

0203-BO-093 Genetic mapping of aggressiveness and fertility barriers in *Gibberella zeae*.

PI: Bowden, Robert; E-mail: rbowden@plantpath.ksu.edu

USDA-ARS, 4007 Throckmorton Hall, Kansas State University, Manhattan, KS 66506

Grant #: NA, \$50,016, 1 Year

Research Area: EDM

PROJECT ABSTRACT

(1 Page Limit)

O'Donnell et al. (2000) recently 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) previously showed that three of the seven lineages could interbreed in the laboratory. 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.

Recently, we used AFLP molecular markers to construct a dense genetic linkage map from a cross between a strain of *G. zeae* from Kansas (lineage 7) and one from Japan (lineage 6). This map has already been used to locate the trichothecene toxin cluster and a second unlinked locus controlling toxin quantity. However, there are at least three regions in the map with distorted segregation of AFLP markers. Two of these can be explained by selection for auxotrophic markers. One appears to be associated with an intercalary chromosome inversion on linkage group II. Inversions and other chromosome rearrangements can be an important genetic isolation mechanism between populations. They can decrease the fertility of crosses because many meiotic recombination events are lethal. They also limit or eliminate recombination of genes within rearranged chromosome segments.

Although the seven lineages appear genetically divergent, much more information is needed about the degree to which their genome organization has diverged through chromosome rearrangements. This will determine chromosome compatibility during sexual recombination. Knowledge of genome organization and interfertility will also aid in the evaluation of whether these lineages deserve status as separate species. If they have diverged significantly, our current genetic map cannot represent all lineages of *G. zeae*.

We propose to develop several new mapping populations that can test the hypothesis that *G. zeae* strains from different lineages have different chromosome arrangements and therefore significant barriers to interfertility. In addition, there is a good chance that aggressiveness will segregate in one or more crosses. This would allow us to identify the genes that control aggressiveness and might eventually lead to improved control measures.

The objectives of this proposed research are:

Objective 1: Create several new mapping populations and genetic maps among different lineages of *G. zeae*. These will help us confirm and extend the results of our first mapping cross (North American by Asian) and to compare genomes of different lineages.

Objective 2: Determine the degree of interfertility between selected lineages.

Objective 3: Determine chromosome number and physical sizes for each parent of crosses. Correlate genetic linkage groups to physical chromosomes.

Objective 4: Test the mapping populations for segregation of aggressiveness. This variation would allow us to locate the genes that control aggressiveness on our genetic map.