Diseases Caused by Bacteria and Phytoplasmas

First Report of Bacterial Soft Rot Caused by *Pantoea agglomerans* on Chinese yam (*Dioscorea opposita*) in China

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Chinese yam (*Dioscorea opposita* Thunb.), which belongs to the family Dioscoreaceae, is widely naturalized throughout China due to its high economic and medicinal value. Since 2019, water-soaked lesions have been frequently observed in the underground tubers of Chinese yams in Xinyang City, Henan Province. To identify the causal agent, 10 pieces of tissue from underground tubers with disease symptoms were collected. Those infected tissues (5 × 5 mm) were crushed in 500 µl of sterilized water after surface sterilization and streaked onto Luria-Bertani agar plates. Pale yellowish and slimy single bacterial colonies with smooth margins were observed after 24 h of incubation, and three bacterial colonies (CY-1, CY-2, and CY-3) were

randomly selected for further biochemical and molecular characterization. These bacteria were rod-shaped, gram-negative cells with a cell length of 1.0 to 3.0 µm and width of 0.5 to 1.0 µm, with peritrichous flagella. Subsequently, the bacteria were biochemically analyzed through BIOLOG (Hayward, CA) and identified as *Pantoea agglomerans* with 99% probability. Furthermore, the phylogenetic analysis results based on 16S rDNA, DNA gyrase subunit B (*gyrB*), and RNA polymerase sigma factor (*rpoD*) showed these three isolates were most closely related to *P. agglomerans*. The sequences of 16S rDNA, *gyrB*, and *rpoD* of each strain were submitted to GenBank with the accession numbers MZ541065, MZ541066, and MZ541067 for 16S rDNA; MZ669846, MZ669847, and MZ669848 for *gyrB*; and MZ669849, MZ669850, and MZ669851 for *rpoD*. A pathogenicity test was performed to complete Koch's postulates. Tubers of two common varieties of Chinese yam were wounded by a sterile needle and inoculated with 500 µl of a 10⁸ CFU/ml bacterial suspension. Sterilized water was used as a control. Five pots were inoculated for each isolate. Water-soaked lesions appeared after 5 days of incubation at 25°C in a biochemical incubator, and no lesions were observed on the control. Bacteria reisolated from the lesions were similar in phenotypic and molecular characteristics to the original isolates. In brief, based on colony morphology, biochemical tests, characteristic sequence analysis, and pathogenicity verification, the pathogen responsible for the soft rot of Chinese yam in Henan Province was identified as *P. agglomerans*. In China, *P. agglomerans* has been reported to be associated with bacterial soft rot on Chinese cabbage (Guo et al. 2020). To our knowledge, this work is the first report of bacterial rot caused by *P. agglomerans* on Chinese yam.

Reference:

Guo, M., et al. 2020. Plant Dis. 104:277.

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