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Sequence adaptations in the symbiosis receptor-like kinase (SymRK) enabling nitrogen-fixing root nodule development

Summary

Plant root symbioses with arbuscular mycorrhiza (AM) fungi and nitrogen-fixing bacteria bear huge potential for sustainable agriculture by reducing the chemical fertilizer input required to maintain high crop yields. The regulation and signal transduction mechanism leading to AM and the nitrogen-fixing root nodule symbiosis (RNS) share a genetic toolkit largely conserved across land plants. It contains a set of signal transduction components including the Symbiosis Receptor-like Kinase SymRK. During evolution, SymRK appears to have acquired novel molecular features that facilitated the development of the nitrogen-fixing root nodule symbiosis, while maintaining its conserved function for AM. In this project, we will explore sequence diversity among SymRK orthologs and paralogs with the goal to narrow down and identify critical sequence adaptations that underlie the rhizobial infection of plant cells. The doctoral student will investigate the mechanistic consequences of these adaptations at the cell biological and biochemical level with a focus on interacting proteins. The relevance of SYMRK paralogs and interacting proteins will be explored by reverse genetics utilizing transposon insertion populations or CRISPR/CAS genome editing technology and quantitative binding studies *in vivo* using advanced light microscopy and *in vitro* using a range of state-of-the-art technologies. We expect novel insights into the molecular mechanisms facilitating the symbiotic infection process of plant cells by nitrogen fixing bacteria.