

Evaluation of a Subset of Ethiopia Sorghum Collection Germplasm from the National Genetic Resources Program of the United States Department of Agriculture for Anthracnose Resistance

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Abstract

Globally, one of the most devastating diseases of sorghum is anthracnose incited by *Colletotrichum sublineola*. During the 2019 and 2020 growing seasons, 94 and 64 accessions from the Ethiopian sorghum germplasm collection maintained by the National Genetic Resources Program of the United States Department of Agriculture were evaluated for anthracnose resistance. Seeds were planted in 1.8 m rows with 0.9 m row spacing in a randomized complete block design. The accessions and checks were replicated three times and 30 days after planting, inoculated by placing *C. sublineola*-colonized grains in the plant whorls. A total of 30 accessions, including PI533918, PI533923, PI534131 and PI534151 were resistant to the disease in both years. These identified resistant sources can be used in breeding programs to develop anthracnose-resistant lines and hybrids.

Keywords

Sorghum, *Colletotrichum sublineola*, Accession, Fungi

1. Introduction

Globally, sorghum [*Sorghum bicolor* (L.) Moench] ranks fifth behind wheat, rice, maize, and barley in cereal production and will play an integral role in fu-

ture food stability, especially in resource-poor drier agro-ecological regions [1] [2] [3]. This versatile drought-tolerant crop will continue to gain in importance for its varied uses as the environment becomes less predictable due to climate change and those looking for healthy diet options [2] [4] [5] [6]. Nevertheless, increases in sorghum production will likely increase biotic stresses due to microorganisms, such as the fungus *Colletotrichum sublineola* (Henn.), a causal agent of anthracnose [4]. Since sorghum anthracnose was first reported in 1902 in Togo, West Africa, the disease is now present in all humid regions where the crop is planted [7]. The pathogen infects all above-ground parts of the sorghum plant; however, the foliar phase of the disease is the most common [7]. Symptoms on infected leaves are characterized by small, circular, or elongated spots, and under favorable conditions, these lesions will coalesce and numerous acervuli are produced at the center [7]. Although estimating yield losses due to anthracnose can sometimes be problematic due to the level of susceptibility of the cultivar/line being evaluated, research has shown that under epidemic conditions, losses may range from 30% - 86% [1] [7] [8] [9]. Acharya *et al.* [10] reported that for every percent increase in sorghum anthracnose severity, 27 to 85 kg/ha losses in grain yield could be expected. In Brazil, 86% yield loss was measured on BR009 when the level of anthracnose severity on the genotype reached 100% [1].

The most effective and environmentally sound management strategy for sorghum anthracnose is the use of resistant genotypes [2] [11] [12] [13] [14] [15]. Many resistant sources from different sorghum-growing regions have been reported [1] [11] [12] [13] [15] [16] [17] [18] [19]. However, due to the hyper-variable nature of *C. sublineola* [8] [20] [21] [22], there is a need to continuously identify sources with diverse resistance genes. Ethiopian sorghum collection from the National Genetic Resources Program (NGRP) of the United States Department of Agriculture is an important genetic resource for sorghum improvement [15].

Thus, the aim of this communication was to evaluate a subset of the Ethiopian sorghum germplasm against *C. sublineola* to identify resistant sources.

2. Materials and Methods

Field trial: A total of 94 accessions in 2019 and 64 accessions in 2020 from the Ethiopian germplasm collection maintained by the USDA-ARS, Plant Genetic Resources Conservation Unit, Griffin, Georgia, and checks (SC748 resistant check and susceptible checks BTx623 and TAM428) were evaluated against *C. sublineola* during the 2019 and 2020 seasons in Isabela, Puerto Rico. Seeds were planted in 1.8 m rows with 0.9 m row spacing in a randomized complete block design. The accessions and checks were replicated three times. Standard field practices were used. Weeds were controlled with hand hoeing.

The protocols for field inoculation and disease assessment were as previously described by Prom *et al.* [23]. Briefly, agar plugs from two isolates of *C. sublineola* were put on autoclaved sorghum grains and mixed periodically to allow the

grains to be completely colonized by the pathogen. The colonized grains were placed in the plant whorls 30 days after planting. Disease assessment was conducted prior to harvest using a 1 - 5 scale: 1 = no symptoms or chlorotic flecks on leaves; 2 = hypersensitive reaction (reddening) with no acervuli; 3 = infected bottom leaves with acervuli; 4 = necrotic lesions with acervuli on bottom leaves and spreading to middle and upper leaves but not the flag leaves; and 5 = most leaves are dead due to infection, including infection on the flag leaf. The symptom types were then categorized into two reaction classes, resistant = rated as 1 or 2; and susceptible = rated as 3, 4, or 5.

Statistical Analysis

Mean scores for anthracnose severity were analyzed using the commands PROC GLIMMIX (SAS Institute, SAS version 9.4, Cary, NC). PROC FREQ was used to calculate the frequencies and probabilities for the resistant and susceptible responses.

3. Results and Discussion

The most effective option for managing sorghum anthracnose in production fields is the use of resistant sources [2] [12] [13] [14] [15] [24] [25]. However, the presence of different pathotypes of the pathogen [8] [20] [21] [22] requires the need to continually evaluate diverse germplasm to identify stable resistant sources.

In this study, a subset of the Ethiopian sorghum collection germplasm was challenged against a mixture of *C. sublineola* isolates from Isabel, Puerto Rico. The results showed that 30 accessions, including PI251637, PI330296, PI533799, PI660638, and PI669636 were resistant during the 2019 and 2020 evaluations (Table 1). With few exceptions, Erpelding [16] and Cuevas *et al.* [18] evaluated different subsets of sorghum accessions from the Ethiopian collection and noted many resistant sources. Accessions PI533799, PI533828, PI533918, PI533923, PI534131, and PI534151 were found to be resistant to anthracnose in this study and when evaluated by Erpelding [16] during the 2008 and 2009 growing seasons in Isabela, PR. In Ethiopia, 366 sorghum landraces evaluated for anthracnose resistance in 2016 and 2017 showed that several landraces, including 71708, 71420, 16133, and 238388 with good agronomic traits exhibited low levels of anthracnose severity [24]. Dessalegn *et al.* [25] also screened 225 Ethiopian sorghum landraces across several locations and identified lines 71552, 2001PWCo II #025, 2001PWCo II #034, and 2001PWCo II #036 with good agronomic performance and resistance reactions to anthracnose.

Variability in anthracnose response to anthracnose by accessions from Ethiopia and other locations from sorghum collections maintained by NGRP has been reported [11] [16] [17] [18]. In the current study, 20 accessions in 2019 and 10 accessions in 2020 had variable responses to anthracnose. There are several factors that may contribute to the different responses between the two evaluation periods such as the weather conditions, the hyper-variability of the anthracnose pathogen, heterogeneity within some of the accessions as a result of seed mixture,

Table 1. Reaction of 94 sorghum accessions from Ethiopia against isolates of *Colletotrichum sublineola* from Puerto Rico.

Accession	Reaction type	2019	Reaction type	2020
PI665168	S	5.0	R	2.0
PI665165	S	5.0	R	2.0
PI534157	S	5.0	S	3.0
PI609251	S	5.0	S	4.0
PI148101	S	5.0	S	3.0
PI570841	S	5.0	S	4.0
PI576380	S	5.0	R	2.0
PI267618	S	5.0	S	4.0
PI533800	S	5.0	S	3.0
PI148086	S	4.0	V	3/2/2
BTx623	S	4.0	S	4.0
TAM428	S	4.0	S	4.0
PI660637	S	4.0	-	-
PI330000	S	4.0	-	-
PI534146	S	4.0	S	4.0
PI267588	S	4.0	S	3.0
PI576377	S	4.0	-	-
PI534115	S	4.0	R	2.0
PI330276	S	4.0	S	4.0
PI668763	S	4.0	V	3/2/2
PI644717	S	4.0	R	2.0
PI533920	S	4.0	R	2.0
PI661148	S	3.0	S	3.0
PI564780	S	3.0	-	-
PI533792	S	3.0	R	2.0
PI329346	S	3.0	V	2/2/3
PI668757	S	3.0	S	4.0
PI669703	S	3.0	V	3/2/2
PI276822	S	3.0	-	-
PI669637	S	3.0	-	-
PI267557	V	2/2/5	R	2.0
PI330819	S	3.0	-	-
PI534121	V	2/3/3	-	-
PI197462	V	1/2/3	-	-

Continued

PI668726	V	2/2/3	R	2.0
PI644502	V	2/3/3	R	2.0
PI669702	V	2/2/3	V	2/3/2
PI329313	V	2/2/3	-	-
PI534152	V	3/2/2	-	-
PI330230	V	3/2/2	-	-
PI669795	V	3/2/2	V	3/2/2
PI669699	V	2/2/3	R	2.0
PI669698	V	3/2/2	V	2/3/2
PI669704	V	3/2/2	-	-
PI534001	V	2/3/2	R	2.0
PI330255	V	2/2/3.	R	2.0
PI147833	V	3/2/2	-	-
PI564778	V	2/3/2	R	2.0
PI330821	V	2/3/2	-	-
PI564777	V	3/2/2	V	2/2/3
PI267655	V	2/2/3	-	-
PI669636	R	2.0	R	2.0
PI330271	R	2.0	-	-
PI257601	R	2.0	-	-
PI660638	R	2.0	R	2.0
PI663869	R	2.0	-	-
PI665166	R	2.0	V	2/2/3
PI330764	R	2.0	-	-
PI533828	R	2.0	-	-
PI576381	R	2.0	R	2.0
PI668723	R	2.0	R	2.0
PI668717	R	2.0	R	2.0
PI564779	R	2.0	R	2.0
PI576375	R	2.0	V	2/4/2
PI665167	R	2.0	R	2.0
PI665169	R	2.0	R	2.0
PI534116	R	2.0	R	2.0
PI669638	R	2.0	R	2.0
PI576431	R	2.0	R	2.0
PI533799	R	2.0	R	2.0
PI576344	R	2.0	R	2.0

Continued

PI267606	R	2.0	R	2.0
PI267565	R	2.0	R	2.0
PI576376	R	2.0	R	2.0
PI576379	R	2.0	R	2.0
PI251637	R	2.0	R	2.0
I330004	R	2.0	-	-
PI533903	R	2.0	R	2.0
PI194355	R	2.0	R	2.0
SC748	R	2.0	R	2.0
PI564776	R	2.0	R	2.0
PI533918	R	2.0	R	2.0
PI534131	R	2.0	R	2.0
PI534151	R	2.0	R	2.0
PI329968	R	2.0	-	-
PI533923	R	2.0	R	2.0
PI267624	R	2.0	R	2.0
PI329697	R	2.0	-	-
PI669639	R	2.0	-	-
PI330275	R	2.0	-	-
PI330299	R	2.0	R	2.0
PI330289	R	2.0	-	-
PI330291	R	2.0	R	2.0
PI330301	R	2.0	-	-
PI330297	R	2.0	-	-
PI330296	R	2.0	R	2.0
PI330295	R	2.0	-	-

Disease assessment was based on a 1-5 rating scale (Prom *et al.*, 2009). The symptom types were then categorized into two reaction classes, resistant (R) = rated as 1 or 2; and susceptible (S) = rated as 3, 4, or 5. V = Variable response.

planting of several different lines in farmers field, place, and method of collection. **Figure 1** shows that 45 accessions exhibited resistance response and 29 accessions were susceptible in 2019, while in 2020, 43 accessions exhibited resistance response and 11 accessions were susceptible. The frequency of scoring an accession as either resistant or susceptible was 61% and 39% in 2019, respectively (**Table 2**). In 2020, the frequency of resistance response was 80% and susceptible response was 20% (**Table 2**). This work confirmed other studies [16] [18] which noted that the Ethiopian sorghum accessions' response to anthracnose was skewed towards resistance.

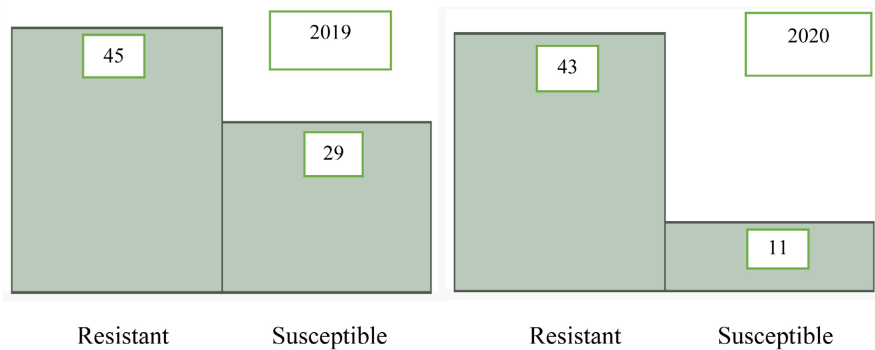


Figure 1. The number of anthracnose-resistant and susceptible lines in 2019 and 2020.

Table 2. Frequencies for resistant and susceptible responses in 2019.

Level	2019		2020	
	Count	Frequency	Count	Frequency
Resistant	45	0.60811	43	0.79630
Susceptible	29	0.39189	11	0.20370
Total	74	1.00000	54	1.00000

4. Conclusion

The hyper-variability of the pathogen coupled with the changing environment requires a continuous need to evaluate sorghum germplasm to identify resistant sources to anthracnose. This study identified resistant sorghum accessions such as PI533918, PI533923, PI534131, and PI534151 that can be used in breeding programs to develop stable anthracnose-resistant lines and hybrids. Future research will include understanding the nature and inheritance of the genes for resistance to these four accessions.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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