Diseases Caused by Fungi and Fungus-Like Organisms

First Report of a Rust Disease Caused by *Puccinia hieracii* on *Taraxacum kok-saghyz* in China

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Taraxacum kok-saghyz Rodin (TKS), commonly known as the Russian dandelion, is a potential alternative crop for natural rubber and inulin production and has gotten widespread attention in recent years (Arias et al. 2016a, 2016b; Cao et al. 2017). From May to July 2019, a rust disease happened in many fields of TKS in Ili, Xinjiang, China, which seriously affected the growth of the crop. The disease severity was found to be moderate to high, more severe in the second year of the TKS life cycle. Symptoms included brown or dark spots (<1.5 mm in diameter) on both sides of the infected leaves, especially on the bottom leaves. The disease was first observed in May when the TKS turned green, reached its peak in June, and declined in July with aestivation. Uredinia were initially borne above the leaf epidermis, and they can break through the leaf epidermis with development. Uredinia were scattered or partly gregarious, naked, pulverulent, and 0.5 to 1.0 mm in diameter. Microscopic observations revealed that urediniospores were globose or ovoid, variable in size (24 to 32 × 21 to 26 µm), and profusely echinulate. Walls were 1 to 2.5 µm thick. No telia were detected on infected leaves. The pathogen was confirmed by

observation of typical microscopic features. To complete Koch's postulates, plants were inoculated by brushing a spore suspension onto the leaves, placed in a moist chamber for 24 h (dark), and kept in a plant growth chamber (20°C, 16/8 h of light cycle, 8,000 to 10,000 lux of light intensity, 100% relative humidity). Urediniospores were formed on the surface of leaves 10 to 12 days after inoculation, and all infected plants showed symptoms similar to those observed in the field, along with spores, whereas the control plants remained symptomless. To confirm the morphological identification, genomic DNA was extracted from urediniospores and was characterized by PCR amplification and sequencing of 28S rDNA using the primer pair NL1 (5'-GCATATCAATAAGCGAGGAAAAG-3')/NL4 (5'-GGTCCGTGTTTCAAGACGG-3') (O'Donnell 1993). The 633-bp sequence (GenBank accession no. MN841787.1) obtained from inoculated plants shared 99.52% nucleotide identity with *Puccinia hieracii* voucher PDD: 98711 (GenBank accession no. KX985752.1). Further, the internal transcribed spacer region was sequenced by rust fungal primer pairs ITS5-u (5'-CAAGGTTTCTGTAGGTG-3')/ITS4rust (5'-CAGATTACAAATTTGGCT-3') (Beenken and Berndt 2012). The 476-bp sequence (GenBank accession no. MT579659.1) obtained from inoculated plants shared 99.06% nucleotide identity with *P. hieracii* strain DAOM 240969 (GenBank accession no. HQ317515.1), which was consistent with the morphological features observed. *P. hieracii* has a wide host range and has been reported from many regions on other species of *Taraxacum*, and a few other rust species have been reported on Asteraceae in China (Liu and Zhuang 2015; Zhang and Wang 2009). To our knowledge, this is the first report of a rust disease caused by *P. hieracii* on *T. kok-saghyz* in China. Occurrence of this disease in China may be a potential threat to the large-scale production of TKS.

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