Genome-wide association analysis of anthracnose resistance response in the NPGS sweet sorghum collection

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Abstract Text:
Anthracnose, caused by the fungal pathogen *Colletotrichum sublineolum* in Kabat and Bubák (syn. *Colletotrichum graminicola* [Ces.] G.W. Wilson), is a prevalent disease in warm and humid sorghum cultivation regions. In highly susceptible lines, anthracnose can cause substantial yield losses (up to 50%) of both grain and biomass. Several recent studies have identified loci responsible for broad-spectrum resistance to anthracnose in sorghum accessions on chromosomes 5 and 9, however, these resistance sources are in grain sorghum germplasm. **The identification of novel anthracnose resistance sources present in sweet sorghum germplasm will expedite the development of new resistant sweet sorghum cultivars and hybrids by avoiding time-consuming introgression breeding approaches with non-sweet sorghums serving as donor of the resistance alleles**.

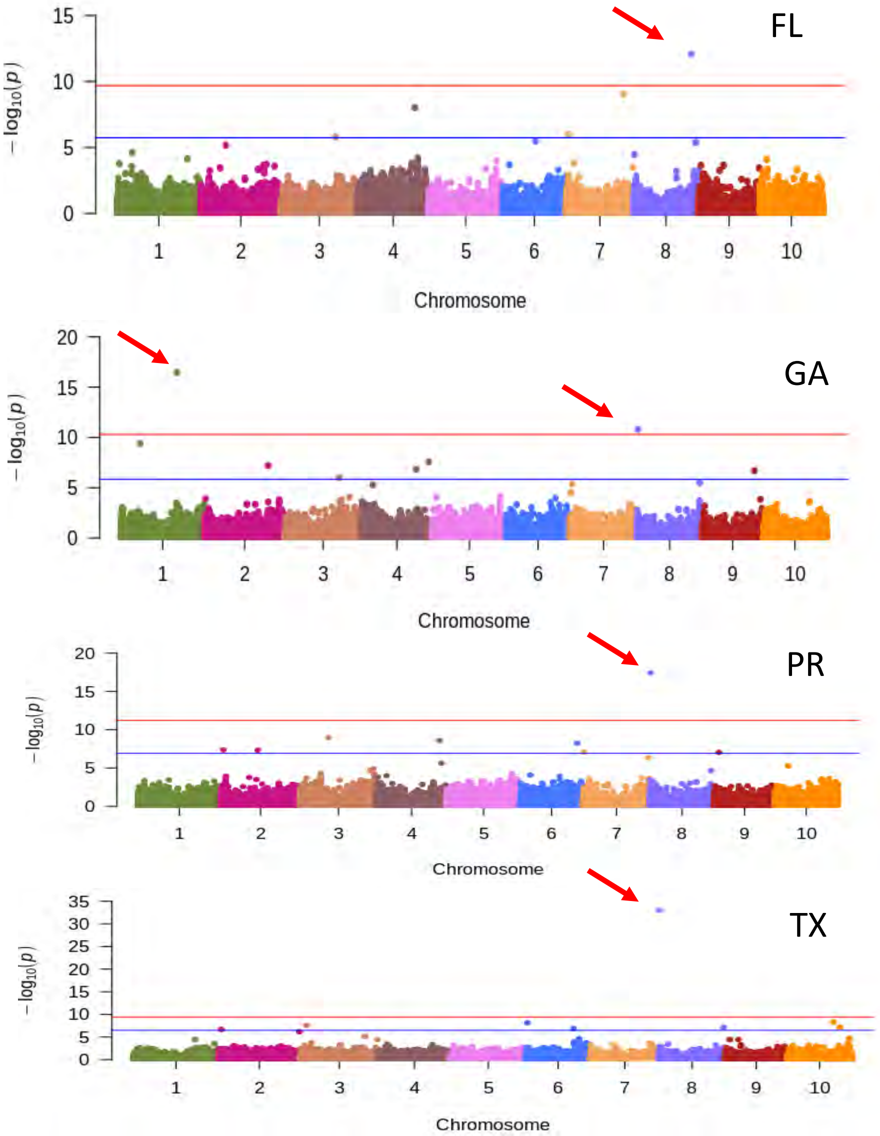
The sweet sorghum collection of the USDA-ARS National Plant Germplasm Systems (NPGS) is the primary source of genetic diversity for the development of new sweet sorghum varieties for biofuel production. Recently, we established a sweet sorghum diversity panel (SWDP) of 233 accessions that includes advanced breeding materials and represent ~15% of the NPGS sweet sorghum collection. A two-year replicated field trial of the SWDP for anthracnose resistance response in Texas, Georgia, Florida and Puerto Rico identified 29 accessions resistant across locations, while another 145 accessions showed variable resistance response against location pathotypes. Phylogenetic analysis among resistant accessions suggests that the SWDP contains multiple sources of resistance. However, it is yet unknown if these resistance sources are identical to those identified in grain sorghum germplasm.

A genome-wide association study (GWAS) based on 157,843 single-nucleotide polymorphisms (SNPs) and employing the fixed and random model Circulating Probability (farmCPU) analysis identified three genomic regions associated with anthracnose resistance (Figure 1). The distal genomic region of chromosome 8 was associated with resistance response observed in Florida, and an associated SNP was located within an *R*-gene. Genomic regions on chromosomes 1 and 8 were associated with resistance responses observed in Georgia. Candidate gene analysis identified a cluster containing genes involved in salt stress/antifungal activity on chromosome 1 and an *R*-gene on chromosome 8. The candidate genes at both loci were in linkage disequilibrium and less than 15 kb downstream of the associated SNP. Resistance response in Texas and Puerto Rico were associated with a genomic region on chromosome 8 that includes an *R*-gene. Candidate *R*-genes among Puerto Rico, Texas and Georgia were 18 kb apart suggesting that each gene might be specific for each location's pathotype.

The results of this study indicate that the NPGS sweet sorghum germplasm collection contains multiple anthracnose resistance sources. A genomic scan revealed these resistance sources are

different from those known in grain sorghum germplasm. It is imperative that these resistance sources be used effectively to increase the durability of anthracnose resistance of new biofuel sorghum varieties. When the goal is to produce a particular cultivar across a large geographic area, multiple sources of resistance effective against the local pathotypes need to be combined.

Figure 1. Genome-wide association analysis for anthracnose resistance response among 233 NPGS sweet sorghum accessions evaluated in Florida (FL), Georgia (GA), Puerto Rico (PR), and Texas (TX) during 2017 and 2018.



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