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DISEASE NOTES

First Report of a New Stunt Nematode *Tylenchorhynchus* sp. From a Soybean Field in North Dakota

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Citation

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Stunt nematodes in the genus *Tylenchorhynchus* are common plant-parasitic nematodes, and several species have been reported to damage crops ([Handoo et al. 2014](#)). In 2015 and 2016, 11 soil samples were collected from a soybean (*Glycine max*) field in Richland County, ND. Nematodes were extracted from soil using the sugar centrifugal flotation method ([Jenkins 1964](#)). Nine samples contained the stunt nematodes, ranging from 125 to 900 per kg of soil. One soil sample with 600 stunt nematodes per kg was planted with a soybean cultivar Sheyenne in three replicates. After 3 months of growth at 22°C under greenhouse conditions, the stunt nematode population increased to a final density of 1,953 ± 674 individuals per kg of soil. The reproductive factor of this nematode was 3.26. Soybean roots were washed with tap water and brown lesions were observed on the roots. Morphological measurements of adult females ($n = 14$) included body length (mean = 744.3 µm, range = 622.0 to 830.0), stylet (21.3 µm, 20.0 to 22.5), body width (25.1 µm, 23.0 to 27.5), head end to posterior end of esophageal glands (134.0 µm, 117.0 to 155.0), anal body width (16.2 µm, 15.0 to 17.5), tail length (47.0 µm, 38.0 to 52.0), tail annules (19.9 µm, 16.0 to 25.0), a (29.6, 25.7 to 34.0), b (5.5, 5.0 to 5.8), c (15.8, 13.5 to 18.1), c' (2.9, 2.6 to 3.3), and V (52.4%, 50.3 to 55.2). Morphological data of adult males ($n = 6$) included body length (711.7 µm, 630.0 to 775.0), stylet (20.8 µm, 20.0 to 22.5), body width (24.1 µm, 22.5 to 26.0), head end to posterior end of esophageal glands (130.3 µm, 123.0 to 135.0), anal body width (15.0 µm, 13.0 to 18.0), tail length (42.0 µm, 38.0 to 45.0), a (30.0, 28.1 to 32.9), b (5.5, 5.1 to 5.7), c (16.9, 16.4 to 17.6), c' (2.8, 2.4 to

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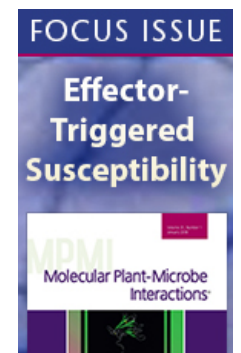
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3.4), spicule (24.3 μm , 22.5 to 25.0), and gubernaculum (12.9 μm , 11.0 to 15.0). DNA was extracted from single nematodes ($n = 6$). D2-D3 expansion domain of 28S rRNA (Yan et al. 2013) and ITS region of rDNA (Subbotin et al. 2005) were amplified and sequenced. The consensus ITS sequence (accession no. KY200668, 861 bp) deposited into GenBank had the highest identity of 92% with a *Tylenchorhynchus* sp. (KJ461594.1) which was then named as *T. thermophilus* (Handoo et al. 2014), and showed 86% identity with *T. annulatus*. The D2-D3 sequence (KY200667, 715 bp) exhibited the highest identity of 98% with a *Tylenchorhynchus* sp. (KJ461562.1), which was *T. thermophilus* based on the paper (Handoo et al. 2014), and showed 96% identity with *T. annulatus*. However, the tail of the unknown species differs from that of *T. thermophilus*, and the 71 nucleotide difference in the ITS sequence does not suggest that it is *T. thermophilus*, although all other morphometric and morphological details fit. The tail resembles that of *T. crassicaudatus* but is not as clavate. No sequence information of *T. crassicaudatus* is available in GenBank. The tail of the unknown and the nature of the inner two lines of the lateral field with oblique striae resemble *T. annulatus*, but the sequence data do not support *T. annulatus*. To our knowledge, this stunt nematode population from the soybean field in North Dakota represents a new *Tylenchorhynchus* sp. Our greenhouse bioassay demonstrated that this new species was capable of infecting soybean plants. The impact of this nematode on soybean growth and yield and resistance levels of soybean cultivars need to be assessed.

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