HOW BENEFICIAL SYMBIONTS ACT: GENE EXPRESSION INDUCED BY ARBUSCULAR MYCORRHIZAL FUNGI IN SUNFLOWER ROOTS


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Arbuscular mycorrhizal (AM) fungi establish beneficial symbioses with the roots of the majority of land plants, including the most important food crops, from cereals to legumes, vegetables and fruit trees. AM fungi are the essential elements of soil fertility, plant nutrition and productivity, facilitating soil mineral nutrient uptake by means of an extensive extra-radical network of fungal hyphae spreading from colonized roots into the soil.

Sunflower (Helianthus annuus) is a non-model, widely cultivated species whose mycorrhizal status was recently assessed in wild accessions, cultivars and inbred lines. Although previous transcriptome analyses on sunflower showed gene differential expression in response to biotic/abiotic stresses, no data are available on molecular changes induced by AM fungi. In this work we used an RNA-seq approach in order to evaluate gene expression variations at early and late stages of mycorrhizal establishment in sunflower roots colonized by the arbuscular fungus Rhizoglomus irregularare.

Sunflower plantlets (inbred HA412-HO) were inoculated with the fungus and total RNA was isolated from roots 4 and 16 days since inoculation, then twelve cDNA libraries were built and sequenced by Illumina technology. A de novo transcriptome was established by assembling Illumina cDNA reads. This transcriptome and a recently released predicted transcriptome of sunflower (inbred XRQ) were used as reference for quantitative analysis of gene expression. Overall 726 differentially expressed genes (DEGs) between mycorrhizal and control plants were identified. The number of over-expressed DEGs was much higher than under-expressed ones and this difference increased in the late stage of colonization. Gene Ontology analyses showed that several DEGs were specifically involved in known mycorrhizal processes, such as membrane transport (ABC transporters, ammonium transporters), cell wall shaping (subtilisins, ascorbate oxidases), gene networking (DELLA, ERF) and defense response (germin-like protein, vinoine synthases). We also identified new mycorrhizal-induced putative transcripts, such as genes belonging to the BAHD-acyltransferase superfamily, involved in endogenous formation of specialized monoterpenoids.

Our data add a valuable contribution for deciphering gene expression related to beneficial fungi and plant symbiosis, adding a new non-model species for future comparative functional genomics analyses.
References

