Characterization of a NAC Domain Protein and a Novel Protein Suppressed in *Pinus taeda* Upon *Cronartium quercuum* f. sp. *fusiforme* Infection

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Cronartium quercuum f.sp. *fusiforme* is the causative agent of fusiform rust, one of the most devastating diseases of southern pines in recent history. Infection generally leads to the development of spindle-shaped galls on loblolly pine. These galls are formed primarily due to swelling, distortion and accumulation of the cells that make up woody tissue. Our lab has identified two partial pine cDNAs, DD55 and H1-F11, that are highly suppressed in galled tissue. DD55 is highly homologous to an unknown gene in *Arabidopsis thaliana* as well as genes in several other unrelated plants. H1-F11 encodes a NAC domain protein. Proteins that contain NAC domains are involved in maintaining the shoot apical meristem of herbaceous plants and in pathogen recognition and defense. The objective of this project is to determine the functions of the DD55 ortholog (ATHDD55) in *A. thaliana* and H1-F11 in pine, and thus infer how their suppression in fusiform rust galls contributes to disease development and (or) gall formation. Based on previous research and computational analyses of the transcripts, we hypothesize that they are involved in suppression of cell expansion, or the formation of areas of low wall flexibility that prevent cells from expanding abnormally in the vascular cambium. Alternatively, these proteins could be receptors of defense elicitors or stress signals. We have cloned the full-length sequence of ATHDD55, and are in the midst of preparing constructs for transgenic overexpression and RNA interference experiments. We will also determine the expression pattern of ATHDD55 with promoter-GUS fusions in *A. thaliana*. We are using a PCR-based method to isolate the full-length sequence of H1-F11. We hope to use immunolocalization to determine the expression pattern of H1-F1, and overexpress H1-F11 in pine to determine the function of this gene directly in pine.