Genomic dissection of anthracnose resistance response in the sorghum nested association mapping populations

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Abstract Text:

Sorghum [*Sorghum bicolor* L. (Moench)] is C4 tropical grass used for food, animal feed, forage, and bioenergy that is drought-tolerant and has lower nutrient requirements compared to many other grasses. The advantages of sorghum as biofuel feedstock are expected to further increase the area of sorghum cultivation. The establishment of sorghum production outside of its natural dry environment presents a challenge due to the presence of multiple abiotic and biotic constraints that can reduce biomass and seed yield and quality. 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.

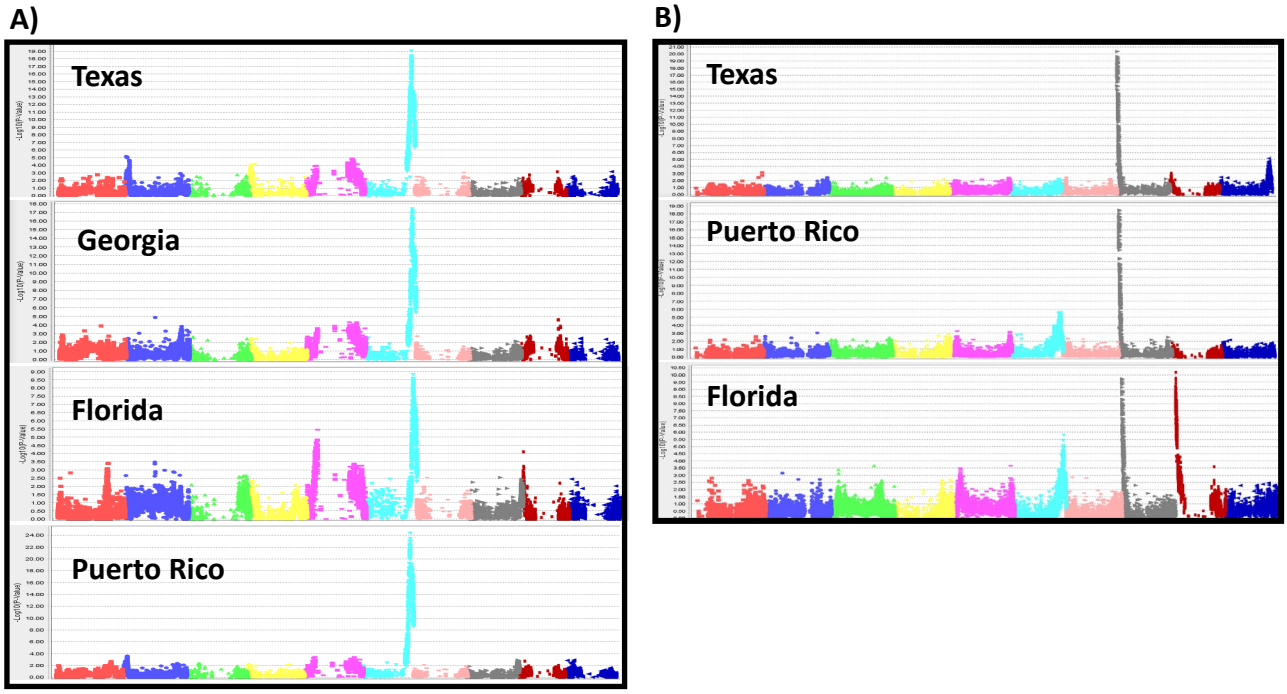
Several recent studies have identified loci responsible for broad-spectrum resistance to anthracnose in tropical and temperate adapted sorghum germplasm. The evaluation of the sorghum association panel (SAP) identified 40 accessions resistant across multiple locations. Genome-wide association analysis identified three loci at the distal region of chromosome 5, which explains 56% of the observed phenotypic variation. Therefore, other resistant sources present in the SAP were not detected due to their low frequency (<0.05) or because they were masked by overcorrection for population structure. Among the 40 resistance accessions identified in the SAP, we determined that three (SC1103, SC265 and SC1345) were used as founder lines in the sorghum nested association mapping (NAM) populations. **Therefore, to uncover resistance sources present in the SAP, we evaluated these three sets of recombinant inbred lines (RILs) populations for anthracnose resistance.**

The NAM population was developed to provide a germplasm and genomic resource that increases the power for the genetic dissection of economically important traits. Ten diverse lines representing the genetic variation of the SAP were crossed with a common parental line (RTx430) for the development of ten sets of >200 RILs each. A two-year replicated field trial of SC1103 and SC265 RILs populations in Texas, Georgia, Florida and Puerto Rico found segregation for anthracnose resistance response. High-density recombination linkage maps previously constructed based on genotyping by sequencing (GBS) of the RILs populations was used to delimit genomic regions associated with resistance response based on linkage analysis. Genome scan for SC265 RILs populations associated the distal regions of chromosome 6 with resistant response across locations (Figure 1A). This genomic region explains up to 46% of the observed phenotypic variation. Genome scan for SC1103 RILs populations associated the top region of chromosome 8 with resistance response in Texas and Puerto Rico (Figure 1B). This region and the top region of chromosome 9 were associated with resistance response in Florida, while no association was detected in Georgia. These genomic regions explain up to 40% of the

observed phenotypic variation. Based on a one year replicated trial of the SC1345 RILs population in Puerto Rico, the distal region of chromosome 5 was associated with resistance response. Since this region include the locus Sb005G172300 (i.e. genetic control similar to previously characterized in line SC112-14) and SC1345 line has the resistant allele this RIL population was not evaluated across location.

The results of this study indicate that SC1103 and SC265 contains new anthracnose resistance sources that could not be detected by the GWAS of the SAP. The development of other RILs populations is necessary to uncover novel resistance sources in the SAP. These new resistance sources present in temperate adapted germplasm are immediately available for sorghum breeding programs.

Figure 1. Anthracnose resistance response in sorghum nested association mapping populations evaluated at Texas, Georgia, Florida and Puerto Rico in 2019 and 2020. A) Genome scan for recombinant inbred lines derived from SC265; B) Genome scan for recombinant inbred lines derived from SC1103.



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