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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 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 phylogenetic 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 might 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. We will test strains of three common lineages for aggressiveness towards the barley variety Chevron, the susceptible wheat variety Norm, and four resistant wheat varieties – Sumai 3, Hondo, Ning 7840, and Chokwang.

As the issue of movement and recombination of lineages is critical to the evolution of this fungus, we will examine the genetic structure of *G. zeae* populations in geographic areas where lineages already are mixed for evidence of lineage displacement or hybridization. We also will compare populations from the United States with those 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 Mexico, South America (Brazil and Uruguay), South Korea, Southeast Asia, and Australia. 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.

Objective 3: Determine pathogenicity/aggressiveness of representative strains from various lineages against susceptible and resistant wheat and barley varieties.