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Editorial

Molecular basics of mycorrhizal symbioses

Mycorrhizas are the most widespread symbioses on earth. These fascinating plant–microbe interactions are established between the root system of terrestrial plants and hyphae from soil-borne fungi, resulting in the intimate connection of plant and fungal structures. Two major types of mycorrhizal symbioses can be differentiated: ectomycorrhizas and arbuscular mycorrhizas. Both symbioses play a vital role in our natural ecosystems that are usually characterized by nutrient limitation, thus requiring a mobilization of mineral nutrients and the recycling of biological matter.

Members of the Fagaceae and Pinaceae families utilize ectomycorrhizal fungi for nutrient acquisition. Trees forming ectomycorrhizal symbioses cover large areas particularly in the Northern hemisphere. While ectomycorrhiza formation is restricted to relatively few plant species, more than 5000 different fungi undergo this partnership. Their fine hyphae more effectively exploit water and nutrients from soils than plant roots can do and thus significantly contribute to host nutrition in particular under conditions of abiotic stress. In contrast to arbuscular mycorrhizal fungi, ectomycorrhizal fungi do not penetrate the cell walls of their host plants, but form the characteristic Hartig net as the major site of nutrient transfer to the plant. In return for the supply of water and minerals, the fungi receive up to 30% of all carbohydrates synthesized by the plants.

Arbuscular mycorrhizas are more widespread than ectomycorrhizas. Under different conditions such as nutrient limitation, heavy metal or salt stress, strong soil acidity, and biotic stress, more than 80% of all higher plants form symbiotic interactions with arbuscular mycorrhizal fungi. In this type of interaction, fungal hyphae extensively colonize the root by penetrating cortical cell walls, forming a network of intraradical hyphae that remains connected to an extraradical mycelium. Arbuscular mycorrhizas are denominated by their ability to form arbuscules, highly branched intracellular structures that are sites of phosphate transfer from the hyphal network to the plant cells. Until now, arbuscular mycorrhizal fungi cannot be grown independently of a host plant. Therefore, despite of an enormous ecological relevance, molecular knowledge on the formation of these endosymbioses is still limited as compared to that of the endosymbioses between rhizobial prokaryotes and legume plants that initiate the formation of root nodules.

Recent technological developments in plant genomics facilitate the comprehensive identification of genes that are activated during mycorrhizal symbioses. Relying on such genomics approaches as tools to inform targeted functional studies, the interaction between fungal and plant partners can be studied at the transcript, protein, and metabolite level. In 1999, the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) established the Priority Program SPP 1084 "Molecular Basics of Mycorrhizal Symbioses" to promote collaborations between German groups working on molecular aspects of both ecto- and arbuscular mycorrhizas. From the beginning, this collaboration was supported by sharing modern technologies in experimental genomics, molecular genetics and plant transformation. Notably, international interactions and integration of the research projects in multinational networks were mandatory for the success of this Priority Program.

In its first topic, the program pursued a *transcriptomics project* covering the interactions of *Medicago truncatula* (barrel medic) with *Glomus intraradices* as a model for arbuscular mycorrhizas and of *Populus tremula* (aspen) with *Amanita muscaria* (fly agaric) for ectomycorrhizas. In the course of the transcriptomics project, almost 20,000 ESTs from both the host plants and the fungal microsymbionts were generated, cDNA and oligonucleotide microarray platforms were developed, and microarray-based transcriptome profiling was performed. Sequence and expression data were evaluated using software developed in the course of the program, and the results were shared with international projects in addition to being deposited in public databases.

The sequence and expression data from the *transcriptomics project* formed the basis for three other main topics of the program. The topic *mycorrhiza development* covered the identification of signals involved in the recognition of symbiotic partners and the analysis of signal transduction

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pathways playing a role in establishing symbioses. In the topic *fluxes*, the transport of carbohydrates, nitrogen and sulfur compounds as well as the adaptation of both the plant and the fungal metabolism to the symbiotic state was investigated. In the fourth topic, *applied aspects* were investigated, e.g. the mycorrhiza-induced heavy metal tolerance and bioprotection.

This Special Issue of PHYTOCHEMISTRY presents a collection of reviews, which summarize the major outcome of a six year financial support by the DFG. The manuscripts focus on own results, which are discussed in relation to international developments in the field. All groups supported within the Priority Program are indebted to the DFG for its generous support, which was a prerequisite for the success of this program. The groups would also like to thank all reviewers of the program for critically examining and accompanying the research projects in a constructive way.

We sincerely hope that this Special Issue, as one major outcome of the Priority Program, apart from receiving a wide international recognition and a broad scientific distribution, will pave the way for future collaborative work on mycorrhizal symbioses.

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