Diseases Caused by Bacteria and Phytoplasmas

First Report of *Burkholderia cepacia* Causing Finger-Tip Rot on Banana Fruit in the Guangxi Province of China

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Banana (*Musa acuminata*) is one of the most popular and widely consumed fruit crops in the world. During late October to early November 2020, a banana finger-tip rot disease was observed in a banana (cultivar Brazil, AAA group) orchard of about 12 ha in Zhongcun, Zhangmu Town, Fumian District, Yulin City, Guangxi province, China. The disease incidence was about 0.5% at the surveyed field. Infected fingers and their tips were usually normal in appearance and then developed brown to black discoloration in the central fruit pulp adjacent to the fingertips. In severe infections, diseased fingers showed brown to black discoloration in both the central and the periphery fruit pulp and along the longitudinal axis throughout the fruit. Symptomatic banana fingers were surface disinfected with 1% sodium hypochlorite for 30 s and 75% ethanol for 30 s, and rinsed three times with sterile distilled water. Flesh tissues were ground in a sterile mortar and soaked in 1 ml of sterile distilled water for 30 min. A tissue suspension of 50 µl was streaked onto Luria-Bertani (LB) medium. Single colonies were picked and restreaked onto new LB medium. The cultures were incubated at 37°C for 24 h. Two representative strains, GX and GX2, were obtained from symptomatic pulps and used in the following studies. To molecularly identify the bacterial species, we performed a polymerase chain reaction (PCR) using *16S rRNA* and *recA* primers (Lee and Chan 2007; Turner et al. 1999) and amplified

1,442- and 1,019-bp sequences, respectively. The amplified sequences were deposited in GenBank under the accession numbers MZ267253 and MZ961355 for the *16S rRNA* and MZ287336 and MZ983484 for the *recA* genes. BLASTn searches shared more than 99% similarity with the reference sequences of *Burkholderia cepacia* strains (MK680073.1 and KC261418.1 for *16S rRNA*; AY598028.1 and KF812859.1 for *recA*). Phylogenetic trees constructed using the *16 rRNA* and *recA* sequences showed that GX and GX2 strongly clustered with *B. cepacia* type strains. To further determine the genomovars of strains GX and GX2, we used specific PCR primers for the *B. cepacia* epidemic strain marker (*BCESM*), type III secretion gene cluster (*bcsV*), and cable pilin subunit gene (*cblA*) (Ansari et al. 2019; Lee and Chan 2007). The presence of *bcsV* and *BCESM* were confirmed by PCR, while *cblA* was not observed in the strains GX and GX2, suggesting that the isolated strains belong to *B. cepacia* genomovar III and are slightly different from the Iranian and Taiwan strains of *B. cepacia* (Ansari et al. 2019; Lee and Chan 2007). A pathogenicity test was conducted on banana fingers (cultivar Zhongjiao No. 3) at the immature and fully ripe stages. A final suspension of 10⁶ CFU/ml was injected into the banana fingers (100 µl/finger) through the center of the stigma (Ansari et al. 2019; Lee and Chan 2007). Fingers inoculated with sterile water were used as a negative control. To maintain humidity, the treated fingertips were wrapped with Parafilm. For each treatment, 10 independent replicates were conducted. At 10 days postinoculation (dpi), the pulp of immature bananas exhibited reddish brown decaying tissue, which were similar symptoms to those observed in the field. Moreover, the pulp tissues of ripe bananas showed a dark brown discoloration in the tip at 5 dpi, whereas the controls remained symptomless. The same bacterium was reisolated from diseased tissues and its identification confirmed by *16S rRNA*, thus fulfilling Koch's postulates. This disease was first described in Honduras in Latin America and then reported in Taiwan province of China and Iran (Ansari et al. 2019; Buddenhagen 1968; Lee et al. 2003). To our knowledge, this is the first report of banana finger-tip rot caused by *B. cepacia* in Guangxi province, China. It is necessary to determine the distribution of *B. cepacia* and to prevent its spread in Guangxi.

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