

## Identification of Adaptive Fungal Pathogen Resistance Loci in Switchgrass

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**Project Goals: Switchgrass (*Panicum virgatum*) is an important target species for domestic production of cellulosic biofuels, but it is susceptible to multiple fungal pathogens. The principle aim of our research is to identify the loci responsible for disease resistance in switchgrass and determine how effective those resistance loci are across geographic space. To accomplish this overarching goal, we will: 1) Characterize the pathogens associated with disease in switchgrass and quantify their geographic distributions. 2) Discover genetic loci for effective switchgrass disease resistance across different geographic locations. 3) Validate QTLs for pathogen resistance through controlled experiments. Overall, the discovery of loci and genes involved in resistance to specific pathogens will make crucial improvements of switchgrass cultivars possible through future breeding and gene editing efforts.**

Switchgrass is an important target species for domestic production of cellulosic biofuels. The principal aim of most switchgrass breeding programs is to develop high-yielding cultivars. However, as feedstock plantings expand, so will pathogen pressure. Unless controlled, fungal pathogens with explosive disease potential will likely drive yield declines and economic losses. Pathogen resistance can be developed through breeding programs that exploit natural genetic variation in disease resistance. Much of the functional genetic variation in switchgrass, including pathogen resistance, is distributed clinally with latitude as well as between ecotypes. In general, southern lowland cultivars are more resistant to fungal pathogens than northern upland cultivars.

Our research will utilize new and powerful genetic mapping populations to identify genomic regions responsible for divergence in disease resistance between northern upland and southern lowland switchgrass ecotypes. The mapping populations include 1) a northern upland X southern lowland four-way, pseudo-testcross F2 tetraploid genetic mapping population for Quantitative Trait Locus (QTL) mapping and 2) a new large panel of ~400 resequenced population accessions for genome-wide association studies (GWAS). These mapping populations have been planted at an unprecedented geographical scale, spanning ten common garden field sites distributed over 17 degrees of latitude in the central United States. Therefore, these populations are ideal for identification of regionally effective disease resistance loci (at one sites) as well as globally effective loci (across multiple sites).

To understand the geographic context for which specific disease resistance loci are effective, we are currently quantifying disease severity and the geographic distribution of pathogens across field sites. Overall, our research will achieve an unparalleled understanding of the genetic basis of disease resistance in switchgrass to multiple pathogens with yield-reducing potential. We will focus on three major goals:

Goal 1. Characterize the pathogens associated with disease in switchgrass and quantify their geographic distributions. We are currently in the process of identifying the specific

fungus pathogens associated with disease at each of the ten field sites, using a combination of microscopy and molecular methods. Analyses of pathogen distribution and environmental factors will be used to develop predictive models for pathogen presence across space.

Goal 2. Discover genetic loci for effective switchgrass disease resistance across different geographic locations. Disease severity of fungus pathogens is being quantified across mapping populations at all ten field sites. We will conduct QTL mapping and GWAS to identify regionally and globally effective disease resistance loci.

Goal 3. Validate QTLs and genes for pathogen resistance through controlled experiments. We will conduct controlled greenhouse experiments to confirm that QTLs identified in the field are effective against fungus pathogens present at particular field sites.

The proposed research builds upon many years of genomic resource, germplasm, and methods development for switchgrass by the collaborators. This strong foundation, combined with the collaborative synergy of the research team, positions this research to make rapid progress in identifying loci involved in disease resistance in this key bioenergy crop.

*This research was supported by the DOE Office of Science, Office of Biological and Environmental Research (BER), grant no. DE-SC0017883.*