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IDENTIFICATION OF PEPTIDE-RESPONSIVE HISTONE MODIFICATION GENES INVOLVED IN ROOT NODULE SYMBIOSIS

Nitrogen (N) is an essential but limiting macronutrient for crop growth in agroecosystems. Biological Nitrogen Fixation (BNF) is a critical biological process where atmospheric-N is converted into ammonia by N-fixing bacteria called rhizobia, forming mutualistic relationship with legume plants. These interactions are mediated by several signaling pathways and may involve epigenetic modifications like DNA methylations and histone modifications, where gene expression is altered without any change in DNA sequence. Histones are proteins which provide structural support to DNA. However, genes encoding enzymes for these post translational modifications are poorly investigated in the Leguminosae family. This project aims to answer the question - Do peptide hormones alter the epigenetic landscape of the genome during root nodule symbiosis? Peptide hormones or Small, secreted peptides are important intercellular signaling molecules that regulate diverse biological processes. To this end, we identified 245 putative histone modifying enzyme encoding genes classified as Methyltransferases, Demethyltransferases, Acetyltransferases, Deacetyl transferases in the model legume *Medicago truncatula*. Next, we leveraged publicly available transcriptomic data to select a subset of genes differentially regulated during nodule formation and affected by peptide application. We selected four genes belonging to the Histone acetyltransferase, methyltransferase, demethyltransferase and deacetyltransferase families which will next be edited using CRISPR-Cas9 technology to generate mutants, and sent for plant transformation and, subsequently examined for their phenotype and expression patterns during nodulation. This research will uncover genes involved in histone epigenetic modifications in *M. truncatula* during nitrogen fixation and their intricate relationship with peptide signaling.