125 Turin (Italy)

**) Genomics Research Centre CRA-GPG, Via S. Protaso 302, I-29017 Fiorenzuola d'Arda (Italy)

***) Human Genetics Foundation (HuGeF), Via Nizza 52, I-10126 Torino (Italy)

****) Department of Agricultural, Forestry and Food Sciences (Di.S.A.F.A.), University of Torino, Largo Braccini 2, I-10095 Grugliasco (Italy)

Solanum lycopersicum, plant microbiota, *Fusarium oxysporum*, pathogen, lignin

In natural and agricultural ecosystems, plants are subjected to multiple biotic and abiotic factors, which modulate their growth. Among them, the soil microbiota (a complex of microbes with different nutritional strategies) is known to influence plant health. While several studies have investigated microbiota biodiversity, highlighting the impact of plant genotype, the comprehension of the mechanisms related to plant response is still at its infancy.

To begin to untangle this complex skein, we investigated in tomato (*Solanum lycopersicum*), a model plant of economic interest, how plants respond when grown on a natural soil. Two tomato genotypes, Cuore di Bue and Battito, respectively susceptible and resistant to *Fusarium oxysporum* f. sp. *lycopersici* (FOL), were maintained in two soils different for geographical origin, history and microbiota: RO sampled in Rosta (TO, Italy), AL sampled in Albenga (SV, Italy), as well as a sterile peat-moss soil (CONT).

As a first explorative analysis, we grew tomato plants in glasshouse on the three different substrates, extracted RNA and proteins from roots and performed i) Illumina HiSeq deep-transcriptome sequencing on 18 cDNA libraries and ii) global proteome profiling for the susceptible genotype only (6 libraries) using LC-MS/MS on Q-Exactive Orbitrap. Transcriptome datasets showed that soil, with its biotic and abiotic components, is the main driving force that induces the plant to activate its defense pathway. Interestingly, KEGG pathway analysis of both transcriptome and proteome profiling datasets highlighted that soil-grown plants activate more efficiently generic defense mechanisms, when compared to plants growing in a sterile substrate, including those related with lignin deposition and plant-pathogen interactions, such as pathogenesis-related proteins (PRs). AL soil, characterized by partial disease suppression was particularly effective in priming elicitation. As a second step, sequencing data were technically validated using qRT-PCR; lignin and total phenol content were assessed in a second experiment performed on root and leaf tissues confirming the transcriptome and proteome results.

Finally, a third experiment was performed by adding a FOL inoculum to the experimental setup. Without pathogen inoculation, the two plant genotypes responded in a similar way, as also observed in the previous experiments, but when FOL was introduced into the system, the resistant genotype showed higher yield and lower disease severity, as expected. Moreover, under pathogen attack, the susceptible genotype activated stronger molecular defenses.

In conclusion, our work is starting to reveal some mechanisms operating in tomato living in natural soils.