

Identification of Adaptive Fungal Pathogen Resistance Loci in Switchgrass

David B. Lowry^{1,*} (dlowry@msu.edu), Acer VanWallendael¹, Shawn C. Kenaley², Gary C. Bergstrom²

¹Michigan State University, East Lansing, MI; ²Cornell University, Ithaca, NY

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.

Abstract:

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.

To identify quantitative trait loci (QTL) responsible for pathogen resistance, we conducted QTL mapping of rust infection on a mapping population planted across the central United States. The mapping population was created by crossing two northern upland accessions with two southern lowland accessions to create a four-way outbred population. This outbred mapping population was planted in 2015 at an unprecedented geographical scale, spanning ten common garden field sites distributed over 17 degrees of latitude in the central United States. Over the following three years (2016-2018), we collect ~149,000 rust infection scores on the mapping population across eight field sites. This data allowed us to identify two major QTLs and many minor QTLs contributing to rust resistance across field sites. The two major QTLs had large effects at northern field sites, but had little or no detectable effect at the southern field sites. This suggests that there are either different rust types in the north or that resistance is modified by local environmental conditions. To examine whether the abundance of different rust species was diverged between the north and the south, we used a combination of microscopy and molecular methods on field collected samples. This analysis found that *Puccinia panici*

was by far the dominant rust species present at all of the sites we surveyed, which suggests that species-level differences in resistance are not responsible for the QTL differences between the north and the south. We are currently developing population genetic approaches to determine whether population structure within *P. panici* could explain the latitudinal QTL patterns. We are also developing GIS maps of each field site to evaluate potential environmental covariates that could explain QTL variation among sites. In the summer of 2018, we planted a genome-wide association study (GWAS) mapping population at all of the field sites, as well as two field sites in central Mexico. We will score rust infection on those plantings and conduct a GWAS analysis, which should allow us to identify genes responsible for variation in rust resistance. Overall, our efforts are providing foundational research that will facilitate the future development of more rust resistant cultivars of switchgrass.

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