Diseases Caused by Bacteria and Phytoplasmas

First Report of ‘*Candidatus Phytoplasma ziziphi*’ in Sweet Potato in China

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Sweet potato (*Ipomoea batatas*; family Convolvulaceae) is an important food crop and serves as a ground cover in orchards of jujube trees. In August 2020, sweet potatoes growing under jujube trees showed obvious jujube witches’ broom (JWB) phytoplasma disease symptoms in an abandoned jujube orchard in Xinzheng county, Henan province, China (34°35′54″N, 113°49′56″E). The sweet potato plants were showing symptoms such as small, yellowing leaves and witches’ broom. The incidence of symptomatic sweet potato plants in the orchard (60 × 100 m) was about 60%. Leaf samples of sweet potatoes and jujube trees exhibiting disease symptoms were collected to confirm the presence of JWB phytoplasma by PCR. The phytoplasma primers R16mF2/R16mR1 (Gundersen and Lee 1996) and secAfor1/sArev3 (Hodgetts et al. 2008) were used. Leaf samples of three sweet potato plants and three jujube trees exhibiting disease symptoms were collected to confirm the presence of JWB phytoplasma by PCR. Two healthy sweet potatoes collected from the experimental station at Henan Agricultural University and two healthy, in vitro-grown jujube plantlets were used as negative

controls. A JWB-diseased in vitro-grown jujube plantlet was set as the positive control. The total DNA of three leaves from each sample was extracted using the Hi-DNA secure Plant Kit (DP350, TianGen, Beijing, China). The phytoplasma amplicon was detected in all leaf samples. The expected 16S rDNA (GenBank accession no. MW990090) amplicon is 1,348 bp, and the expected secA (GenBank accession no. MZ292648) amplicon is 842 bp. These two fragments were detected in the sweet potato samples. The DNA fragment amplified from the diseased sweet potato and the diseased jujube leaf samples exhibiting disease symptoms using the 16S rRNA primers was then sequenced (Sangon Biotech, Shanghai, China) and was 100% identical to that of 23 JWB phytoplasma strains through BLAST analysis. The DNA fragment amplified using the secA primers was sequenced and was 100% identical to that of JWB phytoplasma strain ZQ secA gene (GU471770.1). Restriction fragment length polymorphism (RFLP) analysis of the 16S rRNA sequence fragment by the online tool iPhyClassifier (Wei et al. 2007) indicated that the pathogen strain was a member of subgroup 16SrV-B and a ‘*Candidatus Phytoplasma ziziphi*’-related strain. Sweet potato witches’ broom disease was reported by Gundersen and Lee (1996) and Lee et al. (2004). Sweet potato little leaf disease was reported and classified as a phytoplasma in the 16 SrII group (Tairo et al. 2006). According to the evolutionary analysis, the 16S rRNA nucleotide sequences found in sweet potato in this study were quite different from those detected in sweet potato little leaf disease. Taken together, the results indicated that the phytoplasma associated with sweet potato in the present study is a ‘*Ca. Phytoplasma ziziphi*’ strain. To our knowledge, this is the first report of its presence in sweet potato in China.

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