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Project Title: Diversity of American, Asian and Australian Populations of *Gibberella zae*.

PROJECT 1 ABSTRACT

(1 Page Limit)

Our long-term goals are: 1) to understand the evolutionary potential of *Gibberella zae* (*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. zae* in North America are genetically diverse, but generally well-mixed, even when separated by large geographic distances. *G. zae* has been postulated to contain nine phylogenetic lineages that have been recently described as separate species, with various continental origins, although some intercontinental movement has occurred. We have shown that representatives of at least some of these lineages are cross-fertile, and hypothesize that *G. zae* 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 will examine the genetic structure of *G. zae* populations from areas where lineages are already mixed for evidence of lineage displacement or hybridization. We also will compare well-characterized US and Mexican populations with those from South America, South Korea, and Southeast Asia-Oceania-Australia. These studies should offer a glimpse of the future if Asian or South American strains are introduced into the United States through agricultural trade, and will provide a test of the integrity and utility of the proposed nine-species model. The objectives of the research are:

Objective 1: Determine the population genetic structure of *G. zae* in samples from South America (Brazil and Uruguay), South Korea, Southeast Asia, Oceania, and Australia. Determine the degree of genetic isolation/similarity of these populations to one another. Look for evidence of migration or the formation of inter-lineage hybrids using AFLP and DNA sequence markers.

Objective 2: If putative hybrids or immigrants are found, then markers from the genetic map will be used to estimate introgression. Test aggressiveness of representative hybrids to estimate one component of fitness. Test the ability of hybrids to backcross to putative parental lineages to determine the speed with which foreign genetic information could be incorporated into US pathogen populations.