0203-YE-062 Cloning and analysis of Fusarium and wheat genes essential to FHB development and resistance in wheat.

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Grant #: 59-0790-1-078; $40,000; 1 Year
Research Area: BIO

PROJECT ABSTRACT
(1 Page Limit)

Certain genes, both of the pathogen *Fusarium graminearum* and the host wheat, are essential to FHB pathogenesis; and manipulation of their expression can be done in favor of FHB control. The goal of this project is to clone and study such essential genes, particularly those that control the initiation of FHB pathogenesis in wheat spikes. Our preliminary research compared gene expression profiles between FHB-inoculated and water-inoculated Sumai 3 spikes. Since the two groups of spikes have the same genotype and only differ in FHB infection, any differentially expressed gene observed should associated with either FHB pathogenesis or FHB resistance in Sumai 3. So far, eight FHB- associated expressed sequence tags (ESTs) have been found. Seven of them are only expressed in the FHB-inoculated Sumai 3 in a short window at early stage of FHB invasion. Four of the seven Sumai 3-specific ESTs were cloned and sequenced. Blasting Genbank with these ESTs as query sequences has revealed no homologue with any known *R* or *PR* gene. Our Southern analysis suggested that one of them belongs to a *F. graminearum* -gene, but has no homology with those in the Purdue *F. graminaerum* EST database. Our Northern analysis did not reveal its expression in cultured *F. graminearum*, either. It seems that it expresses after invading Sumai 3. Another group of interesting ESTs is found to be expressed in both the FHB-inoculated Sumai 3 and Wheaton spikes, but much stronger in the former than in the later. One of this kind was cloned and sequenced. Northern analysis indicated that, it belongs to *F. graminearum*, too, suggesting that it may represent an essential *F. graminearum* gene that interacts with wheat causing FHB. The gene expression represented by the two *F. graminearum* ESTs may be necessary to overcome Sumai 3's resistance. Obviously, our preliminary results have let us leap one step closer toward our goal. Therefore, our current objectives in this proposed research are: 1) continuing our screening for and cloning of differentially expressed ESTs of interest, 2) genetically confirming the association of the cloned ESTs with FHB or FHB-resistance and their potential usage as markers in breeding; 3) cloning the full-length cDNAs of the genes represented by the ESTs of interest with 5' race technology, and 4) analyzing the sequences of the full-length cDNAs to reveal their potential functions. Fulfillment of the objectives proposed here will reveal the full coding sequence of these interesting genes and their functions in FHB pathogenesis, and thus establish a solid foundation for cloning the full length genes from the corresponding genomes as well as for increasing our knowledge of *F. graminearum* -wheat interaction. The cloned genes or their derivatives will be used to produce transgenic plants to increase our capability in controlling FHB.