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**Project ID: FY06-LE-056**

**FY05 ARS Agreement #: New**

**Research Area: PGG**

**Duration of Award: 1 Year**

**Project Title: Genetic Diversity and Genetic Mapping of *Gibberella zeae*.**

## **PROJECT 1 ABSTRACT**

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Our long-term goals are: 1) to understand the evolutionary potential of *Gibberella zeae* (*Fusarium graminearum*) either to change in aggressiveness or to adapt to control measures such as fungicides, biocontrol agents, and cultivar resistance; and 2) to study the genetic basis of ecologically or agriculturally important traits of the pathogen such as toxin production, fertility, or aggressiveness with the objective of improving control strategies. Studying population genetic structure can help us understand the evolutionary past and future potential of this pathogen. By using AFLP markers, we have found that populations of *G. zeae* in North America are genetically diverse, but generally well-mixed, even when separated by large geographic distances. *G. zeae* has been postulated to contain nine phylogenetic lineages that have been recently described as separate species. We have shown that representatives of at least some of these lineages are cross-fertile, and hypothesize that *G. zeae* is one large biological species. The difference between one species and nine could be very significant in terms of quarantine regulations and trade barriers. Immigrant strains with higher aggressiveness or that produce higher toxin levels or that have different toxin profiles could displace native strains in the United States or interbreed with the native strains leading to new combinations of genes for aggressiveness, host range, or toxin production.

The issue of movement and/or recombination of lineages is critical to the evolution of this fungus. We have identified interlineage hybrids in areas where multiple lineages occur in the same field. We will develop additional molecular markers to characterize these populations based on known genes and AFLP sequences, and use them as well as fertility and pathogenicity to better characterize the interlineage hybrids thus far identified. If cross-fertility between US and foreign strains is low, then movement of foreign pathogen germplasm into the US population will be slowed or limited to strains that can reproduce profusely in a clonal manner. Collectively, these studies could offer a glimpse of the future if Asian or South American strains are introduced into the United States, and provide a rigorous, independent test of the integrity and utility of the proposed nine-species model. The objectives of the research are:

Objective 1: Look for evidence of migration or the formation of inter-lineage hybrids using AFLP and DNA sequence markers. Identify genome regions that differ between lineages. Test aggressiveness and fertility of representative hybrids to estimate fitness components.

Objective 2: Identify genes for differences in fertility and localize these genes on genetic and/or molecular maps.