Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Vascular Wilt Caused by *Fusarium proliferatum* on Cauliflower in China

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Cauliflower (*Brassica oleracea* var. *botrytis* L.), which belongs to the Brassicaceae, is an economically important vegetable crop in China and worldwide. Statistically, China is the largest cauliflower producer in the world (FAOSTAT 2018). During September 2017 to June 2018, severe outbreaks of root rot were observed on cauliflower in several commercial fields (approximately 3.5 ha), with disease incidence of approximately 25 to 50% in the Acheng District (127°06'E, 45°53'N) of Harbin City, Heilongjiang Province, China. Symptoms included leaf yellowing and wilting, plant stunting, root rot, and vascular discoloration of the stems and roots. A total of 15 symptomatic plants were uprooted and collected from seven fields. Infected tissues were surface sterilized by soaking in 1% sodium hypochlorite for 1 min, followed by three rinses in sterile distilled water, and then placed on potato dextrose agar (PDA) and incubated at 25°C in the dark for 5 days. In total, 21 cultures were obtained and purified by single-spore subcultures on PDA and carnation leaf agar (CLA; Leslie and Summerell 2006) for morphological identification. The colonies on PDA were originally white, later becoming light to dark purple in color with abundant aerial hyphae. Macroconidia were abundant on CLA, hyaline, slightly curved, three- to five-septate, with a distinct basal foot cell, measuring 20.6 to 46.8 × 2.4 to 4.6 µm. Microconidia were in short chains on monophialides and polyphialides, oval or ellipsoid, with a flat base, zero- to one-septate, measuring 4.7 to 15.1 × 2.1 to 4.4 µm. No

chlamydospores were observed. The morphological features were consistent with *Fusarium proliferatum* (Matsushima) Nirenberg (Leslie and Summerell 2006). Pathogenicity tests were performed on the four-true-leaf stage of healthy cauliflower ‘Jingxue no. 88’ seedlings by dipping the roots into a conidial suspension (1×10^6 conidia/ml) for 10 min, which were produced on CLA. Control plants were dipped in sterile distilled water. Seven days later, inoculated plants developed typical leaf yellowing, vascular discoloration, and wilting symptoms identical to those observed in the fields, whereas the control plants remained healthy. *F. proliferatum* was reisolated from symptomatic stems, confirming Koch’s postulates. Genomic DNA was extracted from fungal mycelium using the Plant Genomic DNA Kit (Tiangen, China). The nuclear ribosomal internal transcribed spacer region (ITS), mitochondrial ribosomal small subunit (mtSSU), and translation elongation factor 1- α (TEF-1 α) regions were amplified using primers ITS1/ITS4, NSM1/NSM2 (Li et al. 1994), and EF1/EF2 (Geiser et al. 2004), respectively. The resulting 537-bp ITS, 711-bp mtSSU, and 699-bp TEF-1 α sequences of isolate HYC1410080401 were deposited in GenBank (MT378328, MT378332, and MT379885, respectively). BLAST analysis showed 100% identities to the ITS and TEF-1 α sequences of *F. proliferatum* (MN809262.1 and MF445092.1) and 99.86% similarity with the mtSSU sequence of *F. proliferatum* (DQ831947.1). To our knowledge, this is the first report of *F. proliferatum* causing cauliflower vascular wilt worldwide (Farr and Rossman 2020). The pathogen has a worldwide distribution and an unusually broad host range, which can be of great significance, and control strategies should be followed.

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