Genomic dissection of anthracnose resistant response in sorghum [*Sorghum bicolor* (L.)]

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Project Goals:

The goal of this project is to use a genomics-based approach to identify anthracnose resistance loci from diverse sorghum germplasm, to establish against which pathotypes these loci protect, and to determine the disease resistance mechanism of at least one of these genes. This information will provide plant breeders a tool kit that can be used to maximize levels of resistance in different areas of production.

We developed three sets of recombinant inbred lines (RILs) derived from the cross of three resistant sources (SC112-14, QL3 and IS18760) to a commonly high susceptible line PI609251. A high density linkage map was constructed for the RIL population derived from the cross of SC112-14 x PI609251 using 1,671 single nucleotide polymorphism sites (SNPs). We later used this map to select a reduced sample of individuals with a high number of recombinant breakpoints which were evaluated under greenhouse conditions against 10 pathotypes from Texas, Georgia, Arkansas, and Puerto Rico. In parallel, the three RILs were evaluated under field conditions at Gainesville, FL, Tifton, GA, and College Station, TX. In addition, we identified two QTL associated with the resistant response in sorghum line Bk7 (chromosome 7 and 9; Felderhoff *et al*. 2016,G3), which are now being analyzed in more detail to identify the underlying resistance genes.

Anthracnose resistance responses were observed for the RILs derived from SC112-14 at Gainesville, FL, Tifton, GA, and College Station, TX. However, the RILs derived from QL3 and IS18760 showed a resistance response only against pathotypes from College Station, TX. The linkage mapping analysis of SC112-14 identified one locus at distal region of chromosome 5 which is controlling the resistance response against pathotypes from the three locations (Fig. 1A). Remarkably, some RILs showed variable resistant response across locations indicating this locus may be constituted by a cluster of multiple resistance genes. Greenhouse evaluation against multiple particular pathotypes validated this locus and delimited its location to a 250 Kb genomic region (Fig. 1B). The observed difference among greenhouse and field evaluations indicated that both analysis are complementary and necessary to dissect the anthracnose resistant locus. We also determined that resistant locus of in chromosome 9 present in sorghum line Bk7 enclosed 12 candidate genes that were validated to be expressed in leaves.

We will be evaluating a larger number of segregating progenies to reduce this genomic region to candidate genes for functional analysis. Simultaneously, we are constructing high density genetic maps for RILs derived from QL3 and IS18760 in order to map and study their resistance. The 12 candidate genes from Bk7 inheritance study are now being targeted for down-regulation using virus-induced gene silencing.

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Figure 1. Anthracnose resistant locus present in line SC112-14. **A)** Linkage map analysis based on field evaluations at Florida, Georgia and Texas; **B)** Linkage map analysis based on greenhouse evaluation against particular pathotypes from Texas, Georgia, Arkansas and Puerto Rico.