Disease Notes

First Report of *Iris yellow spot virus* in Onion in Hawaii

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Onion (*Allium* spp.) production in Hawaii is mostly comprised of green onion and the locally prized sweet bulb onions (*Allium cepa* L.) that include short- and medium-day cultivars. *Iris yellow spot virus* (*IYSV*; family *Bunyaviridae*, genus *Tospovirus*) is an important constraint to bulb and seed onion production in many onion-growing regions of the continental United States and the world (3). In June 2010, straw-colored, diamond-shaped lesions with occasional green islands were observed on leaves of sweet onion ‘Linda Vista’ in an insecticide trial on Maui for onion thrips (*Thrips tabaci*) control. Collapse and lodging occurred when lesions on leaves were severe. Seven bulbs with green leaves exhibiting lesions were collected from this onion field in the Pulehu Region of the lower Kula District on Maui. Leaf samples that included a lesion or were within 1 cm of a lesion were found to be positive in indirect ELISA with *IYSV*-specific polyclonal antisera (2). A405nm readings after 1 h ranged from 0.263 to 2.067 for positive samples and 0.055 to 0.073 for healthy onion controls. Four samples that were prepared from leaf tissue several centimeters away from a lesion tested negative in ELISA. Such uneven virus distribution in the plants has been previously reported (4). In July 2010, symptomatic sweet onion from a commercial farm in upper Kula, Maui at the 1,060 to 1,220 m (3,500 to 4,000 foot) elevation tested positive for *IYSV* by ELISA. Green onion samples collected from a commercial farm in Omaopio, Maui, located approximately 0.8 km (0.5 mile) north of Pulehu, have tested negative, suggesting distribution may be limited at this time. RNA was isolated from leaf tissue from the seven ‘Linda Vista’ sweet onions collected from the Maui insecticide trial. Reverse transcription
(RT)-PCR with forward and complementary primers 5′-CTCTTAACATTTAAGGCAC-3′ and 5′-TAAAACAAACATTCAACAA-3′ flanking the nucleocapsid (N) gene encoded by the small RNA of IYSV was conducted as previously described (1). Amplicons approximately 1.1 kb long were obtained from all seven symptomatic onion samples but not from healthy samples or water controls. Sequencing of selected amplicons confirmed IYSV infection. Three sequence variants (GenBank Accession Nos. HM776014–HM776016) were identified from two RT-PCR reactions. Phylogenetic analyses of the three sequence variants with the neighbor-joining procedure available through NCBI-BLASTn Tree View showed that the highest nucleotide identities of 97 to 98% were shared with IYSV isolates from New Zealand (EU477515), Nevada (FJ713699), and northern California (FJ713700). Phylogenetic analyses with the N-gene showed the sequences from Hawaii are most closely related to isolates from the western United States, Texas, and New Zealand. To date, to our knowledge, IYSV has not been detected on the islands of Kauai, Oahu, Molokai, or Hawaii. The distribution and economic consequences of this disease to Hawaii's onion production are under investigation.


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