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Response of the Set of Anthracnose Differentials to other Foliar and Panicle Diseases in Niger

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Abstract

This study was conducted to determine the reactions of 19 sorghum lines, of which 18 had been used for *Colletotrichum sublineola* pathotype determination to other foliar and panicle diseases in two agroecological zones in Niger. The anthracnose resistant check SC748-5 was infected with leaf blight, oval leaf spot, and zonate leaf spot but free of long smut, rough leaf spot, and target leaf spot. BTx623 and TAM428 which are susceptible to anthracnose were infected with leaf blight, long smut, oval leaf spot and zonate leaf spot. Across locations, all the lines tested were infected with leaf blight, caused by *Exserohilum turcicum*. PI570726, an accession from Sudan was infected with only leaf blight but free of all the other diseases observed in both locations. This work showed that some of the sorghum anthracnose differentials, especially PI570726 may possess genes for resistance to multiple sorghum diseases and can be utilized as parents in breeding programs in Niger.

Keywords: Sorghum; Fungal diseases; *Colletotrichum sublineola; Exserohilum turcicum.*

1. Introduction

In the drier regions of Africa and Asia, sorghum (*Sorghum bicolor* (L.) Moench) supplies the daily calorie intake for hundreds of millions of people [1]. As the fifth most important cereal crop, its uses are expanding to include consumers seeking alternate grains for a healthier, gluten free addition to their diet, and as a potential source of biofuel [1-3]. Sorghum ranks second among cereals after pearl millet in Niger, and similar to other African Countries is used primarily as a staple food for the population and secondarily for animal feed, especially their haulms [4-6]. Biochemical studies have shown that 25% of the accessions from Niger tested at ICRISAT exhibited good sources for high seed lysine content [7]. The projected global area for 2019/2020 planting of sorghum will exceed 40.8 Mha, and in Africa, Niger with 3.7 Mha ranks third after Sudan (7.0Mha) and Nigeria (5.9Mha) [8]. By 2050, the world's population is expected to exceed 9 billion and this will require annual increase in cereal production, including sorghum to at least 3 billion tons [9]. New challenges, such as management of existing and emerging plant pathogens, are expected with the increase in sorghum production coupled with climate change. Therefore, one of the factors in obtaining food security in resource poor areas is the effective management of plant diseases, especially the use of resistant sources. This study was undertaken to determine the responses of the set of sorghum differentials used to delimit the anthracnose pathogen races to natural disease infection in two locations in Niger.

2. Materials and Methods

Nineteen sorghum germplasms, including the 18 differentials SC326-6, SC414-12E, BTx378, TAM428, Tx2536, SC328C, QL3, BTx398, SC283, Brandes, SC112-14, Theis, BTx623, SC748-5, PI570841, PI570726, PI569979 and IS18760 that had been used to establish *Colletotrichum sublineola* pathotypes in the United States and

Puerto Rico [10] were evaluated for foliar and panicle diseases in two regions, Tillabéri and Maradi in Niger. Tillabéri and Maradi in Niger represent 2 of the top 5 major sorghum production regions. These regions have a Sahelian type of climate with ferruginous tropical soil type, and annual rainfall of 450 mm and 550 mm, respectively [11, 12]. During the rainy season, the maximum and minimum temperatures are 28˚C and 23˚C [11]. Seeds were planted in single 15-ft rows, with 36 in. row spacing. Standard field management protocol was followed as recommended. Plants were exposed to natural infection. At the soft to hard dough stage of development, incidence of the different diseases that appeared in the nurseries was recorded.

3. Results and Discussion

In Africa, sorghum cultivation is integral to the lives of millions of people where the grain and plant parts are utilized in baked foodstuff, porridge, snack foods, nonalcoholic and alcoholic beverages, fiber, and syrup, among other uses [1, 7]. However, sorghum cultivation and profitability are hampered by biotic stresses due to fungal and other microorganisms [1, 13].

In this study, 19 sorghum lines, including 18 that had been used to establish the pathotypes of *Colletotrichum sublineola* were planted at two locations in Niger to identify lines with resistance to foliar and panicle diseases. SC748-5 has been shown to be resistant to anthracnose and had been used as a resistant check in pathotype determination, while BTx623, TAM428, and PI609251 are used as susceptible checks [10, 14]. In this current study in Niger, SC748-5 was infected with leaf blight, oval leaf spot, and zonate leaf spot but free of anthracnose, long smut, rough leaf spot, and target leaf spot (Tables 1 and 2). SC748-5, BTx378, and SC326-6 were free of long smut when tested in Niger; however, these lines were infected with the disease when evaluated in Senegal [14, 15], indicating that different long smut pathotypes likely exist in the two Countries. Different long smut pathotypes have been documented [15, 16]. The anthracnose susceptible checks BTx623, TAM428, and PI609251 also were infected with leaf blight, oval leaf spot, and long smut but free of target leaf spot (Table 2). In addition, there were differences in the reactions of the sorghum differentials to anthracnose, indicating different pathotypes of *C. sublineola* in the two locations (Tables 1 and 2). Across locations, all the lines tested were infected with leaf blight, caused by *Exserohilum turcicum* (Table 1 and 2). Among the lines, leaf blight incidence ranged from 4 % (QL3 and BTx378) to 100% (PI570841 and SC414-12E). Except for PI570726 and PI609251, all other lines tested were infected with zonate leaf spot, incited by *Gloeocercospora sorghi* while PI570726, QL3, Theis, SC328C, and SC326-6 were free of oval leaf spot, caused by *Ramulispora sorghicola*. Target leaf spot was absent at Tillabéri (Table 1); however, 7 lines were infected with the disease with SC326-6 exhibiting the highest incidence 86% (Table 2). Also, 8 lines were infected with rough leaf spot, incited by *Ascochyta sorghina*, with incidence ranging from 3% (Brandes) to 40% (SC414-12E) (Tables 1 and 2). PI570726, an accession from Sudan was infected with only leaf blight but free of all the other diseases observed in both locations. However, PI570726 was shown to be susceptible to anthracnose when inoculated with *C. sublineola* isolates from the USA [10].

In conclusion, some of the sorghum anthracnose differentials, especially PI570726 may possess genes for resistance to multiple sorghum diseases and can be utilized as parents in breeding programs in Niger. Also, some of these lines could be used as differentials in other pathosystems for pathotype determination. In addition, future work will be needed to determine the inheritance of the resistance genes.

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Table-1. Reactions of sorghum differentials to natural infection in Tillabéri, Niger[1]

Line	ANTH[2]	LB	LS	OVL	RLS	ZLS
SC748-5	-	18	-	18	-	-
IS18760	-	53	21	12	-	-
PI569979	-	36	-	39	-	-
PI570726	-	13	-	-	-	-
PI570841	13	65	-	-	-	-
PI609251	11	46	2	4	7	-
QL3	-	4	-	-	4	-
RTx2536	-	32	4	21	4	-
TAM428	24	28	24	16	-	-
Theis	3	9	34	-	6	-
Brandes	-	47	-	100	-	-
BTx378	3	12	-	26	-	3
BTx623	44	46	51	13	-	3
BTx398	-	70	-	15	-	-
SC112-14	-	68	-	-	-	5
SC283	32	48	14	11	-	-
SC414-12E	-	32	41	-	-	-
SC328C	-	36	9	-	-	-
SC326-6	-	27	-	-	-	16

[1]The sorghum differentials were planted at the experimental plots at Tillabéri, under natural infection. Disease incidence was recorded at the soft to hard dough stage of development.

[2]ANTH=anthracnose (*Colletrichum sublineola*); LB=leaf blight (*Exserohilum turcicum*); LS=long smut (*Sporisorium ehrenbergii*); OVL=oval leaf spot (*Ramulispora sorghicola*); RLS=rough leaf spot (*Ascochyta sorghina)*; ZLS=zonate leaf spot (*Gloeocercospora sorghi*); and TLS=target leaf spot (*Bipolaris sorghicola*).

Table-2. Reactions of sorghum differentials to natural infection in Maradi, Niger[1]

Line	ANTH[2]	LB	LS	OVL	RLS	ZLS	TLS
SC748-5	-	18	-	-	-	6	-
IS18760	11	25	4	100	-	4	-
PI569979	41	26	-	56	-	6	-
PI570726	-	69	-	-	-	-	-
PI570841	32	100	3	16	32	13	-
PI609251	87	76	87	100	7	-	-
QL3	-	29	-	-	-	6	-
RTx2536*	-	25	-	35	-	25	55
TAM428	19	22	-	33	4	4	-
Theis	8	12	4	-	-	58	73
Brandes	-	33	-	53	3	8	-
BTx378*	-	4	-	-	-	4	83
BTx623	50	17	-	42	-	17	-
BTx398	-	9	-	18	-	23	68
SC112-14	-	-	-	44	-	44	-
SC283	17	-	-	78	-	28	44
SC414-12E	-	100	-	-	40	40	-
SC328C	40	25	5	-	-	20	50
SC326-6	14	43	-	-	-	29	86

[1]The sorghum differentials were planted at the INRAN Station, Maradi, under natural infection. Disease incidence was recorded at the soft to hard dough stage of development. Panicles were bagged is some of the differentials and this may be responsible for no or low incidence of long smut.

[2]ANTH=anthracnose (*Colletrichum sublineola*); LB=leaf blight (*Exserohilum turcicum*); LS=long smut (*Sporisorium ehrenbergii*); OVL=oval leaf spot (*Ramulispora sorghicola*); RLS=rough leaf spot (*Ascochyta sorghina)*; ZLS=zonate leaf spot (*Gloeocercospora sorghi*); and TLS=target leaf spot (*Bipolaris sorghicola*).

*Bacterial leaf streak/bacterial leaf stripe 10% and 8% incidence was recorded on RTX2536 and BTx378, respectively.

References

[1] Frederiksen, R. A. and Odvody, G. N., 2000. *Compendium of sorghum diseases. The american phytopathological society*. USA.: St. Paul, MN,. p. 78.

[2] da Costa, R. V., Zambolim, L., Cota, L. V., da Silva, D. D., Rodrigues, J. A. S., Tardin, F. D., and Casela, C. R., 2011. "Genetic control of sorghum resistance to leaf anthracnose." *Plant Pathol*, vol. 60, pp. 1162-1168.

[3] Gonzalez, R., Phillips, R., Saloni, D., Jameel, H., Abt, R., Pirraglia, A., and Wright, J., 2011. "Biomass to energy in the Southern United States: Supply chain and delivered cost." *BioResources*, vol. 5, pp. 2954-2976.

[4] Hamidou, M., Souley, A. K. M., Kapran, I., Soulemane, O., Danquah, E. Y., Ofori, K., Gracen, V., and Ba, M. N., 2018. "Genetic variability and its implications on early generation sorghum lines selection for yield, yield contributing traits, and resistance to sorghum midge." *International Journal of Agronomy*, p. 10 Available: https://doi.org/10.1155/2018/1864797

[5] Manssour, A. M., Alzouma, M. Z., Dan-Lamso, N., Elhadji, S. D., and Ambouta, J. M. K., 2014. "Productivity of the cultivation of sorghum (Sorghum bicolor) in Acacia senegal (L.) Willd. based agroforestry system in Niger." *J. Appl. Biosci.*, vol. 82, pp. 7339-7346.

[6] Ousmane, S. D., Niaba, T., Mamadou, A., Abdoul-Kader, M., Garba, S., and Tongoona, P., 2017. "Survey on crop residues for cattle feeding in Niger." *J. Agric. Food. Tech.*, vol. 7, pp. 7-15.

[7] Upadhyaya, H. D., Reddy, K. N., Vetriventhan, M., Ahmed, M. I., Krishna, G. M., Reddy, M. T., and Singh, S. K., 2017. "Sorghum germplasm from West and Central Africa maintained in the ICRISAT genebank: Status, gaps, and diversity." *The Crop J.*, vol. 5, pp. 518-532.

[8] World Agricultural Production, 2019. *Office of global analysis foreign agricultural service*. USDA, Circular Series WAP, pp. 12-19.

[9] FAO, 2009. "How to feed the world in 2050." Available: http://www.fao.org/fileadmin/templates/wsfs/.../how-to-feed-the-world-in-2050.pdf

[10] Prom, L. K., Perumal, R., Erattaimuthu, S. R., Little, C., No, E. G., Erpelding, J. E., Rooney, W. L., Odvody, G. N., and Magill, C. W., 2012. "Genetic diversity and pathotype determination of Colletotrichum sublineolum isolates causing anthracnose in sorghum." *Eur. J. Plant Pathol.*, vol. 133, pp. 671-685.

[11] Direction of Statistics, 2019. *Assessment report of the 2018 winter agricultural campaign and food outlook 2018/2019*. Republic of Niger: Ministry of Agriculture and Livestock,. p. 45.

[12] Moussa, S., 2013. *Situation of soils in niger: Constraints and needs. Global soil partnership (gsp) in west africa, 4-5 février 2013*. Ghana: Accra, . p. 24.

[13] Prom, L. K., Isakeit, T., Perumal, R., Erpelding, J. E., Rooney, W., and Magill, C. W., 2011. "Evaluation of the Ugandan sorghum accessions for grain mold and anthracnose resistance." *Crop Prot.*, vol. 30, pp. 566-571.

[14] Prom, L. K., Cuevas, H., Perumal, R., Isakeit, T., and Magill, C., 2018. "Inheritance of resistance of three sorghum lines to pathotypes of Colletotrichum sublineola, causal agent of anthracnose." *Plant Pathol. J.*, vol. 17, pp. 75-79.

[15] Prom, L. K., Cisse, N., and Ndoye, O., 2007. "Assessing the vulnerability of selected sorghum lines from the United States of America to long smut (Sporisorium ehrenbergii Vanky) disease." *Crop Prot.*, vol. 26, pp. 1771-1776.

[16] Botros, S. E., Abdel-Rahman, T. M., and Hassan, M. H. A., 1999. "Studies on Tolyposporium ehrenbergii the cause of sorghum long smut in Upper Egypt." *Assiut J. Agric. Sci.*, vol. 30, pp. 97-107.