Abstract

Plants develop beneficial interactions with soil microorganisms driven by various growth-limiting factors. One such factor is the low availability of soil phosphorus, which is taken up by the plants as inorganic phosphate (Pi). Low soil Pi availability promotes the establishment of the arbuscular mycorrhizal (AM) symbiosis, the most common mutualistic plant-fungal interaction, which features a reciprocal exchange of Pi towards the plant and lipids and sugars towards the fungus. In addition, soil Pi deprivation positively affects the development of the beneficial association between the ascomycete *Colletotrichum tofieldiae* (Ct) and the AM non-host *Arabidopsis thaliana*. Under low Pi, Ct colonizes the roots of *A. thaliana*, transfers Pi to the plant and enhances its growth. Despite the various differences, it is likely that there are common, evolutionary conserved genetic factors that play crucial roles in the establishment and development of those Pi-limitation-driven beneficial interactions. In order to identify such genetic factors, an orthology-based comparative analysis of transcriptomics data (OCAT) using experiments with AM hosts and the *A. thaliana*-Ct (AtCt) interaction has been performed. The analysis has revealed a set of conserved genes potentially essential for beneficial plant-fungal associations. Mutants for selected candidate genes in *A. thaliana* were used with the aim of identifying disturbances in the AtCt interaction. This technique yielded phenotypes of differential responses to Ct compared to wild-type and the strongest phenotypic effect was observed in a mutant of a lipid biosynthesis gene.

Transfer of fatty acids to the fungal partner is essential for the successful establishment of both beneficial and parasitic plant-fungal associations. It was, therefore, hypothesized that *de novo* fatty acid biosynthesis, which takes place in the plastids, is crucial for the development and determination of the fate of the beneficial plant-fungal interactions. One of the target genes identified by the OCAT, the plastid *LIPOAMIDE DEHYDROGENASE 1* (*LPD1*), was the E3 component of the plastid pyruvate dehydrogenase complex. The activity of this enzymatic complex leads to the synthesis of acetyl-CoA in a process which underlines the first committed step of the plants for *de novo* fatty acid biosynthesis. To work on the hypothesis, *A. thaliana* mutants in *LPD1* were used in reverse genetics experiments with the model AtCt interaction. In addition, mutants in *WRI3* and *WRI4*, which are regulators of *LPD1* and orthologs of *LjCBX1*, the regulator of the nutrient exchange in the AM symbiosis, were used. Although no differences could be observed under sterile conditions between wild-type plants and mutant lines, inoculation with Ct as well as growth in non-sterile substrates led to dramatic growth inhibition of the mutants. Furthermore, Ct colonization of *lpd1* and *wri3wri4* did not lead to the accumulation of root lipids and shoot nutrients, especially P, as opposed to wild-type. Interestingly, the phenotype developed during Ct inoculation of the mutants was morphologically and transcriptionally similar to infection with the pathogenic relative of Ct, *C. incanum*, indicating a switch of the AtCt interaction from beneficial to parasitic. Moreover, although indole glucosinolates accumulated in significantly lower levels, plant defense was increased in *lpd1* roots which also coincided with changes in the lifestyle of the fungus as observed by enhanced expression of genes related to virulence activity. The findings of this study highlight the importance of *LPD1* as well as *WRI3* and *WRI4* in lipid biosynthesis during the AtCt interaction and suggest that sufficient capacity of *de novo* fatty acid biosynthesis is required in order to maintain the beneficial state of the plant-fungal association.