Diseases Caused by Bacteria and Phytoplasmas

First Report of *Dickeya fangzhongdai* Causing Peduncle Soft Rot of Banana in China

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Banana (*Musa* spp.) is a popular fruit all over the world, and an important cash crop with a planting area of 358,924 ha in southern China. In July 2020, a peduncle soft rot disease occurred on dwarf banana (*Musa* sp. cv. Guangfen) in Guigang City (22°50'29" N, 109°43'34" E), Guangxi Province, China. More than 20% of plants were infected in a banana plantation. The first external sign of the disease appeared on the incisional wound after the flower bud was cut off from the peduncle. The symptoms initially appeared as a black lesion on the wound and then extended into the internal tissue of the whole peduncle. In the later stages, the internal tissue became soft and rotted, occasionally formed a necrotic cavity, and eventually led to black rot of the whole peduncle with a foul smell. To isolate the pathogen, 5- × 5-mm samples of internal lesion tissues were collected from the border of symptomatic and healthy tissue, treated with 75% ethanol for 10 s and 0.1% HgCl₂ for 3 min, and rinsed with sterile water three times. Sterilized tissue fragments were cut into pieces with sterilized surgical shears, soaked in 5 ml of sterile water, and shaken for 10 min in a vortex oscillator. The suspension was diluted 1,000 times with sterilized water, plated on nutrient-agar medium, and incubated at 28°C in darkness for 24 h. Among the 32 isolates, 23 pure bacterial cultures with similar morphology were predominantly obtained from the samples. These bacteria were gram-negative, and their colonies were initially yellowish white with irregular edges and smooth surfaces and turned grayish blue after 72 h of incubation at 28°C. Representative isolates GZF2-2 and GZF1-8 were selected for further identification. Genomic DNA was isolated from the bacteria, and the 16S rDNA was amplified with

primers 27F/1492R (Weisburg et al. 1991) and sequenced. The obtained sequences (GenBank accession nos. MZ768922 and OK668082) showed >99% identities to several records of *Dickeya fangzhongdai* deposited in NCBI GenBank (1400/1404 bp for GZF2-2 to KT992690 and 1409/1417 bp for GZF1-8 to MT613398) based on BLAST analysis. In addition, the *recA*, *fusA*, *gapA*, *purA*, *rplB*, and *dnaX* genes and the 16S-23S intergenic spacer (IGS) regions of the two isolates were also amplified and sequenced (GenBank accession nos. OK634381 and OK634382, OK634369 and OK634370, OK634373 and OK634374, OK634377 and OK634378, OK634385 and OK634386, OK634365 and OK634366, and OK631722 and OK631723, respectively) as described by Tian et al. (2016). All the DNA sequences matched those of *D. fangzhongdai* strains JS5^T (percent identities >99.06%) PA1, and ECM-1 in GenBank. Neighbor-joining phylogenetic analysis by the software MegaX (Kumar et al. 2018) based on the 16S rDNA sequences revealed that the two isolates were in the same clade with reported *D. fangzhongdai* strains. Multilocus sequence analysis of the other seven regions also showed the two representative isolates belonged to *D. fangzhongdai*. Therefore, the isolates were identified as *D. fangzhongdai*. Pathogenicity of isolate GZF2-2 was investigated to demonstrate Koch's postulates. The ends of the banana peduncles of six healthy plants were cut off, and 10 ml of bacterial suspension (10⁸ CFU/ml) was inoculated to the fresh wound on the plants using sterile brushes. Six control plants were inoculated with sterilized water. All the inoculated peduncles were covered with plastic bags to maintain high humidity. After 28 days, all the peduncles inoculated with strain GZF2-2 showed soft rot symptoms similar to those observed in the field, while the controls remained symptomless. The same bacteria were reisolated from the symptomatic peduncles and confirmed by sequencing the 16S rDNA. *D. fangzhongdai* has been reported to cause soft rot on onion (Ma et al. 2020) and bleeding cankers on pear trees (Chen et al. 2020). To the best of our knowledge, this is the first report of *D. fangzhongdai* causing peduncle soft rot on banana in China.

References:

- Chen, B., et al. 2020. J. Int. Agr. 19:889.
- Kumar, S., et al. 2018. Mol. Biol. Evol. 35:1547.
- Ma, X., et al. 2020. Plant Dis. 104:1251.
- Tian, Y., et al. 2016. Int. J. Syst. Evol. Microbiol. 66:2831.
- Weisburg, W. G., et al. 1991. J. Bacteriol. 173:697.

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