Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Taproot Decline Caused by *Xylaria* sp. on Soybean in Tennessee

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Soybean (*Glycine max*) is a major economic crop in Tennessee. In August 2017, foliar interveinal chlorosis progressing to necrosis and root necrosis symptoms consistent with taproot decline, caused by *Xylaria* sp. (Allen et al. 2017), were observed in a production field of ‘Croplan 4886’ soybean cultivar (WinField Solutions, Saint Paul, MN) in Hardeman County, Tennessee. Characteristic stromata were observed in the field at the base of infected plants, with some produced on cotton debris from the previous season. Infected roots of 13 plants were collected, surface sterilized in the laboratory by rinsing in tap water for 10 min, immersed in 10% NaOCl for 1 min, rinsed twice in sterile distilled water, split longitudinally, and plated on potato dextrose agar amended with 0.125 g/liter of streptomycin sulfate salt and 0.075 g/liter of chloramphenicol (Allen et al. 2017). Plates were incubated at 22°C on a 12-h fluorescent light/dark cycle for 1 to 2 weeks. Based on colony morphology, two isolates were selected for subsequent analyses (DMCC2477 and DMCC2478). To fulfill Koch’s postulates, both isolates were used to inoculate the soybean cultivar Asgrow 4632 (Monsanto, St. Louis, MO). Inoculum was grown on sterilized soybean stems for 1 month prior to inoculation. Three treatment groups (nontreated check, sterilized soybean stems, and inoculated soybean stems) were included with four replicates each, for which three plants per pot was a replicate. Six seeds were initially planted in 15-cm pots in potting mix (Pro-Mix BX, Premier Horticulture, Rivière-du-Loup, Canada) and thinned to three plants after emergence. Plants were watered every 1 to 2 days, supplemented with fertilizer, and grown under supplemental

lighting with a 16-h light/8-h dark cycle with temperatures ranging from 25 to 35°C in a greenhouse. Foliar symptoms including wilting and interveinal chlorosis followed by necrosis were observed 3 to 4 weeks after inoculation on the majority of inoculated plants. No symptoms were observed on plants treated with sterilized soybean stems or nontreated plants. This experiment was repeated twice. DNA from original isolates DMCC2477 and DMCC2478 was amplified with PCR using universal primers targeting four loci: α -actin (ACT), nuclear ribosomal internal transcribed spacer (nrITS), RNA polymerase subunit II (RPB2), and β -tubulin (TUB2). DNA sequences were obtained with Sanger sequencing and deposited in GenBank (nrITS: MH046898, MH046900; ACT: MH113624, MH113625; RPB2: MH113626, MH113627; TUB2: MH113628, MH113629). Roots from symptomatic inoculated plants that had mycelial growth in the pith after 3 to 4 weeks were used to obtain pure cultures as described above, and these were sequenced for the nrITS region to confirm presence of the fungus (GenBank accession nos. MH046899, MH046901). Alignment of sequences of each loci with published sequences of taxa in the family Xylariaceae (Hsieh et al. 2010; U’Ren et al. 2016) revealed both isolates DMCC2477 and DMCC2478 (and reisolations) were in the *Xylaria arbuscula* aggregate and were conspecific with the first isolate identified as the causal pathogen of taproot decline, MSU_SB201401 (Allen et al. 2017). To our knowledge, this is the first report of taproot decline in Tennessee, an emerging disease previously reported in Alabama, Arkansas, Louisiana, Mississippi, and Missouri (Allen et al. 2017). This disease has been shown to be economically significant to soybean production, threatening the ~1.64 million acres planted annually in Tennessee (USDA-NASS 2020). Education and monitoring efforts should be provided to Tennessee producers regarding the detection of this disease and management options.

References:

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