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BOOK OF ABSTRACTS

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Physiological and transcriptomic responses of the tomato mutant chloronerva affected in the regulation of iron metabolism to arbuscular mycorrhiza

Víctor Manuel López-Lorca, Olga López-Castillo, Concepción Azcón-Aguilar, Nuria Ferrol
Soil and Plant Microbiology Department, Estación Experimental del Zaidin, Consejo Superior de Investigaciones Científicas, Granada, Spain

Arbuscular mycorrhiza (AM) is a widespread symbiosis in nature whose establishment and function is influenced by environmental factors. Mineral nutrients are known to influence AM. In this work, we investigated the importance of iron homeostasis in the *Rhizophagus irregularis-Solanum lycopersicum* interaction by using the iron inefficient mutant chloronerva (chln) of tomato. AM development was impaired in the chln mutant, but the symbiosis partially reverted its growth defect. RNA sequencing revealed a lower number of differentially expressed genes in the "chln vs wild-type" comparison in mycorrhizal than in non-inoculated roots. Gene Ontology and Kyoto Encyclopedia of Genes and Genomes pathways enrichment analyses revealed differential metabolic responses to AM colonization between roots of wild-type and chln mutant plants. Expression of a subset of genes that have been previously shown to be required for AM establishment and function was lower in the mycorrhizal roots of chln mutants compared to the wild-type. The lower expression levels of the phosphate starvation-induced genes in non-mycorrhizal chln roots compared to wild-type and the higher phosphorus concentration of the chln plants suggests that reduced AM colonization of chln may involve phosphate signalling pathways. Over-expression of iron-deficiency response genes in chln roots was mitigated by AM colonization, which suggests that root AM colonization contributes to increase Fe availability and distribution in the chln mutants. All these data together indicate that there exists a connection between AM and Fe homeostasis.

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