Functional analysis of a peptide receptor module regulating arbuscular mycorrhizal symbiosis

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Arbuscular mycorrhiza (AM) is a mutualistic symbiosis between ancient Glomeromycotina fungi and host plants. In this relationship, the fungus colonizes the plant root cortex cells to form branched hyphae called arbuscules which assist the host plant with water and nutrient uptake, particularly phosphate. Unable to produce carbohydrates, the fungus is provided with carbon from the host plant in the form of sugars and lipids. We previously described a negative regulatory pathway involving a root-derived peptide hormone (CLE53) which acts with the leucine-rich receptor-like kinase SUNN to restrict symbiosis. As a consequence, *sunn* mutants display higher fungal colonization relative to the wildtype. Other proteins involved in regulating this symbiosis pathway have not been identified. Here we use the plant model *Medicago truncatula* to demonstrate that mutants in membrane-associated kinase CORYNE are also impaired in symbiosis regulation. Because *sunn* and *coryne* mutants display similar phenotypes in our preliminary experiments, we hypothesize that they regulate AM through a common pathway which involves CLE53. We will topically apply CLE53 to the plant mutants and use genetic approaches to test this hypothesis. Further, we will perform growth response assays to determine the physiological impacts of uncontrolled symbiosis. Whether these impacts resemble parasitism or provide increased benefit to the plant will be examined. Understanding these topics will allow us to maximally exploit this mutualistic symbiosis for the creation of "supermycorrhizal" mutants. Thus, the need and use of unsustainable, finite chemical fertilizers can be diminished. This ultimately will secure a more sustainable and stable crop food supply.