**DISEASE NOTE**

**FIRST REPORT OF WATERMELON SILVER MOTTLE VIRUS INFECTING TOMATO IN YUNNAN, CHINA**

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Tomato is an economically important vegetable crop in Yunnan province. During a survey in November 2015, about 17% of tomato plants showing chlorosis on leaves and the presence of thrips were observed in Mangshi county, Yunnan province. Leaves of five symptomatic plants were collected and examined by electron microscopy; tospovirus-like spherical particles 80-90 nm in diameter were found in the sap of diseased leaves of two samples. The positive samples were tested in ELISA with polyclonal antisemur of Tomato spotted wilt virus (TSWV), Tomato zonate spot virus (TZSV), Watermelon silver mottle virus (WSMoV), Impatiens necrotic spot virus (INSV), Groundnut yellow spot virus (GYSV), Hibiscus chlorotic ringspot virus (HCRV), and reacted positively with WSMoV polyclonal antisemur. The positive samples were mechanically inoculated onto *Nicotiana benthamiana* and sack of symptomatic leaves reacted positively with WSMoV antisemur. To further characterize this tospovirus isolate infecting tomato, total RNA was extracted from symptomatic leaves using Trizol reagent (Invitrogen, USA) and detected by RT-PCR with tospovirus universal primer J13 (5’-CCCGGATCCAGAG-CAAT-3’) (Cortez et al., 2001). The RT-PCR products were cloned into pGEM-T Easy vector (Promega, USA) and sequenced. The mRNA 5’-end sequence of the isolate from Yunnan (YN-Tomato) was deposited in GenBank (Accession No. KU523691). The amplification was consistent isolated from asymptomatic roots, forming dense, pale orange, aerial mycelium on Komada selective medium. Macroconidia were abundant (19.1 to 42.7 µm × 2.1 to 2.8 µm), curved to lunate, and three to four septate. Pathogenicity tests were carried out in greenhouse by injection of spore suspension (2 ml per plant of 107 spores/ml) into the rhizome of 5-year-old plants of walnut cultivar ‘Qingxiang’. Two months later, the inoculated plants started to yellow and wilt, similarly to those observed in the orchard, while the water-injected controls remained symptomless. The fungus was consistently re-isolated from inoculated plants but not from the controls. The isolate was identified as *Fusarium sp.* based on morphology (Leslie and Summerville, 2006). ITS and TEF-1α regions were PCR amplification using rDNA universal primers ITS1/ITS4 (White et al., 1990) and EF-728F/EF-986R (Carbone et al., 1999), respectively. The sequences of ITS (KP001165) and TEF-1α (KJ019828 and KM044418) showed 99% to 100% identity to *Fusarium solani* (KJ019828 and KM044418). The pathogen was identified as *F. solani* based on its morphological and molecular characteristics. To our knowledge, this is the first report of Fusarium wilt on walnut trees caused by *F. solani* in central China.

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**FIRST REPORT OF FUSARIUM WILT CAUSED BY FUSARIUM SOLANII WALNUT IN CENTRAL CHINA**

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Walnut (*Juglans regia L.*) is widely planted in China. A new Fusarium wilt disease was observed in 5-year-old walnut orchards in Hubei, China in mid-August of 2012 and 2013. The infected trees were found over an area of 50 ha. Yellowing and wilting of leaves, browned vascular tissues, and partially or entirely rotted roots were observed. A fungus was consistently isolated from symptomatic roots, forming dense, pale orange, aerial mycelium on Komada selective medium. Macroconidia were abundant (19.1 to 42.7 µm × 2.1 to 2.8 µm), curved to lunate, and three to four septate. Pathogenicity tests were carried out in greenhouse by injection of spore suspension (2 ml per plant of 107 spores/ml) into the rhizome of 5-year-old plants of walnut cultivar ‘Qingxiang’. Two months later, the inoculated plants started to yellow and wilt, similarly to those observed in the orchard, while the water-injected controls remained symptomless. The fungus was consistently re-isolated from inoculated plants but not from the controls. The isolate was identified as *Fusarium sp.* based on morphology (Leslie and Summerell, 2006). ITS and TEF-1α regions were PCR amplification using rDNA universal primers ITS1/ITS4 (White et al., 1990) and EF-728F/EF-986R (Carbone et al., 1999), respectively. The sequences of ITS (KP001165) and TEF-1α (KU599902) showed 99% to 100% identity to *Fusarium solani* (KJ019828 and KM044418). The pathogen was identified as *F. solani* based on its morphological and molecular characteristics. To our knowledge, this is the first report of Fusarium wilt on walnut trees caused by *F. solani* in central China.

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