TITLE: **Defensin like (DEFL) genes in *Medicago truncatula*: function and patterns of gene expression**

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For optimal plant health, legumes must deter a diversity of pests and pathogens, while encouraging beneficial microbes, such as nitrogen-fixing Rhizobium bacteria. We have previously identified genes encoding putative antimicrobial proteins that are specifically expressed in legume seeds or root nodules, the organ that houses the symbiotic rhizobia (1). Defensins are examples of cysteine-rich antimicrobial proteins made by plants, insects, and mammals. Defensins have been identified previously to inhibit the growth of various Gram-negative and Gram-positive bacteria, many fungi, some viruses and deter predation by some insects. Given these properties, Defensins represent promising candidates to engineer disease resistance in plants. Using computational methods, we have identified several hundred defensin-like genes (DEFLs) in the model legume *Medicago truncatula* (Medicago) and in *Arabidopsis thaliana* (Arabidopsis). These DEFLs have many hallmarks of well-characterized defensins (1). In Medicago, most of the DEFLs studied to date are strongly expressed in nodules. This poster will describe our preliminary work to evaluate the function of DEFL genes in Medicago and outline our continuing research. Preliminary assays have demonstrated the antimicrobial activity of representative DEFLs. We plan to assess global patterns of gene expression for >300 DEFLs and determine the localization of DEFL gene expression and protein activity. Four DEFLs have been selected for GFP tagged promoter-GUS constructs, immunolabelling and insitu RT-PCR studies. Preliminary results will be presented. To further characterize DEFL expression patterns, we plan to perform ~200 DNA microarray experiments using a custom microarray .

References:
1. Graham MA, Silverstein KA, Cannon SB, VandenBosch KA (2004) Computational identification and characterization of novel genes from legumes. Plant Physiology 135: 1179–1197.