Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Fusarium oxysporum* Causing Coriander Wilt Disease in North China

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Coriander or cilantro (*Coriandrum sativum* L.) is extensively used as a fresh herb in China. During the summer of 2019 in Tianjin, China, coriander plants showed a previously unknown wilt in commercial fields. In severely infected fields, approximately 85% of the plants at vegetative stages were stunted, chlorotic, wilted, or dead. Vascular tissues of the main stem and root were discolored. Soil samples were collected from five fields with a history of severe wilt disease in Tianjin since the fall of 2019. Seeds of coriander cultivar ‘Ansemi’ were sown in soil from the five fields and were cultured in a greenhouse at 22°C/20°C (12 h/12 h, light/dark) and 75% relative humidity. After 50 days’ cultivation, infected seedlings exhibited similar symptoms to those of plants in the field. Twenty symptomatic seedlings from each of the collected field soil samples were harvested and washed for 3 min under running water. Then vascular tissue fragments (3 mm²) of stem and root at the boundary of the symptomatic area were excised and placed on improved Komada’s medium, which is selective for *Fusarium* sp. (Komada 1975). After incubation at 25°C for 5 days in the dark, 70% of the isolates generated white to pale pink aerial hyphae on PDA. Microconidia were single-celled, hyaline, nonseptate and ovoid, and measured 5.6 to 14.1 × 2.1 to 3.8 µm (*n* = 40). Macroconidia were three to five-septate, slightly curved at the apex, and ranged from 11.2 to 38.6 × 3.2 to 4.5 µm (*n* = 40). Based on morphological characteristics, these fungi were preliminarily identified as *F. oxysporum* (Leslie and Summerell 2006). For molecular identification, the ITS gene, TEF1-α gene, and mtSSU gene of cultures from two

representative single-spored isolates XC02 and XC03 were amplified and sequenced (Carbone and Kohn 1999; Li et al. 1994; White et al. 1990). The sequences were submitted to GenBank (MT579855 and OK326765 for ITS; MT597425 and OK256882 for TEF1-α; MT587799 and OK330480 for mtSSU). BLASTn analyses indicated that the nucleotide sequences of the three loci of the two isolates were 99.8 to 100% homologous to sequences of *F. oxysporum* in the NCBI database and *Fusarium* MLST database. A multilocus phylogenetic tree was drawn via unweighted pair-group method with arithmetic means (UPGMA) analysis of the combined ITS, TEF1-α, and mtSSU partial sequence data from the *Fusarium* MLST database. Pathogenicity of each isolate was tested on ten 15-day-old healthy coriander seedlings in each treatment according to the method of Yang et al. (2021). The first wilt symptoms developed 3 days after inoculation, and 7 to 10 days after inoculation 90 to 100% of the plants were dead. Control plants remained healthy. To fulfill Koch’s postulates, *F. oxysporum* were reisolated from the diseased tissues and verified based on morphology and sequencing as described above. The experiments were repeated twice with similar results. *F. oxysporum* has been reported to cause coriander wilt disease in India, Argentina, California (Koike and Gordon 2005), and Italy (Gilardi et al. 2019). To our knowledge, this is the first report of *F. oxysporum* causing coriander wilt disease in north China. Compared with *F. equiseti* in the previous report (Yang et al. 2021), *F. oxysporum* isolates possessed higher separation frequency and stronger pathogenicity to coriander seedlings. Thus, attention should be given to *F. oxysporum* causing coriander wilt diseases when developing effective management strategies in north China.

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