011

Title: Characterization of Glycine rich proteins in root nodule development of *Medicago truncatula*

Symbiotic nitrogen fixation is an agronomically important biological process that results in natural input of nitrogen into agricultural soils. Legumes and soil bacteria called rhizobia that convert atmospheric nitrogen into readily available ammonia enter a partnership that leads to formation of specialized organs called nodules on legume roots. Small signaling peptides (SSPs) or peptide hormones are emerging regulators of root nodule formation and are fragments of larger polypeptides, that range from five to 65 amino acids. SSPs are classified into subgroups such as post translationally modified peptides, Cystine rich and Glycine Rich Peptides (GRPs). Although there are several studies investigating the first two subgroups, not much is known about the Glycine rich peptides. In the model legume *Medicago truncatula* there are 57 genes which encode glycine rich proteins, of which three have been implicated in rhizobial infection previously. Glycine rich peptides in nodules range between 60-250 amino acids and are characterized by an N-terminal secretion signal followed by stretches of glycine residues. Our research is focused on the characterization of glycine rich proteins in root nodule development of *M. truncatula,* as they are induced during nodule development. Of 57 glycine rich protein (NodGRP) genes, *MtNodGRP31* is seen to be induced in three out of four time points post inoculation with the rhizobial partner *Sinorhizobium meliloti*; these include 4dpi, 10dpi, 14dpi and 28dpi. Phylogenetic analysis in MEGA X showed that the genes NodGRP31 belongs to a cluster of 13 closely related, tandemly duplicated genes on chromosome five. These 13 NodGRPs do not have orthologues in non nodulating plants such as *Arabidopsis thaliana* or *Nelumbo nucifera*. Our research aims to characterize these proteins using molecular genetics and plant phenotyping. Understanding NodGRP function will help provide insights into genetic control of nodule development and rhizobial infection required for optimizing this process.