

## Genomic regions associated with pathogenicity in *Exserohilum turcicum* identified by linkage mapping in a biparental population

Pummi Singh\* (pummi@illinois.edu), Santiago X. Mideros, and **Tiffany M. Jamann**

University of Illinois at Urbana-Champaign, Urbana

### Project Goals:

Our research seeks to identify host-specificity genes in *E. turcicum* with the goal to understand how pathogens evolve to become pathogens of bioenergy crops. Our approach includes linkage mapping of a biparental population of *E. turcicum* strains with specificity to sorghum and maize and analysis of *in planta* and *in vitro* transcriptomes of the host-specific strains.

### Abstract text

The filamentous fungus *Exserohilum turcicum* is a significant pathogen of sorghum and maize and is the causal agent of sorghum leaf blight (SLB) and northern corn leaf blight (NCLB). Both diseases can cause significant yield losses, and this pathosystem serves as a model for understanding host jumps. Strains of *E. turcicum* are typically host specific and infect either sorghum or maize. Pathogen host specificity is attributed to a single locus for each host, which facilitates host jumps between maize and sorghum in regions where maize and sorghum are co-cultivated. To test the hypothesis that a single locus in *E. turcicum* underlies specificity to maize and a second locus underlies specificity to sorghum, we generated a biparental population of *E. turcicum*. We crossed strains specific to maize and sorghum, phenotyped the population for virulence on sorghum and maize, genotyped the population to create a linkage map of *E. turcicum*, and located candidate pathogenicity genes. A total of 190 ascospores from 35 pseudothecia were isolated from the biparental cross. Greenhouse phenotyping of the biparental population (n = 144) showed independent inheritance of virulence, as indicated by a 1:1:1:1 segregation for virulence to maize, sorghum, both maize and sorghum, and avirulence to both crops (p=0.09). The population and host specific parent strains were genotyped using genome skim sequencing on an Illumina NovaSeq platform, resulting in over 780 million reads. A total of 32,635 variants including single nucleotide polymorphisms and indels were scored. A genetic map consisting of 17 linkage groups spanning 3,069 centimorgans was constructed. The maize and sorghum host specificity genes mapped to distinct loci on different linkage groups, confirming that a single locus in *E. turcicum* strains confers pathogenicity to sorghum and maize. Fungal transcriptome analysis from *in planta* infections and axenic cultures is in progress. The results from current research are expected to have significant impact on targeted breeding efforts towards improved host resistance and reduction in yield losses of biofuel crops along with a better understanding of the *E. turcicum*- Andropogoneae pathosystem.

*Funding statement- This work is funded by DOE award number DE-SC0019189 (Plant Feedstocks Genomics).*