Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium brachygibbosum* Causing Root Rot on Soybean in Northeastern China

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In August 2017, soybean plants exhibiting root rot were observed in Baiquan County (47°60'N, 126°10'E), Heilongjiang province, China. The disease occurred on approximately 65% of soybean (cv. Heihe43) plants in five fields (>10 ha). The disease resulted in yellowing or wilting and smaller sized leaves, absence of lateral roots, and black lesions on tap roots. Infected root tissues from 10 individual plants (two plants per field) were surface disinfested with 0.5% NaOCl for 2 min, rinsed three times in sterile distilled water, placed on potato dextrose agar (PDA), and incubated at 26°C for 3 days. Eight fungal isolates were obtained by transferring hyphal tips. Colonies on PDA were initially white to rose and then yellow in color with abundant aerial mycelium. The fungal colonies grew to a size of 7.4 cm in diameter 4 days after inoculation. Macroconidia were scarce and scattered, measuring $19.7 \times 3.5 \mu\text{m}$ ($n = 50$) on carnation leaf agar. Typical macroconidium had three to five septa, slightly sharp apices with a distinct basal foot cell. Microconidia had zero to two septa and were slightly curved, measuring $10.7 \times 3.2 \mu\text{m}$ ($n = 50$). Spherical chlamydospores had a mean diameter of $13.7 \mu\text{m}$ ($n = 50$) and were terminal and intercalary on PDA. According to these

morphological characteristics, the fungus was identified as *Fusarium brachygibbosum* (Padwick 1945). Genomic DNA of a representative isolate (P13-1) was extracted. The *Ef-1 α* , *RPB1*, and *RPB2* regions were amplified using primers ef1/ef2, Fa/G2R, and 5f2/7cr (O'Donnell et al. 2010). The consensus sequences (accession nos. MH748277, MH748278, and MH748279) showed 98.65, 98.91, and 99.54% identity to the sequences of *F. brachygibbosum* strain NRRL 34033 (accession nos. GQ505418.1, HM347172.1, and GQ505482.1). Isolate P13-1 was preserved in the Agricultural Culture Collection of China, and stock ID number is ACCC 39715. To confirm pathogenicity of P13-1, soybean (cv. Heihe43) seeds were grown in 15-cm pots containing a commercial potting mix (five seeds per pot, three pots per treatment). Sorghum seeds (10 g) fully colonized by *F. brachygibbosum* (Li et al. 2018) were uniformly distributed in each pot and then covered with a 0.5-cm layer of sterile potting soil, sterilized sorghum seeds (10 g) were added to control pots, and pots were incubated in a growth chamber at 25°C (12-h day)/20°C (12-h night). Ten days after inoculation, all inoculated plants showed symptoms consistent with those observed in the fields. The experiment was repeated two times. *F. brachygibbosum* was reisolated from diseased plants and identified as *F. brachygibbosum* based on morphological and gene sequences analysis. No fungal pathogens were isolated from non-treated controls. To our knowledge, this is the first report of *F. brachygibbosum* on soybean in China. The soybean is the prime oil seed crop and the source of protein cultivated in Northeast China, and this disease seriously affects the seedling growth. So, our findings are very important for the establishment of control strategies and breeding for resistance to soybean root rot.

References:

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