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PROJECT 1 ABSTRACT
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We have sequenced and analyzed a cohort of over 12,000 ESTs from *Fusarium graminearum* strain PH-1 grown in culture. We have generated six cDNA libraries from cultures as follows: carbon-starved, nitrogen-starved, forming perithecia (two stages), and from infected heads (two different strains). Analysis of the ESTs from the fungus grown in culture, identified 1088 contigs and 1022 singleton sequences for a total of 2110 putative genes. We estimate these genes represent roughly one quarter of the *F. graminearum* genome. We expect *F. graminearum* has infection mechanisms that are different from foliar pathogens such as the rice blast pathogen *Magnaporthe grisea*. Our approach in this proposal is to continue to emphasize the functional aspects of genomics that will lead to new means of control, and to use existing ESTs to identify genes importance for *F. graminearum* pathogenesis. Our specific objectives are (1) To continue to search for new means of control by identifying processes essential for pathogenesis. To disrupt the genes identified by ESTs that may be important in pathogenicity or inoculum production. Experiment proposed for this objective will also serve to test different gene knockout approaches, including transposon and *Agrobacterium*-based approaches. (2) To use microarray analyses to identify genes that are important to inoculum development. Genomic sequencing will greatly enhance and facilitate identification of genes important to pathogenicity and inoculum development.