Diseases Caused by Bacteria and Phytoplasmas

First Report of *Streptomyces stelliscabiei* Causing Potato Common Scab in Guizhou Province, China

U. Handique, R. F. Zhang, Z. X. Zhang, Z. W. Feng, Q. H. Sun, and J. Wu[†]

Inner Mongolia Potato Engineering and Technology Research Center, Inner Mongolia University, Hohhot 010021, China

Funding: Funding was provided by Start Funding of Inner Mongolia University (no. 30300-5205162) and China Agriculture Research System of MOF and MARA. Plant Dis. 106:311, 2022; published online as <https://doi.org/10.1094/PDIS-06-21-1242-PDN>. Accepted for publication 17 August 2021.

Potato (*Solanum tuberosum* L.) common scab can be caused by multiple pathogenic *Streptomyces* spp. worldwide (Braun et al. 2017; Doering-Saad et al. 1992). Potato tubers (cv. Favorita) with severe pitted common scab symptoms were observed at a small farm (2 ha) during harvest in Anshun, Guizhou province, in early May 2020. The disease incidence was around 10%, and symptomatic samples were collected to isolate the pathogen. Potato peels with lesions were peeled off, soaked in 75% ethanol for 2 min, rinsed with sterile distilled water, and ground. The solution was then serially diluted, plated onto glucose yeast malt extract agar (GYM) (Han et al. 2005), and incubated for 7 days at 28°C to obtain individual colonies. Colonies that showed *Streptomyces* phenotype were further transferred onto GYM agar to obtain pure colonies. Amplification of the 16S rRNA gene was performed using the universal primer set 8F/1492R (Weisburg et al. 1991), and the amplicons were sequenced and blasted against the NCBI GenBank database. Two isolates, ZR-IMU141 and ZR-IMU146 (accession nos. MW995958 and MW995959 respectively), showed more than 99% sequence identity to *Streptomyces stelliscabiei* sequences (accession no. HM018085). *S. stelliscabiei*-specific PCR primers Stel3 and T2st2, produced a 476-bp fragment. Five housekeeping genes

for multilocus sequence analysis (MLSA) of *Streptomycetaceae* (Guo et al. 2008) were amplified, sequenced, and uploaded to NCBI: *atpD* (MZ343164 and MZ343165), *gyrB* (MZ343162 and MZ343163), *recA* (MZ343166 and MZ343167), *rpoB* (MZ343168 and MZ343169), and *trpB* (MZ343170 and MZ343171). All the genes show over 98% identity with *S. stelliscabiei*. Phylogenetic trees of 16S rRNA gene sequence and MLSA were constructed by using Molecular Evolutionary Genetics Analysis (MEGA X) software. The two isolates contain pathogenicity genes *txtAB*, *nec1*, and *tomA* (Wanner 2006), which was confirmed by PCR. To complete Koch's postulates, nine potato seedlings (cv. Favorita, 15 cm high), were transferred to new pots and inoculated with spore suspensions of ZR-IMU141 and ZR-IMU146 (10^4 CFU/ml), or water as a negative control. Two months later, potato tubers inoculated with either ZR-IMU141 or ZR-IMU146 exhibited typical symptoms of potato common scab, such as superficial or deep, raised, pitted, or polygonal lesions like the field symptoms, but the negative controls remained asymptomatic. Potting experiments were repeated twice. The pathogens were reisolated from the lesions and confirmed identical to the original isolate by 16S rRNA gene sequences. To our knowledge, this is the first report of *S. stelliscabiei* causing potato common scab in Guizhou province, China. We believe that this report will draw attention to the study and management of the increased pool of scab pathogens in China.

References:

- Braun, S., et al. 2017. Am. J. Potato Res. 94:283.
- Doering-Saad, C., et al. 1992. Appl. Environ. Microbiol. 58:3932.
- Guo, Y., et al. 2008. Int. J. Syst. Evol. Microbiol. 58:149.
- Han, J. S., et al. 2005. J. Appl. Microbiol. 99:213.
- Wanner, L. A. 2006. Phytopathology 96:1363.
- Weisburg, W. G., et al. 1991. J. Bacteriol. 173:697.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: *Solanum tuberosum* L., *Streptomyces stelliscabiei*, potato common scab

[†]Indicates the corresponding author.
J. Wu; jianwu@ufl.edu