Diseases Caused by Bacteria and Phytoplasmas

First Report of *Pseudomonas aeruginosa* Causing Basal Stem Rot of *Solanum lycopersicum* in China

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Tomato (*Solanum lycopersicum* L.) is an economically important crop in China and elsewhere. A previously unreported basal rot of tomato affecting as much as 15% of the stems was first observed in greenhouses in Northwest China (Jingyuan County, Baiyin City, Gansu Province) in March 2015, and the same disease was observed every year from 2016 to 2021 in the region. The loss of local agricultural income from this plant disease in greenhouses is up to 2 million Chinese yuan each year. Symptoms on the basal stems were initially characterized by water-soaked lesions, which developed rapidly into a soft, watery, decayed mass within 5 to 10 days after their appearance. Ten symptomatic stem samples were collected from basal stems exhibiting decay and were processed for microbiological analysis. Three strains of the bacteria (BBSR1 to BBSR3) isolated from symptomatic samples were gram-negative, rods with a single polar flagellum, 0.5 to 1.0 × 1.5 to 3.5 µm. Colonies on nutrient agar (NA) medium were round, smooth, translucent, with flat edges and elevated center (“fried egg” appearance), and yellowish green to light purple in color. All isolates were positive for oxidase, gelatin liquefaction, denitrification, lipase, arginine dihydrolase, growth at 41°C, utilization of mannitol, and production of pyocyanin. They were negative for levan formation; lecithinase; hydrolysis of starch; growth at 4°C, utilization of maltose, xylose, γ-aminobutyrate, and ethylene glycol; and growth in media supplemented with 8.5% NaCl. The representative bacterium (BBSR1) was identified as *Pseudomonas aeruginosa* using Biolog-based Bacterial Identification System

version 4.2 (Biolog, Hayward, CA), revealing 88% similarity to *P. aeruginosa* in the OmniLog Biolog database. The identity was further confirmed as *P. aeruginosa* based on 16S rRNA sequence (1,387 bp) analysis with universal primers 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3'). A BLASTn search of GenBank revealed a 100% identity to that of *Pseudomonas aeruginosa* strains JCM5962 (LC069033), SM-1 (KP794924), and KUN4 (KR025537). The 16S rRNA gene sequence of strain BBSR1 (1,387 bp) was deposited in GenBank (KT454095). Strain BBSR1 was further evaluated in pathogenicity tests. One-month-old tomato (cv. Tomo608) potted plants were spray inoculated with BBSR1 bacterial suspensions (~3 × 10⁸ CFU/ml) and wounded with a sterilized needle prior to inoculation. Controls were wounded similarly and inoculated with sterile water. The experiment was maintained at 28°C with 80 to 85% relative humidity in a greenhouse. Three replicates were used for each treatment with three mature plants in each pot. Symptoms developed within 14 days and were similar to those originally observed, whereas symptoms did not occur on the control plants. Strains recovered on NA were identified as *P. aeruginosa* based on physiological and biochemical characteristics and Biolog (Biolog). Although *P. aeruginosa* is generally regarded as a human conditional pathogen, it has been reported to cause disease on a variety of plants including ginseng (Gao et al. 2014), tinda (Mondal et al. 2012), onion (Abd-Alla and Bashandy 2012), and sweet basil (Walker et al. 2004). This is the first report of *P. aeruginosa* causing basal stem rot on tomato in Gansu Province, China. Under globalization, people should give great importance to bacterial pathogens that cross kingdoms to cause infection and become copathogenic in plants and animals.

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