First Report of High Plains Wheat Mosaic Emaravirus Infecting Foxtail Barley and Wheat in Canada

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High Plains wheat mosaic virus (HPWMoV) is a monocistronic octapartite single-stranded negative-sense RNA virus in the genus *Emaravirus*, family *Fimoviridae* (ICTV 2018). It infects a number of cereal crops including wheat (*Triticum aestivum* L.), maize (*Zea mays* L.), barley (*Hordeum vulgare* L.), and some weeds (Seifers et al. 1998). HPWMoV is transmitted by the wheat curl mite *Aceria tosichella* Keifer (Seifers et al. 2009). It can coinfect wheat with some cereal viruses including wheat streak mosaic virus (WSMV) (Burrows et al. 2009). A field survey in southern Alberta, Canada, in late June 2017, evaluated 34 and 37 plants of wheat and grassy weed species, respectively, for the presence of cereal viruses. The sampled wheat plants showed yellow flecks and streaks, with some heavily chlorotic leaves showing necrotic patches along margins. Leaves with extreme symptoms were completely scorched and/or desiccated. Grassy weed species were collected nearby symptomatic wheat but did not show any typical symptoms. The incidence of symptoms varied among the sampled wheat fields, ranging from trace levels to 75% infected. RT-PCR was performed using primers WMoV-F (Byamukama et al. 2016) and WMoV-RR targeting the RNA 3B region of HPWMoV, after total nucleic acid extraction using an in-house procedure (SOP L036-02(a): KingFisher ml total nucleic acid extraction procedure, Sidney Laboratory, Canadian Food Inspection Agency, North Saanich, BC). All primer sequences, their location in the genome, and amplicon sizes are given in the supplementary table. Four wheat plants (one plant of cultivar AAC Elevate and three plants of unknown cultivar) and one foxtail barley plant (*Hordeum jubatum* L.) from Lethbridge County tested positive for HPWMoV. One wheat plant (cv. Glenn) from the Medicine Hat area also

tested positive for HPWMoV. Results were confirmed by two independent RT-PCRs with primers targeting the RNA-6 segment (WmoV-F1 and WmoV-R1) and RNA-2 segment (WmoV-F2 and WmoV-R2), respectively. BLASTn analysis of a representative of each of the two fragments, which have been submitted to NCBI under accession numbers MT124696 and MT124697, showed that they share more than 99% sequence identity with respective RNA sequences of some HPWMoV isolates from the United States (KT988861, KJ939624, KJ939629, and KT988866). All but one of the HPWMoV-infected wheat plants were also positive for WSMV. WSMV infection was confirmed using DAS-ELISA (Agdia, U.S.A.) and RT-PCR with primers targeting the WSMV coat protein (WSMV-CP2 and WSMV-CP4, Dwyer et al. 2007). Next-generation sequencing analysis of one RT-PCR positive sample yielded 10,012,849 clean reads. The dsRNA extraction method, library preparation, sequencing, and bioinformatics analyses were done according to the method of Rott et al. (2017). The obtained clean reads were searched for viral sequences using Virtool software (<https://www.virtool.ca>), revealing 31 HPWMoV-specific contigs. Sixteen contigs, ranging in length from 252 to 1,728 bp, covered 72.92% of the HPWMoV KS7 isolate genome (KT988860 to KT988868) and shared 95 to 100% identity with it. This virus could be present in, or spread to, other parts of the Canadian prairies where coinfections with other wheat curl mite-transmissible viruses could occur. Coinfections of WSMV and HPWMoV have been reported to correlate with increased symptom severity (Burrows et al. 2009). WSMV infections have led to wheat yield losses of 7 to 18% in the Texas panhandle and in the North American prairies, including Alberta, Canada (Hadi et al. 2011). The appearance of HPWMoV in Canada is concerning because coinfections with WSMV could increase severity and yield loss.

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