Disease Note

FIRST REPORT OF TOMATO SPOTTED WILT VIRUS INFECTING TREE TOMATO (SOLANUM BETACEUM CAV.) IN ECUADOR

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The tree tomato (Solanum betaceum Cav.) is an important edible fruit crop from the family Solanaceae that is native to South America. In 2014-2015 mosaic and necrotic symptoms on young leaves and stems were observed on tree tomato plants in Azuay provinces of Ecuador. Based on the type of symptoms, infection by a tospovirus was suspected. The presence of Tomato spotted wilt virus (TSWV, genus Tospovirus, family Bunyaviridae) was ascertained in symptomatic tissue by triple antibody sandwich (TAS)-ELISA using specific antibodies (Agdia, USA). TSWV was confirmed by RT-PCR using total RNA isolated from ELISA positive samples with the RNAs easy Plant Mini kit (Qiagen). DNA fragments of ca. 800 bp were amplified using degenerate universal tospovirus primers (Chu et al., 2001). A PCR product was sequenced (Macrogen, Seoul, Korea) and the sequence was deposited in GenBank as accession no. KP772268. Sequence analysis (BioEdit v. 7.05) of TSWV isolate Ecuador with other tospovirus isolates showed 99.5% and 99.1% identity at the nucleotide and amino acid levels, respectively. A phylogenetic tree based on nucleotide sequences constructed using MEGA version 4.1 revealed a clustering of TSWV-Ecuador with other tospovirus isolates in five serogroups. PhyClassifier, showed that TSWV-Ecuador was consistent with that of Peanut witches’-broom phytoplasma, a 16SrII-A subgroup phytoplasma. To our knowledge, this is the first report of the occurrence of TSWV on tree tomato in Ecuador.


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Disease Note

FIRST REPORT OF A 16SrII-A PHYTOPLASMA INFECTING CELOSIA ARGENTEA IN CHINA

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Celosia argentea L. (Amaranthaceae), is an annual herb and ornamental plant frequently seen in China. In 2015, symptoms of witches’-broom and phyllody were observed on C. argentea in Haikou, Hainan province, China. Three symptomatic plants and two asymptomatic ones were collected for phytoplasma detection and classification (Dickinson and Hodgetts, 2013). Total DNAs were extracted, and phytoplasma diagnosis was performed by nested PCR using primer pairs P1/P7 and R16F2n/R16R2n. Fragments about 1.8 (P1/P7) and 1.2kb (R16F2n/R16R2n) were only detected in all symptomatic plant samples, which confirmed phytoplasma infection. For phytoplasma classification, 16SrRNA gene and rp (ribosomal proteins) gene were amplified by high-fidelity DNA polymerase with primers P1/P7 and rp(II)F1/rp(II)R1, and three clones of each amplicon from each sample were sequenced. The consistent sequences were deposited in GenBank with accession number KX426374 (16SrRNA) and KX426375 (rp). Partial 16SrRNA gene sequences (between R16F2n and R16R2n) were used for C. argentea phytoplasma identification at group and subgroup levels. Phylogenetic tree analysis, performed by MEGA 5.0 using neighbor-joining method, showed C. argentea phytoplasma was grouped with 16SrII-A group phytoplasmas. Virtual RFLP analysis, carried out by iPhyClassifier, showed that RFLP profile from C. argentea phytoplasma was consistent with that of Peanut witches’-broom phytoplasma, a 16SrII-A subgroup phytoplasma. To our knowledge, this is the first report about a 16SrII-A subgroup phytoplasma associated with phytoplasma disease on C. argentea in China, although 16SrII phytoplasmas were detected in the same host showing little leaf and witches’-broom on Guadalcanal in the Solomon islands (Davies and Tsatsia, 2009).


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