Seed-transmitted Wheat Mosaic Virus in Sweet Corn in Utah

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Wheat mosaic virus (WMoV) (syn. High Plains virus) was first observed in corn in 1993 in Colorado, Idaho, Kansas, and Texas (Seifers et al. 1997). The virus causes chlorotic streaks and mosaic on corn foliage, and it stunts ear development. When infected early in the season, plants frequently die. There are anecdotal reports of reduced seed germination rates in infected seed lots. The host range of the virus includes corn, small grains, and yellow and green foxtail. The virus is transmitted by the wheat curl mite (*Aceria tosichella* Keifer 1969). Seed transmission of WMoV at extremely low rates was demonstrated in sweet corn in greenhouse grow-out tests by Forster et al. (2001), but due to the low transmission rate of three seedlings out of >38,000 tested, this mode of transmission was considered to be negligible.

In each of 2016 and 2017, plants in a sweet corn crop on a commercial farm in northern Utah developed chlorotic streaking on leaves, and the plants remained stunted (Fig. 1) throughout the growing season but did not die after emergence. The disease was more severe in the 2016 crop than in the 2017 crop. Many symptomatic seedlings had yellow to white streaks in leaves as they emerged. The grower reported lower than expected seed germination rates and a 40% yield loss in 2016. Over time, symptoms ranged from bright yellow to nearly white streaks in stunted plants, to faint chlorosis in plants that grew to normal height but only developed one or no ears. The symptoms resembled those caused by WMoV. Wheat curl mites were not detected on the leaves and no other corn plantings or small grains in the area were similarly affected. Imaging using an unmanned aerial vehicle (UAV) with a near infrared (near-IR) camera showed that infected plants were scattered randomly across the field, a pattern often observed with seed transmitted pathogens (Fig. 2a). In near-IR images, all green plant tissues appear red, while yellow and white symptomatic tissues remain yellow and white thus making it easier to detect infected plants (Fig. 2b). Plants identified in the images were collected and tested by antibody-based DAS-ELISA for WMoV (Agdia, Elkhart, IN). All five symptomatic plants tested positive for WMoV. The results were verified by extracting total RNA (Norgen Biotek,Thorold, ON, Canada) and using a RT-PCR assay with WMoV specific primers (Lebas et al. 2005). The resulting PCR products were sequenced at Eton Bioscience Inc. (San Diego, CA) and the sequences compared in a BLAST search to deposited sequences in the NCBI GenBank. The sequences (GenBank accession number: MT027518 for the consensus sequence) matched 100% with those of WMoV sequences from Ohio sweet corn GG1 (KT988872) and Kansas barley KS7 (KT988863) with 100% coverage. To confirm that no other virus was present, two samples of symptomatic plants were sent to a commercial lab (Agdia, Elkhart, IN) were they were screened for the following viruses: Barley yellow dwarf virus – pav (BYDV-pav), Brome mosaic virus (BMV), Cereal yellow dwarf virus – rpv (CYDV-rpv), Johnsongrass mosaic virus (JGMV), Maize chlorotic mottle virus (MCMV), Maize dwarf mosaic virus (MDMV), Maize stripe virus (MSpV), Maize white line mosaic virus (MWLMV), Sugarcane mosaic virus (SCMV), WMoV, and Wheat streak mosaic

virus (WSMV). They only tested positive for WMoV. Based on the UAV image analysis it was determined that, in 2016, 2% of the plants in the field showed symptoms. The UAV image also shows the gaps in the rows from poor seed germination. Forty remnant seeds obtained from the grower were tested using ELISA in 2016, and 20 seeds of the same variety were obtained from the grower in 2017 and tested. In addition, seed was purchased at a store off a different sweet corn variety as a control treatment for ELISA testing. The seed was soaked for one hour in general extract buffer in mesh bags on ice to soften the seed. Samples were then tested according to the ELISA kit manufacturer's protocol. In 2016, 70% of the remnant seed tested positive for WMoV and, in 2017, 20% were positive. The lower incidence of positive seed in 2017 was also mirrored by very few symptomatic plants in the field in 2017. None of the store- bought seed tested positive. The ELISA results for the seed were confirmed using the RT-PCR assay for WMoV and DNA sequencing (MT027517). In greenhouse grow-out tests in 2016, 216 seeds were planted. The seeds were planted in 72-cell flats with Miracle Gro potting mix. One seed was planted per cell. Eighty-three percent of the seed germinated, and six plants developed symptoms in the first 5 weeks after emergence. The symptomatic seedlings from the grow-out test also were tested for WMoV using the DAS-ELISA and RT-PCR assays, which confirmed infection. The isolates from the seed and grow- out tests were identical in sequence (MT027516) and matched the GenBank accessions KT988872 and KT988863 by 100%. Although this study confirmed the virus was transmitted through seed, conclusions on the seed transmission rate cannot be inferred due to the small sample size. Our results showed that WMoV can be seed transmitted under field conditions. Information on the sweet corn variety in the growers' field, beyond that it was the same variety planted in 2016 and 2017, was not available. The name of the original company that supplied the seed lots was not provided by the Utah grower. Our finding that WMoV was readily seed transmitted indicates a need for further research to determine the frequency of seedborne infections, seed transmission rates, and if development of a sweet corn seed testing program for WMoV is warranted.

Literature cited:

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Figure 1. Stunted, chlorotic plants infected with Wheat mosaic virus (WMoV) adjacent to healthy, dark green plants in a commercial sweet corn crop in northern Utah.

Figure 2a. a) Near-infrared (NIR) image of a sweet corn field using an unmanned aerial vehicle (UAV). Yellow circles show symptomatic plants infected with Wheat mosaic virus (WMoV) in a random pattern, indicating potential seedborne inoculum as the source of the infection. b). Image of two infected plants taken with the UAV, and the corresponding ground images

Fig 1.

Fig. 2 a and b