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Assessment of sorghum germplasm from Burkina Faso and South Africa to identify new sources of resistance to grain mold and anthracnose

Hugo E. Cuevas [a, *], Louis K. Prom [b], Thomas Isakeit [c], Ghada Radwan [c]

[a] USDA-ARS, Tropical Agriculture Research Station, 2200 Pedro Albizu Campos Ave. Ste. 201, Mayaguez, PR, 00680, USA
[b] Southern Plains Agricultural Research Center, USDA-ARS, College Station, TX, 77845, USA
[c] Department of Plant Pathology and Microbiology, Texas A&M University, College Station, TX, 77843, USA

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ABSTRACT

Sorghum is an important worldwide crop whose yield can be significantly reduced by anthracnose (*Colletotrichum sublineola*) and grain mold diseases (multiple fungi). The identification of new genetic sources of resistance to both diseases is imperative for the development of new sorghum varieties. To this end, a total of 80 exotic germplasm accessions from Burkina Faso (BFA) and South Africa (ZAF) were evaluated for anthracnose and grain mold resistance during two planting periods in 2012 at the USDA-ARS experimental farms in Isabela, Puerto Rico. Twelve accessions were resistant to anthracnose during both evaluations of which 10 are originally from BFA. The anthracnose resistant accessions identified herein had a hypersensitive reaction characterized by lesions having red and purple color. Likewise, 9 accessions exhibited grain mold resistance after being inoculated with a mixture of a conidial suspension of *Fusarium thapsinum*, *Fusarium semitectum*, and *Curvularia lunata* during both periods. Eight of these accessions (PI 586182, PI 586186, PI 647705, PI 647706, PI 647707, PI 647708, PI 647710, and PI 647712) originated from BFA, while one (PI 61666) is from ZAF. The PI 586186 was the only accession that exhibited resistance to both anthracnose and grain mold. The grain mold resistant accession PI 61666 has a panicle shape that resembles a standard United States commercial type sorghum and is also photoperiod insensitive. The results presented herein indicate that the BFA germplasm could be an important source for anthracnose and grain mold resistance genes. The integration of these anthracnose and grain mold resistant germplasm into sorghum breeding programs should aid in expanding the genetic diversity and in the development of new resistant varieties.

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1. Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], a crop originally from tropical Africa, is currently grown worldwide in an array of different environments. Sorghum is the fifth most import grain crop behind maize, wheat, rice and barley (FAO, 2012). Nevertheless, sorghum productivity and profitability are limited by several biotic constraints, including the fungal pathogens causing anthracnose and grain mold. Yield losses of up to 50% have been reported from anthracnose infected fields (Thakur and Mathur, 2000), and up to 100% in fields where highly grain mold susceptible cultivars are planted (Williams and Rao, 1981). Moldy seeds are characterized by discoloration inside and outside of the grain, softening of the endosperm, and reduced acceptability for food and feed processing (Rooney and Serna-Saldivar, 1991).

Anthracnose is caused by the fungus *Colletotrichum sublineola* P. Henn., in Kabát & Bubák (syn. *Colletotrichum graminicola* (Ces.) G. W. Wilson), and is most prevalent in warm and humid sorghum production regions. It is considered one of the most destructive diseases of sorghum because it infects all aerial tissues of the plant. Resistant varieties have been deployed worldwide to control the disease; however, the pathogen population is highly diverse genetically which makes it difficult to obtain widespread or durable control with this approach (Prom et al., 2012b). Indeed, the virulence patterns of *C. sublineola* is not well understood since genetic diversity analysis among 232 isolates from United States [U.S.; Texas, Arkansas and Georgia], and Puerto Rico could not associate

* Corresponding author.
E-mail address: hugo.cuevas@ars.usda.gov (H.E. Cuevas).

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the genetic variation of pathotypes with particular geographical regions (Prom et al., 2012b). In contrast, there was a high level of genetic differentiation and limited gene flow among isolates from Ethiopia (Chala et al., 2011). Therefore, the deployment of multiple resistance genes is necessary to adequately control the disease in a particular region. Results from recent evaluation of subsets of sorghum germplasm accessions from China, Ethiopia, Mali, Mozambique, Sudan, Uganda and Zimbabwe has identified highly-resistant germplasm (Cuevas et al., 2014b; Erpelding and Prom, 2006a; Erpelding and Prom, 2004; Prom et al., 2012a, 2011). Nevertheless, the identification of additional resistance sources is still required to adequately control the disease worldwide.

Grain mold is another important disease affecting sorghum production worldwide (Thakur et al., 2006). This disease is caused by a complex of pathogenic and opportunistic fungi, including various *Fusarium* species such as *Fusarium thapsinum* Klittich, Leslie, Nelson, & Manasas, *Fusarium semitectum* Berk. & Ravenel, *Fusarium proliferatum* (Matsushima) Nirenberg, and *Fusarium andiyazi* Marasas, Raheeder, Lamprecht, Zeller & Leslie, *Curvularia lunata* (Wakk.) Boedijn, *Alternaria alternata* (Fr.) Keissler, and *C. sublineola*, which are the most prevalent species worldwide (Das et al., 2012; Williams and Rao, 1981). The prevalence of the disease varies among geographic locations and climate conditions. In fact, regions with moist conditions late in the growing season are the most affected (Bandyopadhyay et al., 2000). Mycoflora analysis of sorghum seeds collected from production fields in south Texas during 2008 and 2009 detected *Alternaria* spp, *Bipolaris* spp., *Fusarium* spp., and *C. lunata* as the most predominant fungi in the region (Prom et al., 2015). Seed of sorghum collected from fields in Isabela, Puerto Rico had *F. semitectum* as the most predominant fungus, in addition to *F. thapsinum*, and *C. lunata* (Erpelding and Prom, 2006b). Resistant cultivars provide the most effective method to control grain mold. In this regard, high levels of grain mold resistance have been identified in germplasm from West and Central Africa (IS 14384, CGM39/17-2-2), Uganda (PI534117), and Sudan (PI 570011, PI570027, PI569992, PI569882, PI571312, PI570759 and PI267548) (Prom and Erpelding, 2009; Prom et al., 2011; Ratnadass et al., 2003). However, the genetic control of grain mold resistance is complex due to the presence of several fungal pathogens associated with the disease and the controlling mechanisms of the plants (Waniska et al., 2001). Generation means analysis based on several familial generation derived from the cross of Sureño (resistant) × RTx430 (susceptible) estimated broad and narrow-sense heritability for grain mold resistance to range from 0.46 to 0.82, and 0.39–0.59, respectively. In addition suggest at least 10 genes might contribute to grain mold resistance (Rodriguez-Herrera et al., 2000). Indeed, five genomic regions associated with grain mold resistance located in chromosome 4, 6, 7, 9 and 10 explained 10–24% of the phenotypic variation (Klein et al., 2001). The identification of new sources of grain mold resistance is imperative to develop new varieties with greater levels of resistance.

The National Plant Germplasm System (NPGS) of United States Department of Agriculture (USDA) holds the largest sorghum collection with more than 44,000 accessions. This collection is a valuable genetic resource for the identification of new sources of disease resistance, including anthracnose and grain mold. Nevertheless, the majority of these accessions have not been characterized for their disease response, and approximately 80% of the collection is photoperiod sensitive (i.e. flowering with day-length less than 12 h), which makes their evaluation in temperate regions difficult. Thus, the screening of exotic germplasm in tropical regions to identify potentially valuable germplasm which can later be converted for use in temperate regions is necessary for the development of new resistant sorghum varieties. Grain mold resistant sources presently employed in breeding programs are originally from Sudan. For instance, the grain mold resistant lines Tx2911 [PI 607931; Rooney et al. (2000)] and Sureño [PI 531472; Meckenstock et al. (1993)] were derived from the Sudanese germplasm SC719 (PI 534047) and SC423 (PI 533758), respectively. Likewise, the line SC748 (PI 533991) from Sudan has proven to be an important anthracnose resistance source for sorghum breeding programs in the U.S. Nevertheless, the identification of novel sources of resistance in sorghum germplasm from other African regions is needed to develop new cultivars having greater levels or more durable resistance. Therefore, the objective of this study was to identify new sources of resistance to anthracnose and grain mold among exotic sorghum germplasm from Burkina Faso (West Africa) and South Africa.

2. Material and methods

2.1. Germplasm material

A total of 80 sorghum germplasm accessions from Burkina Faso (BFA; 40 accessions) and South Africa (ZAF; 40 accessions) were selected based on their limited phenotype information in the Genetic Resources Information Network (GRIN) database. The accessions were grown at the USDA-Agricultural Research Services (ARS) Tropical Agriculture Research Station (TARS) experimental farm at Isabela, Puerto Rico from February to May 2012 (Experiment # 1) and from October 2012 to January 2013 (Experiment # 2). The lines RTx2536 and RTx430 were used as susceptible checks, and Sureño as a resistant check for the grain mold evaluation; whereas, BTx623 and PI 609251 were susceptible checks, and SC748-5 was a resistant check for the anthracnose screening. The experimental designs in both seasons were randomized complete block designs (RCBD) consisting of three blocks. Seed from each accession were planted in a single, 1.8-m long row, with 0.9 m spacing between rows. Plants were maintained using standard management practices, and weeds were controlled with mechanical tillage and hand hoeing.

2.2. Phenotypic evaluation

2.2.1. Agronomical traits

Flowering date (FL), plant height (PH), panicle length (PL), panicle shape and plant color were recorded for each accession/plot. Flowering time was defined as the numbers of days where 50% of the plants within a row reached anthesis. Plant height refers to the distance from the base of the main stalk (i.e. soil) to the top of the panicle recorded at maturity and represents the average height for three plants within each experimental unit. Panicle length refers to the distance from the first rachis to top of the panicle. Panicle shapes were classified according to the sorghum descriptor (IBPGR and ICRISAT, 1993), which consisted of 12 categories: 1) very lax panicle (typical wild sorghum), 2) very loose erect primary branches, 3) very loose drooping primary branches, 4) loose erect primary branches, 5) loose dropping primary branches, 6) semi-loose erect primary branches, 7) semi-loose drooping primary branches, 8) semi-compact elliptic, 9) compact elliptic, 10) compact oval, 11) half broom corn and 12) broom corn. Plant colors were according to the Sorghum Crop Germplasm Committee (SCGC).

2.2.2. Disease resistance response

2.2.2.1. Anthracnose. The inoculation and disease assessment methods were similar to those described by Prom et al. (2009). Briefly, fungal cultures were prepared with five different isolates of *Colletotrichum sublineolum* [AMP170, 205, 207, 222, and 224 (Prom et al., 2012b)] which represent the pathotypes present at the TARS experimental farm at Isabela. The pathotypes were cultured on ½