Why is so important to have a kinase that is capable to interact with a ROP GTPase as well as a ROPGEF? GEF proteins have the potential to transfer signals from receptors to ROP GTPases. A huge family of receptor-like kinases (RLKs) has been found in plants but their downstream signaling events are hardly known. Similarly, it is not known what are the upstream signaling steps resulting in ROP activation. What we currently know is that a tomato protein called KPP (kinase partner protein) has been identified as binding partner of the cytosolic domains of the pollen-specific RLKs, LePRK1 and LePRK2. This KPP protein is a homolog of *Arabidopsis* ROPGEF1 and is phosphorylated in vitro by LePRK1. Our results indicate that a further type of kinase (RLCK) might be involved linking ROP- and RLK-mediated signaling pathways.

In order to prove this hypothesis, as a first step, we showed the interaction between the MtGEF and MsROP3 proteins. In our yeast two-hybrid experiments, MtGEF displayed strong interaction with the non-nucleotide bearing wild-type and the constitutive active (CA) mutant of MsROP3. Wild type, CA- and dominant negative (DN) mutants of MBP-fused MsROP3 and His tagged-MtGEF fusion proteins expressed in *E. coli* were used for pull down assay. With this in vitro protein-protein interaction assay we were able to confirm our yeast results. Then the expression level of MtGEF was investigated in different *Medicago truncatula* tissue types by QRT-PCR, but it showed very low expression in almost all tissues therefore a correlation with MsROP3 or RRK1 expression could not be made. Recently, the full length MtGEF cDNA sequence has been amplified by PCR from a *Medicago truncatula* cDNA library and cloned into various expression vectors. In the future we would like to confirm our previous observations with this full length form as well as to further characterize the potential signaling interactions. This will include the determination of GEF activity toward MsROP3 and the RRK1 kinase activity towards MtGEF. We suppose that MtGEF could be an elusive link between RLKs and ROPs in a plant-specific signal transduction mechanism that also includes a ROP-dependent feedback regulation of GEF activity through RRK1.

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Phylogeny of Alloxysta (Hymenoptera, Cynipoidea, Figitidae, Charipinae) species – morphology vs. molecules

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Members of the figitid genus Alloxysta (Förster 1869) are parasitoids of hymenopteran natural enemies of economically important aphid species. Therefore these hyperparasitoid species have large impact on the biological control of insect pests. Due to their minute size most of the morphological characters which are widely used in the taxonomy of other cynipoid taxa, are variable and highly reduced. Most of the species are hardly distinguishable morphologically and it is impossible to determine if the variablility is intra- or interspecific. According to some authors there are only a few, very variable and generalist Alloxysta species whereas others suggest that the genus containes much more species which are less variable but more specialized. Current phylogenetic relationships of the genus are based on the same, often questionable morphological characters. So far no studies were carried out using molecular markers determining species limits and resolving the phylogeny of the genus. 20 morphological characters were widely used for Alloxysta species determination. On the basis of three characters: presence of the propodeal carina, pronotal carina, radial cell, the genus might be divided into six species groups. Mapping morphological characters on a molecular-based phylogeny enabled examination of character evolution. In this study, 20 morphological characters from western Palaearctic Alloxysta were mapped on a phylogenetic tree reconstructed from region of the cytochrome-c-oxidase I (COI) and the ribosomal 28S D2 genes analised with parsimony Bayesian, maximum-likelihood and distance based methods. The COI and 28S D2 trees were congruent. The above mentioned morphological characters may have evolved in parallel in different species groups of Alloxysta and, taken alone, may be unsuitable for a subgeneric division of the genus, however, are suitable for species differentiation.

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