

**PI: Leslie, John F.**

**PI's E-mail: [jfl@ksu.edu](mailto:jfl@ksu.edu)**

**Project ID: FY08-LE-117**

**FY07 ARS Agreement #: 59-0790-6-064**

**Research Category: PBG**

**Duration of Award: 1 Year**

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

### **PROJECT 1 ABSTRACT**

(1 Page Limit)

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 eleven phylogenetic lineages that have been described as separate phylogenetic 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 eleven could be very significant in terms of quarantine regulations and trade barriers.

Objective 1: Determine DNA sequences for genes encoding pheromones and pheromone receptors from North and South American strains of *G. zeae*. We will sequence the genes encoding both pheromone/receptor gene pairs from the standard lineage tester strains of O'Donnell *et al.* and up to 500 strains from the field populations collected in different parts of North and South America. We will use these sequences to test the following hypotheses: (1) The *ppg1* and *pre2* pheromone/receptor pair are under purifying selection, the *ppg2/pre1* pheromone receptor pair are not. (2) Sequences will show evidence of recombination among phylogenetic lineages. (3) Gene genealogies of pheromones and pheromone receptors will be consistent with the phylogenetic lineages described by O'Donnell *et al.* (2004). These genes are of special interest since the changes may be used to help determine the age of the species and since mutations in them can adversely affect sexual fertility and homothallic reproduction.