

Plant secondary metabolites constitute an unusually large group of structurally diversified compounds that have long been suggested to contribute to the interactions of plants with other organisms. Numerous functions of plant secondary metabolites include their roles in plant response to abiotic stresses, defense against insects and plant immunity. These compounds play also important roles in interactions with symbiotic microbes that can support plant growth by nutrient delivery. However, so far function of secondary metabolites in these beneficial interactions has not been studied in detail. A well know example of interactions that promote plant growth is mycorrhiza, association of plants with fungi the phylum Glomeromycota that are capable to colonize plant roots and deliver important nutrients including phosphorus. Mycorrhiza represents an ancient form of symbiosis that have been observed in 80-90% of land plants. However, despite the ubiquity of the mycorrhizal symbiosis ability to form this association had been lost in several plant lineages. Among such plants are species belonging to the Brassicaceae (cabbage) family that includes some important vegetables, crop plants and the model plant species *Arabidopsis thaliana* (Arabidopsis). Recent studies indicated that function of mycorrhizal fungi had been replaced in Arabidopsis by other fungal endophytes that colonize roots of this plant in natural soils and are capable to promote growth by delivering phosphorus to the host. Concerning the wealth of genetic tools and resources available for Arabidopsis this plant species together with its growth promoting endophytes constitutes an excellent system to study molecular mechanism underlying microbe-induced growth promotion. For this reason we will employ this model system in our study to address function of plant secondary metabolites in interactions of plants with growth promoting fungi. This will include identification of involved metabolites as well as enzymes required for their biosynthesis. Obtained results will expand our fundamental knowledge on the mechanisms that control microbe-induced plant growth promotion. Knowledge on the biosynthetic pathways leading to phytochemicals with function in microbe-induced growth promotion is of significance for future crop cultivation strategies. This may facilitate rational breeding or genetic design of plants with secondary metabolite optimal for interaction with beneficial microbes. In this context, it is important that the model plant Arabidopsis belongs to the cabbage family that includes a large number of agriculturally important crops. Finally, understanding of function of particular plant metabolites in assembling beneficial for plants microbial communities could provide structural scaffolds of molecules which field application could support development of the microbial species beneficial for crop plants.