Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium* Root and Stem Rot Caused by *Fusarium oxysporum* f. sp. *radicis-cucumerinum*, a Destructive Disease on Greenhouse Cucumbers in Saudi Arabia

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Cucumber (*Cucumis sativus* L.) is an important vegetable crop in Saudi Arabia. During May 2018, 45 to 60% of 5-month-old cucumber plants showed symptoms of a previously unknown wilt in commercial greenhouses around Al Kharj area of Riyadh region. Symptoms consisted of crown and root rot, wilting, and stem disintegration, along with yellowish brown to brown external discoloration extending throughout the affected tissues. As the disease progressed, a pinkish-orange mycelial growth was often observed at the basis of affected stems, while vessels were discolored. Subsequently, the affected plants collapsed and died. Crown, stem, and root fragments (4 × 4 mm) were cut from symptomatic tissues, surface sterilized in 2.5% NaOCl, cultured on potato dextrose agar with 25 mg/liter of streptomycin sulfate, and incubated at 26°C in darkness for 6 days. Single-spore cultures produced white mycelium with pink, white, or purple pigmentation in the center. The mycelium produced sporodochia. Macroconidia were mainly slightly curved with three to five septa. Microconidia were single-celled, oval, and produced on short lateral phialides. Chlamydospores were single or in short chains. Morphologically, the isolated fungus was characterized as *Fusarium oxysporum* (Leslie and Summerell 2006). To further confirm the fungus identification, DNA was extracted from a single-spore culture. Three different fungal nuclear regions of internal transcribed spacer (ITS), elongation factor 1- α , (TEF1- α), and the second largest subunit of DNA-directed RNA polymerase

II (rpb2) were amplified with the following primers: ITS4 and ITS5 (White et al. 1990), EF-1 and EF-2 (O'Donnell et al. 1998), and fRPB2-5F and fRPB2-7cR (Liu et al. 1999), respectively. The ITS, TEF1- α , and rpb2 sequences of the isolate FCKSU17 were submitted to GenBank (MT232918, MW471131, and MW449833, respectively). Phylogenetic analysis based on the alignment of the ITS, TEF1- α , and rpb2 sequences using MEGA7 placed this strain in the *F. oxysporum* clade. To confirm the *forma specialis radicis-cucumerinum*, amplification with the specific primers ForcF1/ForcR2 was conducted (Lievens et al. 2007). The amplified fragment (~250 bp) was sent for sequencing, and the sequence was submitted to GenBank (MW471132). BLASTn analysis of the sequences showed 100% identity with *F. oxysporum radicis-cucumerinum* (KP746408). To fulfill Koch's postulates, a pathogenicity test was conducted on 7-day-old plants of cucumber cultivar Beit Alpha grown in pots filled with soil mix (2:1 sandy loam/peat moss, vol/vol). The plants were inoculated through drenching with 100 ml of conidial suspension in sterile distilled water (10⁶ spores/ml) per pot. Control plants were treated with sterile distilled water. Each treatment included 10 replicates (pots), with two plants per pot. The pathogenicity test was repeated once. Cucumber plants inoculated with the fungus showed early wilting symptoms within the first 2 weeks postinoculation. At the sixth week postinoculation, 90 to 100% of the inoculated plants developed typical symptoms. No symptoms were observed on the control plants. The pathogen was successfully reisolated from the inoculated wilted plants and identified morphologically. To our knowledge, this is the first report of *F. oxysporum* f. sp. *radicis-cucumerinum* on cucumber in Saudi Arabia. It is recommended that preventive management should be considered, because this disease may cause significant economic losses on cucumbers in Saudi Arabia.

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