Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Sclerotinia Blight on Peanut Caused by *Sclerotinia sclerotiorum* in Qinghai Province, China

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Historically, peanut has not been produced in Qinghai Province located in northwestern China because of the high elevation and cold climates. However, since 2020, field studies have been conducted to evaluate peanut cultivars for suitability for field production. In 2020, peanut cultivation was successful for the first time in Haidong City, Qinghai Province, China. In August 2020, brown, irregular-shaped lesions were observed on peanut stems from Qinghai Province in China. In the early stage, the water-soaked spots were formed on the stems; then, lesions expanded rapidly and became brown. In advanced stages of the disease, stems became bleached and eventually died. The inside of the stems was rotten and hollow, and the diseased stem wilted and died. White hyphae and black, irregular-shaped sclerotia were observed on the infected stems. Finally, parts of the plant or the whole plant rotted and died at the end. Approximately 10% of the plants in a field were infected. Symptomatic stems were cut into small pieces, disinfected with 75% ethanol for 1 min and 0.5% NaClO for 2 min, and rinsed with sterile water three times. Pieces then were plated on potato dextrose agar (PDA) media and incubated at 25°C

in darkness. Fungal colonies were initially white, becoming gray; then, black sclerotia (2.4 to 6.0 mm in diameter) appeared at the edge of colonies. Genomic DNA of the pure cultures of an isolate (ZHX7) was extracted and PCR was carried out using glyceraldehydes-3-phosphate dehydrogenase gene (*G3PDH*) region primer pair G3PDH-F/G3PDH-R, heat-shock protein 60 gene (*HSP60*) region primer pair HSP60-F/HSP60-R, and DNA-dependent RNA polymerase subunit gene (*RPB2*) region primer pair RPB2-F/RPB2-R (Staats et al. 2005). The *G3PDH* region (accession no. MZ388475) showed 99.44% sequence identity (887 of 909 bp) to *Sclerotinia sclerotiorum* (accession no. AJ705044, 887 of 887 bp). The *HSP60* region (accession no. MZ388476) showed 99.90% sequence identity (972 of 984 bp) to *S. sclerotiorum* (accession no. AJ716048, 972 of 980 bp). The *RPB2* region (accession no. MZ388477) showed 100.00% sequence identity (1,096 of 1,129 bp) to *S. sclerotiorum* (accession no. AJ745716, 1,096 of 1,096 bp). Phylogenetic analysis was done using neighbor-joining analysis based on those gene sequences. The isolate was identified as *S. sclerotiorum* based on molecular analysis and morphological characteristics. For the pathogenicity assay, 10-day-old potted peanut seedlings ('Luhua No. 12') were each inoculated with one mycelial plug (8 mm in diameter) by placing the inoculum on the base of the stem in a growth chamber (30°C in the day and 25°C at night, with a 12-h photoperiod and 80% RH). All inoculated seedlings exhibited typical basal stem rot, roots showed different degrees of damage, and plants wilted 5 days after inoculation. No symptoms were observed on control plants treated with sterile distilled mycelial plugs, and *S. sclerotiorum* was consistently reisolated from symptomatic tissue. *S. sclerotiorum* has been reported on peanut in northeastern China (Yan et al. 2014). To our knowledge, this is the first report of *S. sclerotiorum* causing Sclerotinia blight on peanut in Qinghai Province, China. The peanut planting area in Qinghai has been further expanded this year, and *S. sclerotiorum* has a broad host range (Boland and Hall 1994); therefore, Sclerotinia blight is a potential threat to peanut production and, as a result, it is critical for commercial producers to monitor plants for *S. sclerotiorum*.

References:

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