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Project Title: Genetic Mapping in *Gibberella zeae*.

PROJECT 2 ABSTRACT

(1 Page Limit)

The long-term goals of our genetic mapping project are to: 1) create genetic linkage maps of important strains of *Gibberella zeae* (*Fusarium graminearum*); 2) use the maps to choose unlinked markers for population diversity studies, 3) use the maps for comparative genomics to understand the evolutionary potential to change in aggressiveness or to adapt to control measures such as fungicides, biocontrol agents, and cultivar resistance through sexual recombination; 4) study the genetic basis of ecologically or agriculturally important traits of the pathogen, *e.g.* toxin production or aggressiveness; and 5) use the maps to help order the genomic sequence. We have made good progress on each of these goals.

We propose to follow-up our successful lineage 6 x 7 linkage mapping and aggressiveness QTL research with a new lineage 3 x 7 map. Lineage 7 is present in the US and lineage 3 is present in central Mexico, so it is a relatively high risk for introduction to the US. This approach will allow us to genetically dissect both aggressiveness QTLs and fertility QTLs in the two lineages. This may be useful for expanding basic knowledge and may also give us information about future hybridization events between these lineages. For example, interlineage or interspecies hybrids are implicated in studies of new aggressive strains of *Phytophthora* (Brasier and Kirk, 2001). This genetic approach to aggressiveness may reveal different genes than knock-out studies for three reasons: 1) regulatory mutants may be missed in knock-out studies, 2) transgressive segregation and epistasis can be revealed in segregating progenies, and 3) we may reveal important genetic differences between lineages in wide crosses that could go unnoticed with other approaches. We also propose continued work on resolving unanchored sequences, ambiguities, and misalignments in genetic maps to continue the development of the genetic infrastructure for research on this fungus.

The objectives of this research are:

Objective 1: Create a new mapping population and linkage map of *G. zeae* lineages 3 x 7.

Objective 2: Locate QTLs that control aggressiveness on the new 3 x 7 map.

Objective 3: Locate QTLs that control interfertility on the new 3 x 7 map.

Objective 4: Continue anchoring of genetic and physical maps and resolve ambiguities