

**0203-LE-091 Diversity of North and South American and Korean populations of *Gibberella zeae*.**

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PROJECT ABSTRACT

(1 Page Limit)

For several years, we have studied the genetic structure (amount and distribution of genetic variation within and among populations) of populations of *Gibberella zeae* in North America. Genetic structure is affected by sexual and asexual reproduction, mutation, migration, genetic drift, and selection. Information on genetic structure and the processes that affect it can help us understand the evolutionary potential of this pathogen. Using AFLP markers, we found that populations in North America are genetically diverse, but well mixed, with no evidence of population subdivision.

O'Donnell et al. (2000) constructed a phylogeny of a worldwide collection of *G. zeae* based on sequences of six genes. They argued 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. Bowden and Leslie (1999) had previously reported interfertility between strains corresponding to three of these lineages.

An important question for growers is whether different lineages of *G. zeae* have already colonized North America through agricultural trade or human travel. Migrant aggressive strains could possibly displace our native strains. Fortunately, our unpublished data for North America found no evidence that this has yet occurred. Another critical issue is whether migrants could interbreed successfully with native strains. If they did interbreed, strains could arise with new combinations of genes for aggressiveness, host range (Carter et al., 2000), or toxin production.

Because the issue of movement and recombination of lineages is so important for the potential evolution of this fungus, we propose to study the genetic structure of *G. zeae* populations in geographic areas where lineages are probably already mixed to look for evidence of lineage displacement or hybridization. Our two areas of study will be South Korea and South America. It could offer a glimpse of the future if Asian or South American strains were accidentally introduced here.

The objectives of this research are:

Objective 1: Determine the population genetic structure of *G. zeae* in samples from Korea.

Objective 2: Determine the population genetic structure of *G. zeae* in samples from Brazil and Uruguay.

Objective 3: Compare populations from Korea and South America to North American populations. Look for evidence of migration and possible hybrids.

Objective 4: If putative hybrids are identified, use the genetic map to analyze the introgression of genes. Test aggressiveness of hybrids to estimate one component of fitness. Test ability of hybrids to backcross to parental lineages.