Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium fujikuroi* Causing Root Rot and Seedling Elongation of Soybean in Indiana

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In summer 2020, 127 soybean (*Glycine max* (L.) Merr) seedlings (V1–V3 stage) showing reduced vigor or crown lesions were collected at Purdue's Agronomy Center for Research and Education in West Lafayette, Indiana. Root tissues from two seedlings with necrotic cotyledons and root rot were surface-sterilized and plated on dichloran-chloramphenicol-peptone agar (Andrews and Pitt 1986). Emerging hyphal tips were transferred to potato dextrose agar (PDA). Single-spore cultures were obtained and grown on PDA. Both isolates developed floccose white aerial mycelia with reddish-pink coloration in the media in 2 weeks on the benchtop. On carnation leaf agar, macroconidia formed on orange sporodochia within 2 weeks in darkness at 25°C. Macroconidia were 3 to 5 septate, measuring 26 to 41 × 2.5 to 3.7 µm (avg. 34.8 × 3.2 µm, *n* = 40). Microconidia were abundant in chains and false heads forming on both mono- and polyphialides, and measured 2.5 to 8.75 × 2.5 µm (avg. 5.9 × 2.5 µm, *n* = 40). These characteristics were consistent with species descriptions of *F. fujikuroi* [Sawada] Wollenw. (teleomorph *Gibberella fujikuroi*) (Leslie and Summerell 2006). DNA was extracted from mycelium and the following genes were amplified and sequenced: the internal transcriber spacer (ITS) region using ITS1/ITS4 primers (White et al. 1990) (GenBank accessions MW463362/MW463363), the mitochondrial small subunit (mtSSU) rDNA using MS1/MS2 primers (White et al. 1990) (MW465310/MW465307), and the partial translation elongation factor 1-alpha (TEF1α) gene using 983F/1567R primers (Rehner and Buckley 2005) (MW475297/MW475298). In GenBank BLAST searches, these sequences showed 100% identity to both *F. proliferatum* and *F. fujikuroi*. Species-specific forward primers Fuji1F and Proli1F were then used in combination with reverse primer TEF1R to amplify another region in the TEF1α

gene (Amatulli et al. 2012). Proli1F/TEF1R primers failed under a variety of annealing temperatures while Fuji1F/TEF1R primers succeeded, and the products were sequenced (MW475299/MW475300). GenBank BLAST searches revealed 100% identity of both isolates to *F. fujikuroi* (MT448248.1). A pathogenicity test was conducted with isolate AC13 in the greenhouse following the protocol of Ellis et al. (2013). Ten seeds (cv. Williams) each were used for inoculation and control, respectively, with one seed per cup. Root rot symptoms similar to those observed in the field were observed 14 days after planting on all inoculated plants but not on controls (VC stage). Infected plants showed symptoms of pre-emergence damping off, reddish-brown lesions on the tap and lateral roots, and root necrosis. Three plants also exhibited hyper-elongation of the stem (12.5, 11.1, and 18 cm, versus controls: avg. 6.8 cm, max. 8.5 cm, stdev 0.78 cm). *F. fujikuroi* was successfully reisolated from inoculated plants but not from controls and identified as described above. *F. fujikuroi* has been reported causing soybean root rot in China (Zhao et al. 2020), Korea (Choi et al. 2019), and the state of Kansas (Pedrozo et al. 2015). To our knowledge, this is the first report of *F. fujikuroi* infecting soybeans in the state of Indiana. *F. fujikuroi* is known to cause elongated seedlings in rice (Leslie and Summerell 2006). Pedrozo et al. (2015) reported that *F. fujikuroi* isolated from soybean caused seedling elongation in rice but not in soybean. The increased distribution and new host symptomatology observed here warrants heightened attention for the control of this pathogen.

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