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**Project Title: Agroecology of *Fusarium graminearum* at a Cereal-Natural Grassland Interface.**

### PROJECT 3 ABSTRACT

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The relationship between *Fusarium graminearum* populations in agricultural fields and natural reservoirs is not well characterized. To better define their connection to each other, this project will examine pathogen populations found in three cereal fields surrounding a large natural grassland, Montezuma National Wildlife Refuge. This minimally managed preserve contains diverse grass species and has the potential to contribute inoculum and genetic diversity to pathogen populations in neighboring fields. Three objectives are proposed: 1) measure genetic diversity of *F. graminearum* in wheat fields and Montezuma, 2) assess the likelihood of inoculum exchange between grasslands and cereal crops, and 3) determine host specificity of genotypes using wheat and *Bromus inermis*

Pursuit of these objectives will increase our understanding of population biology at the interface of a natural space rich in host species and land devoted to agricultural production while providing the data to construct an ecological model. Genotypes from each of these locations will be characterized and compared using single nucleotide polymorphisms called from reduced representation genome sequences. Examining population structure across landscapes will allow us to assess the likelihood that significant amounts of inoculum and genetic diversity move between populations. Comparing genotypes collected from wheat and *B. inermis* will allow for assessment of host specificity.

The first of two hypotheses is that the overall population is highly structured, with genotypes clustering based on location or host. The alternative is that the population is largely homogenous and little structure is discernible. Clustering will indicate a potential for novel genotypes to move from grasslands to cereal fields, introducing heightened virulence, fecundity, or other detrimental traits to agricultural populations. A lack of structure could support the theory that reservoirs with diverse hosts preserve less virulent genotypes and act as a buffer against the development of detrimental traits in agricultural populations.

A model based on the results of this project could improve disease forecasting systems, estimate the impact of host reservoirs on field populations, and predict the emergence or suppression of genotypes from either location. The location chosen serves as a model system, and inferences will apply to interactions between cereal crops and any other nearby hosts or reservoirs such as weedy grasses, road sides, ditches, and fallow fields.

Exploring these facets of *F. graminearum* agroecology will bring new ideas for management strategies while building our fundamental understanding of the pathogen's evolution. The ability to better measure inoculum transfer will have direct implications for disease management and land use decisions while measuring the genetic diversity contained in fungal reservoirs is especially important to plant breeders as they consider the durability of crop resistance. A large culture collection including diverse and potentially unique genotypes and phenotypes will be maintained and made available for studies of plant-fungal interactions and breeding line susceptibility assays.