Diseases Caused by Bacteria and Phytoplasmas

First Report of *Pectobacterium versatile* Causing Aerial Stem Rot of Potato in China

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Pectobacterium species cause blackleg, soft rot, and stem rot in potato and many other vegetable crops (Charkowski 2015). In July 2020, potato plants showing characteristic symptoms of aerial stem rot were observed in a field (cv. Xisen 6) in Fengning Manchu Autonomous County, Chengde, Hebei Province (North China). The disease incidence in that field (5 ha in size) was more than 50%. Putative pectolytic bacteria were obtained from symptomatic stem tissues (light brown and water-soaked stem sections) by culturing on crystal violet pectate (CVP) medium. Bacterial colonies producing pits were restreaked and purified on Luria-Bertani (LB) agar. The isolates causing stem rot were gram-negative and rod shaped, negative for oxidase, urease, indole production, gelatin liquefaction, and acid production from maltose and D-sorbitol. All isolates were catalase positive, produced acid from lactose, rhamnose, saccharose, raffinose, and D-arabinose, and were tolerant to 5% NaCl, and able to utilize citrate. The bacterial gDNA was extracted using the EasyPure Bacteria Genomic DNA Kit (TransGen Biotech, Beijing). The 16S rDNA region was amplified by PCR using the universal primer pair 27F/1492R and sequenced. Result of the BLASTn analysis of the 16S rDNA

amplicons (MZ379788, MZ379789) suggested that the isolates FN20111 and FN20121 belonged to the genus *Pectobacterium*. To determine the species of the stem rot *Pectobacterium* isolates, multilocus sequence analysis (MLSA) was performed with six housekeeping genes *acnA*, *gapA*, *icdA*, *mdh*, *proA*, and *rpoS* (MZ403781–MZ403792), and the phylogenetic tree was reconstructed using RAxML v8.2.12 (<https://github.com/stamatak/standard-RAxML>). The result of phylogenetic analysis showed that the stem rot *Pectobacterium* isolates FN20111 and FN20121 clustered with *P. versatile* (syn. '*Candidatus Pectobacterium maceratum*') strains CFBP6051^T (Portier et al. 2019), SCC1 (Niemi et al. 2017), and F131 (Shirshikov et al. 2018). The isolates FN20111 and FN20121 were more closely related to the type strain CFBP6051^T than to strains SCC1 and F131. Potato seedlings (cvs. Xisen 6 and Favorita) were inoculated with the isolates FN20111 and FN20121 by injecting 100 µl of bacterial suspensions (10⁸ CFU·ml⁻¹) into the upper parts of the stems of potato plants, or injected with 100 µl of 0.9% saline solution as control. The seedlings were grown at 28°C and 50% relative humidity. Three days postinoculation, only the bacteria-inoculated seedlings showed diseased symptoms resembling those observed in the field. Bacterial colonies were obtained from the infected stems and were identified using the same PCR primers of housekeeping genes as described above, fulfilling Koch's postulates. *Pectobacterium versatile* causing soft rot and blackleg on potato plants has been reported in Finland (Niemi et al. 2017), Russia (Shirshikov et al. 2018), the Netherlands (Portier et al. 2019), Poland (Waleron et al. 2019), and in New York State (Ma et al. 2021). To our knowledge, this is the first report of *P. versatile* causing aerial stem rot of potato in China.

References:

- Charkowski, A. O. 2015. Am. J. Potato Res. 92:223.
- Ma, X., et al. 2021. Plant Dis. 105:2585.
- Niemi, O., et al. 2017. Stand. Genomic Sci. 12:87.
- Portier, P., et al. 2019. Int. J. Syst. Evol. Microbiol. 69:3207.
- Shirshikov, F. V., et al. 2018. Genome Announc. 6:e00260-18.
- Waleron, M., et al. 2019. Plant Dis. 103:1409.

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