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 Northwest China because of the high elevation and cold climates. However, since 2020 field studies have been conducted to evaluate peanut cultivars for suitability to 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 watersoaked 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, local or 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 minute, 0.5% NaClO for two minutes, and sterile water for 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) were 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 primers G3PDH-F/G3PDH-R, heat-shock protein 60 gene (HSP60) region
primers HSP60-F/HSP60-R, and DNA-dependent RNA polymerase subunit gene
(RPB2) region primers RPB2-F/RPB2-R (Staats et al., 2005), respectively. G3PDH
region (Accession No. MZ388475) showed 99.44% sequence identity (887 bp out of
909 bp) to Sclerotinia sclerotiorum (Accession No. AJ705044, 887 bp out of 887 bp).
HSP60 region (Accession No. MZ388476) showed 99.90% sequence identity (972 bp
out of 984 bp) to S. sclerotiorum (Accession No. AJ716048, 972 bp out of 980 bp).
RPB2 region (Accession No. MZ388477) showed 100.00% sequence identity (1096 bp
out of 1129 bp) to S. sclerotiorum (Accession No. AJ745716, 1096 bp out of 1096 bp).
Phylogenetic analysis was done using Neighbor-Joining (NJ) analysis based on those
gene sequences. The isolate was identified as S. sclerotiorum based on molecular
analysis and morphological characteristics.

For pathogenicity assay, ten-days-old potted peanut (Luhua No.12) seedlings were
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, a 12-h
photoperiod and 80% RH). All inoculated seedlings exhibited typical basal stem rot,
and root showed different degrees of damage, and wilted 5 days after inoculation. No
symptoms were observed on control plants treated with sterile distilled mycelial plugs,
and S. sclerotiorum was consistently re-isolated from symptomatic tissue. S.
sclerotiorum has been reported on peanut in Northeastern China (Yan et al., 2005). 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),
so 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.
Reference:

