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DISEASE NOTES

First Report of the Stubby Root Nematode *Paratrichodorus allius* on Potato in North Dakota

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- Citation

Stubby root nematodes (*Paratrichodorus* and *Trichodorus*) are migratory ectoparasites that feed on roots and vector tobraviruses (Riga et al. 2007). They are important to the potato industry as they transmit *Tobacco rattle virus* (TRV) causing corky ringspot disease, which has a direct economic impact on growers due to abandonment or rejection by processing or fresh markets (Charlton et al. 2010). TRV associated with corky ringspot on potato in North Dakota was reported but stubby root nematodes (SRN) were not investigated (David et al. 2010). In October 2014, three soil samples were collected from a potato field in Sargent Co., ND, to determine the occurrence of SRN. Most of the field was harvested but a portion of the field was abandoned due to 80 to 90% of the tubers (cv. Milva) exhibiting the typical brown necrotic ring, arc, and spot symptoms of corky ringspot. Diseased tubers from this field were tested and found to be infected with TRV. Nematodes were extracted from soil using sugar centrifugal flotation and one of the samples was found to contain SRN (44/kg soil). In April 2015, 49 soil samples were collected from the same field and seven of the samples had SRN with population densities ranging from 135 to 300 (mean = 175) per kg of soil. Nematodes were examined morphologically and molecularly for species identification. Morphological measurements of adult females (n = 10) included body length (range = 550.0 to 690.0 µm, mean = 606.8 µm), onchiostyle (40.0 to 47.5, 43.9), body width (35.0 to 58.0, 42.3), anterior end to basal bulb (90.0 to 150.0, 114.7), a (10.3 to 18.6, 14.7), b (4.0 to 6.7, 5.3), and V (50.0 to 60.0%, 53.8%). The anus and caudal pores were

subterminal. The nematode species was identified as *P. allius* (Jensen 1963) Siddiqi, 1974, by morphological and morphometric characteristics (Decraemer 1980). DNA was extracted from single nematodes (*n* = 7) isolated from three soil samples in 20 µl of extraction buffer. The D2/D3 region of 28S rRNA, partial 18S rRNA, and ITS1 rDNA were amplified with primer pairs D2A/D3B, SSUF07/SSUR26, and BL18/5818, respectively (Ye et al. 2015; Riga et al. 2007). PCR products were cloned using pGEM-T easy vector and sequenced. Since sequences from all samples for each genomic region were identical, only one of the sequences from that region was submitted to GenBank and therefore represents a consensus sequence. The 18S rRNA sequence (GenBank Accession No. KU094058, 919 bp) was 100% identical to one population of *P. allius* (AJ439572) from Washington, 99% identical to *P. teres*, a closely related species of *P. allius*, and less than 99% identical to other *Paratrichodorus* spp. The ITS1 rDNA sequence (KU094059, 832 bp) was 99% homologous with two populations of *P. allius* from North Carolina (KJ934124) and Washington (AM087124), but had no significant similarity with *P. teres* and other *Paratrichodorus* spp. The 28S D2/D3 sequence (KU094057, 799 bp) was 91% or less homologous with *P. teres* and other *Paratrichodorus* spp., but no *P. allius* sequence was available for comparison. The molecular tests confirmed the identity as *P. allius*. *P. allius* is known to be the most prevalent vector of TRV in Washington and Oregon (Riga et al. 2007). To our knowledge, this is the first report of *P. allius* in North Dakota.