Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Aloe vera* Rust Caused by *Uromyces aloes* in an Ornamental Nursery in the United States

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Aloe vera (L.) Burm. f. is a tropical evergreen perennial in the family Liliaceae. Native to the Arabian Peninsula, it is sold in Pennsylvania as an ornamental and for its medical and topical purposes due to its high levels of amino acids, anthraquinones, saponins, and vitamins A, B, C, and E (Sahu et al. 2013). In February 2020, at an ornamental plant nursery in Lancaster County, Pennsylvania, five out of 15 mature *A. vera* plants in 15-cm pots showed symptoms and signs of rust on the leaves, exhibiting dark-brown erumpent pycnial spots with a chlorotic band surrounding the infected tissue that turned necrotic after 3 days of incubation at 20°C. Only the telial stage was present. Sori ($n = 25$) were rounded, concentrically arranged, 0.2 to 3.7 mm, and covered by a brown epidermis. Teliospores ($n = 40$) were amphigenous, orange-brown, globose to ellipsoidal, measuring $(29.2) 30.4$ to $36.1 (39.5) \times (27.4) 27.6$ to $30.1 (30.5) \mu\text{m}$, with a wall thickness of 4 to 5 μm and a persistent hyaline pedicel ranging from 5 to 57.1 μm in length and 5.2 to 9.3 μm in width. These measurements were comparable to the descriptions of *Uromyces aloes* previously reported from India (teliospore size 25 to 42.5 $\times$ 20 to 30 μm , wall thickness 3 to 5 μm , and pedicel size 25 to 95 $\times$ 5 to 6.25 μm) and South Africa (teliospore size 30 to 44 $\times$ 24 to 32 μm , wall thickness 4 to 6 μm , and pedicel size 6 to 20 μm) (Maier et al. 2007; Soni et al. 2011). Based on these morphological traits and the plant host, the causal agent was identified as *U. aloes* (Cooke) Magnus (Pucciniaceae, Uredinales). The sample was also independently identified as *U. aloes* by the USDA APHIS PPQ Beltsville laboratory (interception no. APEMD20055255001) based on morphological characteristics. Teliospores were harvested with a sterile pin,

transferred to a 1.5-ml tube with DNA extraction buffer (100 mM Tris-HCl, 10 mM EDTA, 1 M KCl, pH 8), and macerated using a plastic minipestle. The DNA was precipitated using isopropanol, washed with 70% ethanol, and reconstituted in 50 μl of PCR-grade water. The segment of the internal transcribed spacer region (ITS) was amplified using ITS4/ITS5 primers (White et al. 1990). The nuclear ribosomal small subunit (18S) was amplified with rust-specific primers Rust18S-R (Aime 2006) and NS1 (White et al. 1990). The nuclear ribosomal large subunit (28S) was amplified with primers LR0R and LR7 (Vilgalys and Hester 1990). Amplified PCR products were cleaned using ExoSap (Affymetrix, Santa Clara, CA) or a QIAquick PCR Purification Kit (Qiagen, Valencia, CA) and sequenced at Penn State Genomics Core Facility. The nucleotide sequences were trimmed, analyzed, and aligned using Geneious 11.1.5 software (Biomatters, Auckland, NZ). The resulting 692-bp segment of the ITS, 1,633-bp segment of the 18S, and the 1,324-bp segment of the 28S regions were deposited in the GenBank database under accession numbers MT136509, MZ146345, and MZ146342, respectively. Based on GenBank BLAST analysis, a 529-bp fragment of our 28S product was found to share 98.87% (523/529) identity with *U. aloes* isolate WM3290 (DQ917740) from South Africa, with three nucleotide differences and three gaps between the two strains. Comparisons among ITS and 18S sequences could not be made because no ITS or 18S sequence data from *U. aloes* have previously been deposited in GenBank. To our knowledge, this is the first report of *U. aloes* from *A. vera* in the United States. Infected plants were confined inside a greenhouse and have been destroyed. Because the plants were purchased from either Florida, U.S.A., or Ontario, Canada, the extent of infection in the United States is unknown.

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