

Anthracnose resistant response of the USDA-NPGS sweet sorghum [*Sorghum bicolor* (L.)] germplasm collection

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Project Goals:

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. Although it has been demonstrated that the collection contains valuable genes/alleles that can aid the commercial production of biofuels, few sweet sorghum varieties have been phenotyped for biofuel applications. Anthracnose is a disease caused by the fungal pathogen *Colletotrichum sublineolum* that currently limits large-scale commercial production of sorghum in the southeastern U.S. and Caribbean. **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.**

We evaluated 1,801 sweet sorghum accessions from the NPGS in single replicated trial in Puerto Rico during 2015 and 2016. The analysis identified 654 accessions with Brix value >10.0° of which 171 accessions had values >15.0°. Based on Brix values and geographic origin a subset of 233 sweet sorghum accessions were selected for further genotypic and phenotypic characterization. This diversity panel is composed of accessions from 19 countries, including advanced breeding materials and it represents ~10-15% of the NPGS sweet sorghum collection.

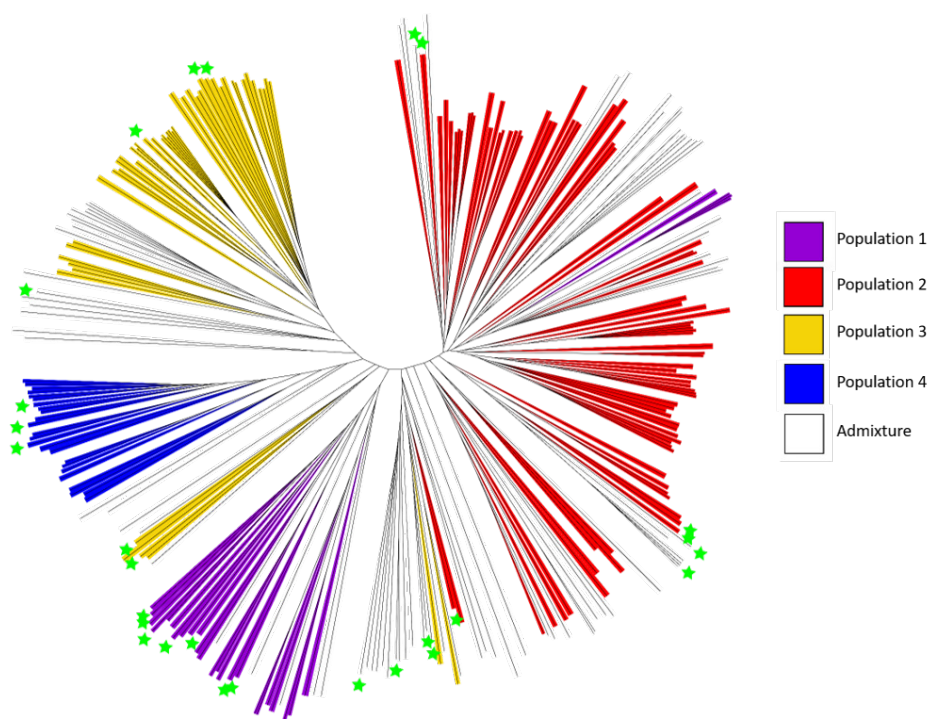
Genotype-by-sequencing analysis of the diversity panel identified 157,843 single-nucleotide polymorphism (SNPs). Population structure analysis based on 2,345 unlinked SNPs separated most of the accessions (~70%) of the panel into four populations and an admixture group (~30%) (**Figure 1**). The population structure could be related with breeding programs, since most of the advanced germplasm is highly genetically related and is distributed among three populations. The anthracnose resistance response of the diversity panel was determined based on replicated trial evaluations in Texas, Georgia, Florida and Puerto Rico during 2017 and 2018. The average of anthracnose resistance response in the diversity panel was less than 3.0 (on a 1 to 5 scale), indicating that most of the accessions were infected at the bottom leaves. A total 145 accessions showed different anthracnose resistance responses among different locations, while 29 and 59 were resistant and susceptible, respectively, at all four locations. The 29 resistant accessions were found at higher frequency in one population (**Table 1**).

An adequate knowledge of the genetic diversity in anthracnose-resistant sweet sorghum germplasm is necessary to effectively use the diversity in sorghum breeding programs. An unrooted neighbor-joining tree was generated to understand the genetic relationships among the 29 resistant accessions across locations (**Figure 1**). Anthracnose resistant accessions were present in each of the four populations. Nevertheless, the high genetic relationship among some resistant accessions suggests that the genes in these accessions are identical by descent (i.e., the accessions share the same resistance genes). Certainly, a limited number of anthracnose resistance genes are controlling the resistance response observed in the NPGS sweet sorghum collection.

Table 1. Frequency of the anthracnose resistant response in a subset of sweet sorghum germplasm from NPGS germplasm collection

Population	Resistant	Susceptible	χ^2	Means \pm S.D.
Population 1	8	19	0.00	2.2 \pm 0.2
Population 2	4	69	0.08	3.0 \pm 0.7
Population 3	5	30	0.60	2.4 \pm 0.5
Population 4	3	15	0.45	2.8 \pm 0.6
Admixture	8	63	0.72	2.7 \pm 0.7

Figure 1. Unrooted neighbor-joining tree of a subset of sweet sorghum accessions from NPGS germplasm collection. Anthracnose resistant accessions are labeled with green stars.



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