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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 such as toxin production 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 eight phylogentic lineages with various continental origins, although some intercontinental movement has occurred. We have shown that representatives of a number of these phylogenetic lineages are cross-fertile, and thus that *G. zeae* is a single biological species that is continuing to evolve. Immigrant strains with higher aggressiveness or that produce higher toxin levels or different toxin profiles might displace native strains in the United States. It also is possible that immigrant strains could interbreed with the native strains leading to new combinations of genes for aggressiveness, host range, or toxin production.

As the issue of movement and recombination of lineages is critical to the evolution of this fungus, we propose to study the genetic structure of *G. zeae* populations in geographic areas where lineages already are mixed to look for evidence of lineage displacement or hybridization. In addition to studies of populations in the United States, we will examine strains from South Korea, South America, 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. The objectives of this research are:

Objective 1: Determine the population genetic structure of *G. zeae* in samples from the United States, Mexico, South America (Brazil and Uruguay), South Korea, Viet Nam, Sulawesi (Indonesia), and Australia. Determine degree of genetic isolation/similarity of these populations to one another. Look for evidence of migration or the formation of inter-lineage hybrids.

Objective 2: If putative hybrids or immigrants are found, then markers from the genetic map will be used to estimate introgression. Test aggressiveness of hybrids to estimate one component of fitness. Test ability of hybrids to backcross to putative parental lineages.