Diseases Caused by Oomycetes

Occurrence of Root Rot Caused by *Pythium aphanidermatum* on Mung Bean (*Vigna radiata*) in China

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In August 2019, approximately 10% of mung bean plants at the experimental farm of the Jiangsu Academy of Agricultural Science (32.03°N; 118.88°E) showed symptoms of stunting and wilting. Brown and water-soaked stem lesions were often observed at the base of the diseased plants. In severe cases, the plants collapsed and cumulous aerial mycelia were visible on the basal stem surface. To identify the causal agent, a total of 20 tissue fragments (5 mm long) were excised from roots and basal stems of five symptomatic plants. The fragments were surface sterilized in 2% sodium hypochlorite solution and plated on 2.5% potato dextrose agar (PDA) plates containing 10 µg/ml pimarin, 100 µg/ml ampicillin, 10 µg/ml rifampicin, and 10 µg/ml pentachloronitrobenzene (PARP; Beckerman et al. 2018). After 3 to 4 days incubation at 25°C in the dark, 14 colonies with white and cumulous mycelia grew from the tissue pieces (named as JS19-1 to JS19-14). JS19-1 and JS19-2 were purified by hyphal tipping, then grown on PDA medium for 7 days for morphological observation using a compound microscope. Width of coenocytic hyphae ranged from 3.7 to 8.9 (avg. 6.1, $n = 20$) µm. Terminal oogonia were globose with a diameter of 13.8 to 25.8 (avg. 22, $n = 20$) µm. Antheridia were barrel-shaped and mostly intercalary, sometimes terminal. Most of antheridia were declinuous, 6.2 to 12.5 (avg. 9.3, $n = 20$) µm in width and 7.6 to 15.3 (avg. 12.8, $n = 20$) µm in length. Oogonia were fertilized with one or rarely two antheridia. Oospores were aplerotic, 10.1 to

23.5 (avg. 20.4, $n = 20$) µm in diameter. Sporangia had terminal inflated hyphal branches. The two isolates were preliminarily identified as *Pythium aphanidermatum*. For molecular identification, the sequences of internal transcribed spacer (ITS) rDNA, cytochrome oxidase subunit I (CoxI) (Robideau et al. 2011), and β-tubulin (Kroon et al. 2004) of JS19-1 were detected and deposited in GenBank (MT949538, MT949539, and MT949540). The ITS and CoxI sequences were identical with *P. aphanidermatum* CBS28779 ITS (759/759 bp, HQ643439.1) and PYT01 CoxI (640/640 bp, MH760243.1), respectively; the β-tubulin sequence showed 99% (830/840 bp) similarity of *P. aphanidermatum* P2 (AY564048.1). Thus, JS19-1 was confirmed as *P. aphanidermatum*. To fulfill Koch's postulates, the pathogenicity of JS19-1 was tested using the procedure of Kiyoshi et al. (2021) with some modifications. Barley grains infested with JS19-1 were as inoculum and thoroughly mixed with potting mixture at a rate of 10% by volume. Six mung bean seeds were sown per pot and then grown in a greenhouse. Potting mixture with no inoculum was used as control. Three pots of replicate plants were used for inoculation and control. After 3 weeks, emergence in the inoculated pots was 33% and symptoms of stunting and root rot similar to those in field were observed, while control plants were asymptomatic. *P. aphanidermatum* was successfully reisolated from symptomatic plants of both methods. The pathogenicity tests were repeated twice. *P. aphanidermatum* causes seed rot, pre- and postemergence damping-off, and stem/root rot of a wide range of industrial crops and vegetables (Liu et al. 2018). To our knowledge, this is the first report of *P. aphanidermatum* causing disease on mung bean in China. Since *Phytophthora vignae* (Sun et al. 2021) and *P. myriotylum* (Yan et al. 2021) have been reported causing mung bean root rot, integrated disease management should be adopted to reduce damage.

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