Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum sublineola* Causing Anthracnose on *Sorghum bicolor* in South Korea

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Sorghum (*Sorghum bicolor* [L.] Moench) is one of the top five cereal crops in the world, but the cultivation area in Korea is estimated to be about 3,000 ha (MIFFAF 2012). In August 2014, anthracnose symptoms on sorghum leaves were observed in two fields in Yecheon (36.62°, 128.41°) and Youngwol (37.20°, 128.49°), South Korea. Symptoms on leaves were brownish-red irregular lesions with yellow and tan borders. Some darkened conidiomata and setae were observed on the lesions of infected leaves. Approximately 20% of sorghum plants (cv. Hwanggeumchal) were affected in each field with an area of about 0.1 ha. Fragments of diseased leaves were surface sterilized with 1% NaOCl for 30 s. The pieces were placed on water agar and incubated at 25°C for 7 days. Two isolates were obtained through single sporing and cultured on synthetic nutrient poor agar at 25°C for 14 days. Conidia ($n = 30$) of YN1458 isolate were falcate and measured 22.0 to 32.7 × 4.2 to 6.4 µm. Brown to black setae ($n = 20$) had one to three septa, with tapering acute apices and 53.7 to 95.2 × 4.7 to 7.8 µm in size. Appressoria ($n = 30$) were dark brown, usually irregular, and 10.5 to 16.9 × 8.6 to 13.6 µm in size. Colonies on PDA produced salmon spore masses in the center of the colony and were whitish gray to dark color in reverse. The morphological characteristics of two isolates were similar. Based on morphology, two isolates were tentatively identified as *Colletotrichum graminicola* species complex (Cannon et al. 2012; Crouch and Tomaso-Peterson 2012). To clarify taxonomic placement, DNA extracted from mycelia of the two isolates was

PCR amplified and sequenced targeting internal transcribed spacer (ITS) regions of rDNA, actin (ACT), chitin synthase 1 (CHS-1), and beta-tubulin (TUB) genes (Weir et al. 2012). The sequences of the above four loci of YN1458 and YN1728 were deposited in GenBank with accession numbers KY351801, KY351802 (ITS); KY769869, KY69870 (ACT); KY769871, KY769872 (CHS-1); and KY769873, KY769874 (TUB), respectively. The sequencing results of two isolates showed 99.6% (ITS), 99.6% (ACT of YN1458), 100% (ACT of YN1728), 100% (CHS-1), 100% (TUB of YN1458), and 99.8% (TUB of YN1728) similarity with *Colletotrichum sublineola* CBS 131301 (JQ005771, JQ005834, JQ005792, and JQ005855) by BLASTn. Based on the morphological characteristics and multigene sequence analysis, the two isolates were identified as *C. sublineola*. Pathogenicity of two isolates was confirmed by spraying conidial suspensions (10⁶ conidia/ml) on leaves of 3-week-old sorghum seedlings (cv. Hwanggeumchal) using a pot assay (five plants per isolate). The same number of seedlings were sprayed with sterile distilled water and served as controls. All plants were maintained in a greenhouse at 25/32°C with natural light. After 1 week, symptoms similar to those in the field were observed on the leaves inoculated with the pathogen but not on the control leaves. *C. sublineola* was consistently reisolated from the inoculated leaves showing anthracnose symptoms, and the pathogen identity was confirmed by observing morphological characteristics. Previously, *C. graminicola* was the only known causal agent pathogen of sorghum anthracnose in South Korea (KSPP 2009). To our knowledge, this is the first report of *C. sublineola* causing anthracnose on sorghum in South Korea. Although sorghum is a small-scale crop in South Korea, it is necessary to study the biological and pathogenic characteristics of *C. sublineola* for effective control of sorghum anthracnose.

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