Diseases Caused by Viruses

First Report of Impatiens Necrotic Spot Virus Infecting Lettuce in Arizona and Southern Desert Regions of California

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Impatiens necrotic spot virus (INSV; family *Tospoviridae*, genus *Orthotospovirus*) is a thrips-borne pathogen that infects a wide range of ornamental and vegetable crops. INSV was first reported in lettuce (*Lactuca sativa*) in the Salinas Valley of California (CA) (Monterey County) in 2006 (Koike et al. 2008). Since then, the pathogen has continued to impact lettuce production in the region, causing severe economic losses with increasing incidence and severity in recent years. Tomato spotted wilt virus (TSWV; *Tospoviridae*, *Orthotospovirus*), also infects lettuce, but its occurrence is much less frequent than INSV (Kuo et al. 2014). While INSV has not been reported in the desert areas of CA and Arizona (AZ), there are concerns that the virus could become established in this region. In early March 2021, symptoms resembling those caused by orthotospovirus infection were observed in several romaine and iceberg lettuce fields in the Yuma and Tacna regions of Yuma County, AZ. Symptoms included leaves that exhibited tan to dark brown necrotic spots, distorted leaf shapes, and stunted plant growth. Similar symptoms were also reported in romaine fields and one green leaf and iceberg lettuce field in the neighboring Imperial and Riverside Counties of CA. A total of 14 samples (five from Tacna, four from Yuma, four from Imperial, and one from Riverside) were tested using ImmunoStrips (Agdia, Elkhart, IN) for INSV and TSWV. Results confirmed the presence of INSV in 13 out of 14 samples and the absence of INSV in one sample originating from Yuma. All 14 samples tested negative for TSWV. The 13 INSV positive samples were processed for RT-PCR validation. Total RNA was extracted from each sample using the Rneasy Plant Mini Kit (Qiagen, Valencia, CA). RT-PCR was performed with the OneStep Ahead RT-PCR Kit (Qiagen) with primers to the N gene of INSV S RNA (accession KF745140.1; INSV F = CCA AATACTACTTTAACCGCAAGT; INSV R = ACACCCAAGACACAG GATTT). All reactions generated a single amplicon at the correct size of 524 bp. One sample each from Yuma, Tacna, and Brawley (Imperial County), as well as a romaine lettuce sample collected from the Salinas Valley in March 2021, were sent for Sanger bidirectional sequencing (Eton Biosciences, San Diego, CA). Sequence analysis revealed that all three desert samples (Yuma, Tacna, and Brawley with accessions OK340696, OK340697, and OK340698, respectively) shared 100% sequence identity and 99.43% identity to the Salinas Valley 2021 sample (SV-L2, accession OK340699). Additionally, all desert samples shared 99.24% sequence identity to the Salinas Valley lettuce isolate described in 2014 (SV-L1, accession KF745140.1) (Kuo et al. 2014), while the SV-L2 and SV-L1 sequences shared 99.43% identity. By the end of the season (April 2021), a total of 43 lettuce fields in Yuma County, AZ, and nine fields in Imperial and Riverside Counties, CA, were confirmed to have INSV infection using ImmunoStrips. Impacted fields included romaine, green leaf, red leaf, and head lettuce varieties and both direct-seeded and transplanted lettuce under conventional and organic management regimes. In AZ, INSV incidence in fields ranged between 0.2 and 33%, while in Imperial and Riverside Counties, CA, field incidence remained low at less than 0.1%. It is possible that INSV was introduced from the Salinas Valley of CA through the movement of infected lettuce transplants and/or thrips vectors. To our knowledge, this is the first report of INSV infecting lettuce in AZ and the southern desert region of CA.

References:
Koike, S., et al. 2008. Plant Dis. 92:1248.
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