Transcriptome analysis of *Solanum lycopersicum* roots provides novel insights into the plant response to a beneficial fungus

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The globally pressing need for increasing agriculture yield while reducing environmental impact has promoted the utilization of sustainable plant protection strategies based on natural biocontrol agents, among which, rhizosphere-competent Plant-Growth-Promoting Fungi (PGPF) have inspired great interest. In this scenario, beneficial strains of *Trichoderma* have proved to be very effective for crop protection against pathogens. Therefore, "omic" data of the plant response to *Trichoderma* can be effectively exploited in sustainable agriculture and could also be a useful model of the plant-beneficial microorganism interaction through "translational research".

Our work investigated the transcriptional response of tomato roots (*Solanum lycopersicum*) to *Trichoderma harzianum* strain T22 at early stages of the interaction (24, 48 and 72 h), using a Next Generation Sequencing approach (RNA-seq). This analysis revealed an intense remodelling of the plant transcriptome already after 24 h, involving more than 75% of the detected Differentially Expressed Genes (DEGs), while smaller effects on gene expression were observed at 48 and 72 h. Enrichment analysis of the 24 h DEGs based on Gene Ontology (GO) showed involvement of "defence response" and "cell wall organization" activities as well as of macromolecules "metabolism", "transport" and "localization". Data inspection via the MapMan tool assigned 151 DEGs to bin 27 ("RNA"-related), suggesting the activation of the transcriptional machinery in tomato roots responding to the PGPF. Moreover, MapMan annotation highlighted a considerable enrichment of bin 35 (*i.e*. "not assigned") over the three time points, mostly due to the large presence (155) of proteins with unknown functions.

Along with plant transcripts, RNA-sequencing of roots also identified 448 Trichoderma genes, which were searched for differential expression over the time course. GO enrichment analysis of the differentially expressed genes revealed that, at 24-48 h, 'macromolecules metabolic processes' were affected; on the other hand, "response to stimulus"–related, as well as cellular processes ("communication", "amino acid metabolism") and their regulation, were involved at 48-72 h.

Taken together, our data were used to develop a model of the early tomato root response (within 72 h) to stimulation by the beneficial fungus *T. harzianum*.