

PI: Bowden, Robert

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Project Title: Genetic Mapping of Aggressiveness and Fertility Barriers in *Gibberella zeae*.

PI's E-mail: rbowden@plantpath.ksu.edu

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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, e.g. toxin production or aggressiveness, with the objective of improving control strategies. O'Donnell et al. (2000) reported that *Gibberella zeae* was composed of at least seven "phylogenetically distinct species among which gene flow has been very limited during their evolutionary history." They correlated these seven putative species with continent of origin, but also postulated some intercontinental movement of these lineages. From our preliminary studies of the population structure of *G. zeae* in Mexico, Uruguay, and Brazil (Vargas et al, 2001), we have evidence that several different lineages of *G. zeae* can be found in the same field. If different lineages of *G. zeae* come together and interbreed successfully in the field, hybrid strains could arise with new combinations of genes for aggressiveness, host range, toxin production, etc. Our preliminary data indicate that all lineages can cross with Lineage VII from North America, but with different degrees of fertility.

The objectives of this research are:

Objective 1: Create new mapping populations and genetic maps of *G. zeae*.

Objective 2: Determine the degree of interfertility between different lineages, and localize genes that control lineage interfertility on our genetic map.

Objective 3: Locate the genes that control aggressiveness on our genetic map

Understanding the genetic basis of important traits like interlineage fertility and aggressiveness could be important for future management strategies for Fusarium head blight. Our proposed experiments will continue the development of the genetic infrastructure for genomic research on this fungus. Mapping populations and associated genetic maps are valuable resources for locating and investigating both qualitative and quantitative traits. The maps can be used to compare genome organization among lineages and help determine chromosomal synteny and constraints on introgression of traits between lineages that could lead to more aggressive hybrid strains. We will determine levels of interfertility between lineages, which will help resolve whether the lineages deserve status as separate species. In selected crosses, we will analyze segregation of aggressiveness genes in the fungus. This genetic approach may reveal different genes than knock-out studies for three reasons: 1) regulatory mutants may be missed in knock-out studies, 2) epistasis can be revealed in segregating progenies, and 3) we may reveal important genetic differences between lineages in wide crosses that could go unnoticed with other approaches.