Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium* Wilt of Gerbera Daisy Caused by *Fusarium kyushuense* in China

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Gerbera daisy, *Gerbera jamesonii* H. Bolus ex. Hooker, is an important flower grown globally. In September 2020, gerbera seedlings in a greenhouse farm in the region of Fujian, China, developed symptoms of severe wilting and stunting. The main stem exhibited reddish to light brown vascular discoloration. Approximately 30% of the 60,000 plants showed symptoms. To isolate the causal agent, necrotic tissue pieces (3 × 3 mm) from the symptomatic stem were surface disinfected with 1% NaClO for 1 min and washed three times with sterile water. The disinfected pieces were dried and placed on potato dextrose agar (PDA) at 25°C in the darkness for 4 days inside a dark chamber. Reddish-white and floccose mycelia developed on PDA after 3 days of incubation. Ten single-spored isolates were identified as *Fusarium kyushuense* based on morphological features (Aoki and O'Donnell 1998). Hyaline and straight or slightly curved macroconidia were observed with three to five septate, 24.5 to 46.6 × 3.6 to 5.7 μm (*n* = 100). Microconidia were ellipsoidal to clavate, zero to one septate, and 6.3 to 19.5 × 3.2 to 5.3 μm (*n* = 100). No chlamydospores were observed. In order to validate this result, partial RNA polymerase second largest subunit (*RPB2*) combined with translation elongation factor (*EF-1α*) gene regions were amplified and sequenced from three isolates with primers 5f2/11ar (Liu et al. 1999) and primers EF1/EF2 (Geiser et al. 2004), respectively. *Fusarium* MLST analysis showed that the *RPB2* (GenBank accession nos. MZ130468, MZ130469, and MZ130470) matched 99.72% (MH582170) to

F. kyushuense, and the *EF-1α* (MZ130471, MZ130472, and MZ130473) matched 99.84% (MH582297) to *F. kyushuense* in the *Fusarium* MLST. Besides, a phylogenetic analysis was conducted using the neighbor-joining algorithm based on the *RPB2* and *EF-1α* gene sequences. The isolates clustered with *F. kyushuense*. To assess pathogenicity, the three molecularly identified isolates were used. The isolates were grown on carboxymethyl cellulose medium (carboxymethyl cellulose [Sigma C-4888] 15.0 g, NH₄NO₃ 1.0 g, KH₂PO₄ monobasic 1.0 g, MgSO₄·7H₂O 0.5 g, yeast extract 1.0 g, distilled water filled to 1.0 liter) for sporulation. The roots of 12 healthy 30-day-old gerbera plants were inoculated by treating them with 10 ml of conidial suspension (1 × 10⁶ conidial/ml). A group of 12 seedlings of the same age was treated with sterile water to serve as the control. Plants were grown in a glasshouse at 23°C, relative humidity >70%, and 16 h of light per day. Typical symptoms of wilt and discoloration of the vascular system in roots and stems developed within 10 days. Uninoculated plants remained healthy. Isolates were consistently reisolated from the symptomatic stem, and the recovered isolates were identified as *F. kyushuense* by amplifying the *EF-1α* gene. The assays were conducted twice. *F. kyushuense* has been reported to cause wilt and rot of tobacco (Wang et al. 2013), maize ears (Wang et al. 2014), and rice (Zhao and Lu 2007) in China. To the best of our knowledge, this is the first report of *F. kyushuense* causing stem and root wilt on *G. jamesonii*. The disease must be considered in existing management practices.

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