Diseases Caused by Bacteria and Phytoplasmas

Occurrence of *Dickeya fangzhongdai* Causing Soft Rot of Banxia (*Pinellia ternata*) in China

Fanfan Wang, Tao Tang, Ting Mao, Jie Guo, Xiaoliang Guo, Yuanyuan Duan, and Jingmao You[†]

Institute of Chinese Herbal Medicines, Hubei Academy of Agricultural Sciences, Enshi, 445000, China

F. F. Wang and J. M. You contributed equally to this work.

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Banxia (*Pinellia ternata* [Thunb.] Breit., Araceae) is a perennial herbaceous plant whose tuber is commonly used in traditional Chinese herbal medicine. In the summer of 2020, an outbreak of soft rot of banxia was observed in Zhugentan Town (30.50°N, 112.91°E), Qianjiang City, Hubei Province, with about 56% of plants being infected. Symptomatic plants initially appeared with small water-soaked spots on leaves that progressed into extensive translucent spots when facing a light source. The bacteria further spread to the stems and tubers. Infected tubers appeared normal, but inner macerated inclusions exuded when touched. The whole plant was macerated and collapsed within a few days. Ten leaves with typical symptoms were obtained from a diseased field, surface sterilized in 75% ethanol for 30 s and 0.3% NaClO for 5 min, and the tissue sections washed three times in sterile water. Small pieces of tissue (5 × 5 mm) were removed from lesion borders, plated

on nutrient agar medium, and cultivated at 37°C for 48 h. Five representative isolates were selected for further identification. Colonies were all smooth and transparent. In addition, these strains were gram negative and had the ability to reduce D-arabinose, melibiose, galactose, raffinose, rhamnose, inositol, and mannitol but not reduce 5-keto-D-gluconate, L-xylose, amygdalin, and sorbitol. Genomic DNA was extracted from isolate stain ZG5. The 16S rDNA gene, recombinase A (*recA*) gene, and DNA polymerase III subunits gamma and tau (*dnaX*) were amplified by PCR with the primers 27f/1492r (Weisburg et al. 1991), *recF/recR* (Waleron et al. 2002), and *dnaXf/dnaXr* (Sławiak et al. 2009), respectively. The PCR products were sequenced and then submitted to GenBank (MW332472, MW349833, and MW349834, respectively). BLAST search showed that the sequences of 16S rDNA, *recA*, and *dnaX* respectively matched ≥99% with *Dickeya fangzhongdai* strains DSM 101947 (CP025003), QZH3 (CP031507), and PA1 (CP020872). Pathogenicity tests were performed on 10 healthy, 3-month-old *P. ternata* plants. Five plants were injected with 20 µl of bacterial suspension (10⁸ CFU/ml) of isolate ZG5, and other plants were injected with sterile water as a negative control. All tested plants were incubated at 28°C and individually covered with a plastic bag. After 24 h, soft rot symptoms all appeared on the pathogen-inoculated leaves, whereas no symptoms appeared on the control leaves. The pathogenicity test was repeated three times and the same results obtained. Koch's postulates were fulfilled by reisolating *D. fangzhongdai* from inoculated plants. Meanwhile, PCR was performed on the reisolated bacteria as described above, and the pathogen was identified and confirmed as *D. fangzhongdai*. Here we report that *D. fangzhongdai* causes soft rot of *P. ternata* in China. The disease progressed rapidly and reduced the yield and quality of tubers. Thus, more research is needed to implement effective strategies to manage this disease.

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[†]Indicates the corresponding author.
J. M. You; jingmaoyou@126.com