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Project ID: FY12-LE-020 **ARS Agreement #: 59-0206-1-113**

Research Category: **PBG** **Duration of Award: 1 Year**

Project Title: Vegetative Compatibility Genes for the Control of Fusarium Head Blight.

PROJECT 1 ABSTRACT

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Vegetative compatibility/incompatibility (vic) is a fungal version of self/nonself recognition and interaction that is known in many ascomycete fungi that results from two different alleles at a single locus being combined in the same cell and collectively triggering apoptotic cell death. Genes responsible for the vic interaction are neither similar to one another nor necessarily evolutionarily conserved. Thus, individual *vic* loci may have this function in only a relatively few species. New anti-fungal control measures that rely on the ability to trigger apoptotic cell death on demand could result from an understanding of the mechanism used to trigger apoptotic cell death in response to the presence of *vic* heteroalleles in a common cytoplasm.

The immediate goals of this proposal is (i) to map functional *vic* loci of *F. graminearum* onto an existing genetic map and localize them in the physical genomic sequence, and (ii) to clone and sequence several of these loci and prove that the vegetative incompatibility phenotype can occur in response to a difference in a single pair of alleles. Longer term goals include: (i) determining if the alleles detected are the only ones present in existing populations of *F. graminearum*, (ii) determining the extent to which polymorphism is found in field populations, and (iii) to identify transcription factors that are important in the regulation of the vegetative incompatibility phenotype. *F. graminearum* is an ideal fungus in which to conduct this research because the fundamental tools needed to conduct the project (recombination and physical maps, ability to make controlled crosses, and reliable transformation system) are in hand and need not be developed before the central question regarding the identity of the *vic* loci could be asked and answered.

vic loci cannot be placed directly on a physical map we will localize them first on a genetic map and then use the correlation of the genetic map and the physical genomic sequence to identify candidate open reading frames (ORFs). We will make a cross in which multiple *vic* loci are segregating and select progeny that all have the same set of alleles at the *vic* loci. ORFs in the identified regions of the physical sequence will be screened for their ability to confer a vegetative incompatibility phenotype, with ORFs near or containing HET or WD0 domains in these regions tested first. ORFs corresponding to one to several *vic* loci will be sequenced from Z-3639 during the term of the present proposal. Hypotheses regarding mode of action for triggering cell death can be formulated once at least two alleles have been sequenced for several loci.