

LOCAL AND SYSTEMIC EFFECTS OF THE AM SYMBIOSIS ON GENE EXPRESSION PROFILES IN *SOLANUM LYCOPERSICUM*

FIORILLI V.*, CATONIM.**, NOVERO M.*, ACCOTTO G.P.**, LANFRANCO L.*

*) Department of Plant Biology, University of Turin, Viale Mattioli 25, 10125 Turin, Italy

**) Institute of Plant Virology – CNR, Strada delle Cacce 73, 10135 Turin, Italy

arbuscular mycorrhizal symbiosis, tomato, microarray, laser microdissection, Glomus mosseae

In nature one of the most widespread mutualistic association is the arbuscular mycorrhizal (AM) symbiosis formed between soil fungi belonging to Glomeromycota and most land plants. The symbiosis develops in the plant roots where the colonization involves epidermal and cortical cells. In the root cortex the fungus develops intercellular hyphae and extensively branched intracellular hyphae called arbuscules which are considered crucial components of the interaction. The AM symbiosis has a multifunctional character: AM fungi improve plant nutrient acquisition and provide protection from biotic and abiotic stresses. To obtain an overview of transcriptional changes triggered in roots and shoots of tomato (*Solanum lycopersicum* L.) as a result of the colonization by the AM fungus *Glomus mosseae* the TOM2 microarray platform (Cornell University) was used. Expression profiles of 17 selected genes was confirmed for qRT-PCR. This analysis revealed 362 up-regulated and 293 down-regulated genes in mycorrhizal roots. Significant gene modulation was also observed in shoots: 85 genes showed increased transcript levels while 337 genes were down-regulated. Most responsive genes are ascribed to the following functional categories: primary metabolism, defence and response to stimuli, cell organization, protein modification and transcriptional regulation. In addition, to identify possible plant determinants of arbuscule formation, the cell-type expression profiles of a subset of genes induced in mycorrhizal roots were monitored taking advantage of the laser microdissection technology. Six genes specifically expressed in arbusculated cells have been identified: they are involved in auxin and abscisic acid metabolism, cell wall biogenesis and cytoskeletal dynamics.