Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Anthracnose Leaf Spot Caused by *Colletotrichum americanae-borealis* on Oat in China

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Oat (*Avena sativa*), an important source of crude protein, fiber, and crude fat needed for livestock, is increasingly being cultivated in China. In August 2020, leaf spots were observed on oat cv. Bayan 7 plants in an experimental field of 3 ha with a disease incidence of 12% and a severity of 20% in Daqiao Town (26.42°N, 103.22°E), Huize County, Yunnan Province, China. Symptoms mainly consisted of reddish-brown spots that were oval to irregularly circular in shape and 3 to 4 mm in diameter (occasionally confluent). The spots were surrounded by chlorosis involving the affected leaf surfaces, which was due to the spread of the disease. Infected tissues (10 diseased leaves) of 10 different plants were cut into small pieces (5 × 5 mm) at the junction of diseased and healthy tissues, surface-sterilized in 75% ethanol solution for 30 s and 1% NaClO solution for 2 min, rinsed three times with sterilized distilled water, air dried, and transferred to potato dextrose agar plates. A total of nine single-spore isolates with similar colony morphologies were obtained. After 7 days, the colonies showed white to gray aerial mycelia and appeared dark brown at the center of the reverse view. Setae were brown, smooth walled, cylindrical at the base, rounded at the tip, contained one to four septa, and measured 50 to 190 µm long. Conidia were hyaline, aseptate, cylindrical to spindle shaped, straight to slightly curved, rounded at both ends, and measured 14.5 to 17.5 × 3.6 to 4.1 µm in size ($n = 50$). Based on the morphological characteristics, the fungal pathogen was identified as being

closely related to *Colletotrichum americanae-borealis* (Damm et al. 2014). To further substantiate the identification, the ITS region of rDNA, beta-tubulin (*TUB*) gene, chitin synthase (*CHS*) gene, and histone H3 (*HIS3*) gene were amplified by the primers described previously (Damm et al. 2014) and sequenced. Sequences of the representative isolated strain YNC-1 were deposited in GenBank (MZ676033 for ITS, MZ686211 for *TUB*, MZ686214 for *CHS*, and MZ686217 for *HIS3*). BLAST analysis showed 99 to 100% identity to *C. americanae-borealis* type strain CBS 136232 (GenBank accessions: KM105224, KM105504, KM105294, and KM105364, respectively). The four locus datasets were combined by SequenceMatrix 1.8 (Vaidya et al. 2011), and the strain YNC-1 and *C. americanae-borealis* (CBS 136232 and CBS 136855) formed a subclade with 97% bootstrap support. To test pathogenicity, five pots each containing five 5-week-old oat seedlings (cv. Baiyan 7) were sprayed with the YNC-1 isolate conidial suspension (1×10^5 conidia/ml), while the other five pots were sprayed with sterile water as a control. All plants were kept for 48 h at 100% RH and then moved to a nursery shelf in a greenhouse maintained at 26/18°C day/night temperatures. After 5 to 7 days postinoculation, reddish-brown spots were observed on the inoculated plants and *C. americanae-borealis* was reisolated and confirmed by morphological and molecular features. No disease was observed on control plants. To our knowledge, this is the first report of *C. americanae-borealis* causing leaf spot on oat in China. *C. americanae-borealis* has been reported being associated with leaf spot in alfalfa (Li et al. 2021) and licorice (Lyu et al. 2020). The disease can cause a serious threat to oat crops in China and disease management strategies are needed to control its proliferation.

References:

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