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Research Note

First Report of *Hemicycliophora conida* (Nematoda: Criconematidae) on *Juncus maritimus* in Jordan

F. A. SHABAN¹, N. SALEM¹, M. WAHSHA², L. AL-BANNA^{1,*}¹Department of Plant Protection, School of Agriculture, The University of Jordan, Amman 11942, Jordan, *E-mail: labanna@ju.edu.jo;²Marine Science Station, The University of Jordan, Aqaba Branch, Aqaba 77110, Jordan

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Summary

During a study of nematodes associated with aquatic plants in Jordan, a species of the sheathoid nematode *Hemicycliophora conida* Thorne, 1955 was recovered from soil associated with roots of sea rush plants, *Juncus maritimus* Lam., from the Zarqa River. Morphological, morphometric, and molecular data of recovered females and males of this nematode are included. This study represents the first record of *H. conida* in Jordan. This sheathoid nematode's presence could adversely affect plants like *J. maritimus*, which are of industrial, medicinal, and environmental significance. The impact of *H. conida* on this aquatic and other aquatic plants in the Zarqa River needs to be studied further.

Keywords: sheathoid nematode; sea rush; Zarqa River; molecular characterization

Introduction

Jordan is a highly diversified area in terms of variation in biogeographic regions and richness in biological diversity elements, especially plant biodiversity. Aquatic plants, also called hydrophytes or macrophytes, are natural and beneficial parts of Jordan's water bodies (fresh and marine water). Their growth forms define aquatic plants as emergent, submerged, floating-leaved, or free-floating. Aquatic plants offer numerous benefits to ecosystems, including habitat provision, influencing water flow and biogeochemical cycles, and providing food and oxygen (French & Chambers, 1996; Chambers *et al.*, 1999). They are valuable for various human uses like fisheries, medicine, and recreation (Suren *et al.*, 2000; Gross *et al.*, 2001; O'Hare *et al.*, 2018). The health of aquatic plant communities reflects the overall health of the ecosystem. Environmental factors can significantly impact these plants. Nematodes play vital roles within these ecosystems as a major component of aquatic sediments. Plant-parasitic nematodes can severely damage aquatic plants, yet they remain understudied. For example,

Hirschmanniella caudacrena attacks the roots of coontail (*Ceratophyllum demersum* L.), causing symptoms like chlorosis, stem deformation, and ultimately, plant death when present in high numbers (Gerber & Smart, 1987).

In Jordan, no prior records of nematodes are associated with aquatic plants. To address this knowledge gap, we conducted a study to investigate the nematode community structure of aquatic plants in Jordan. During this survey, a sheathoid nematode belonging to the genus *Hemicycliophora* was recovered from soil surrounding the submerged aquatic plant, *Juncus maritimus* Lam., growing on the banks of the Zarqa River. The genus *Hemicycliophora* de Man, 1921 (Nematoda: Criconematidae) represents a large group of migratory root-ectoparasites of various plant species, including aquatic plants, that cause poor root development and damaged foliage.

This study represents the first record of this sheathoid nematode, *Hemicycliophora conida* Thorne, 1955, in Jordan associated with roots of *J. maritimus*, including its morphological and molecular characterization.

* – corresponding author

Materials and Methods

During a study of nematodes associated with aquatic plants in Jordan, soil samples were collected from the rhizosphere of sea rush plants, *Juncus maritimus* Lam., from the Zarqa River (32°08'52.6" N, 36°03'25.2"). Nematodes were extracted using the Baermann funnel method (Niblack & Hussey, 1985) and the centrifugation-sugar flotation method (Christie & Perry, 1951). After extraction, some of the collected nematodes were kept at -80 °C

for molecular characterization and others were killed, fixed in hot buffered formalin, and mounted in glycerin for morphological identification (Humason, 1972; Seinhorst, 1959).

Morphological identification of the species *Hemicyclophora* was confirmed by sequencing two regions of rDNA (18S gene and D2/D3 expansion segments of the 28S rRNA gene). Two sets of primers were used: the D2A forward primer and the D3B reverse primer for amplification of the D2/D3 expansion segment of the 28S rRNA gene (Subbotin *et al.*, 2006). Meanwhile, the forward

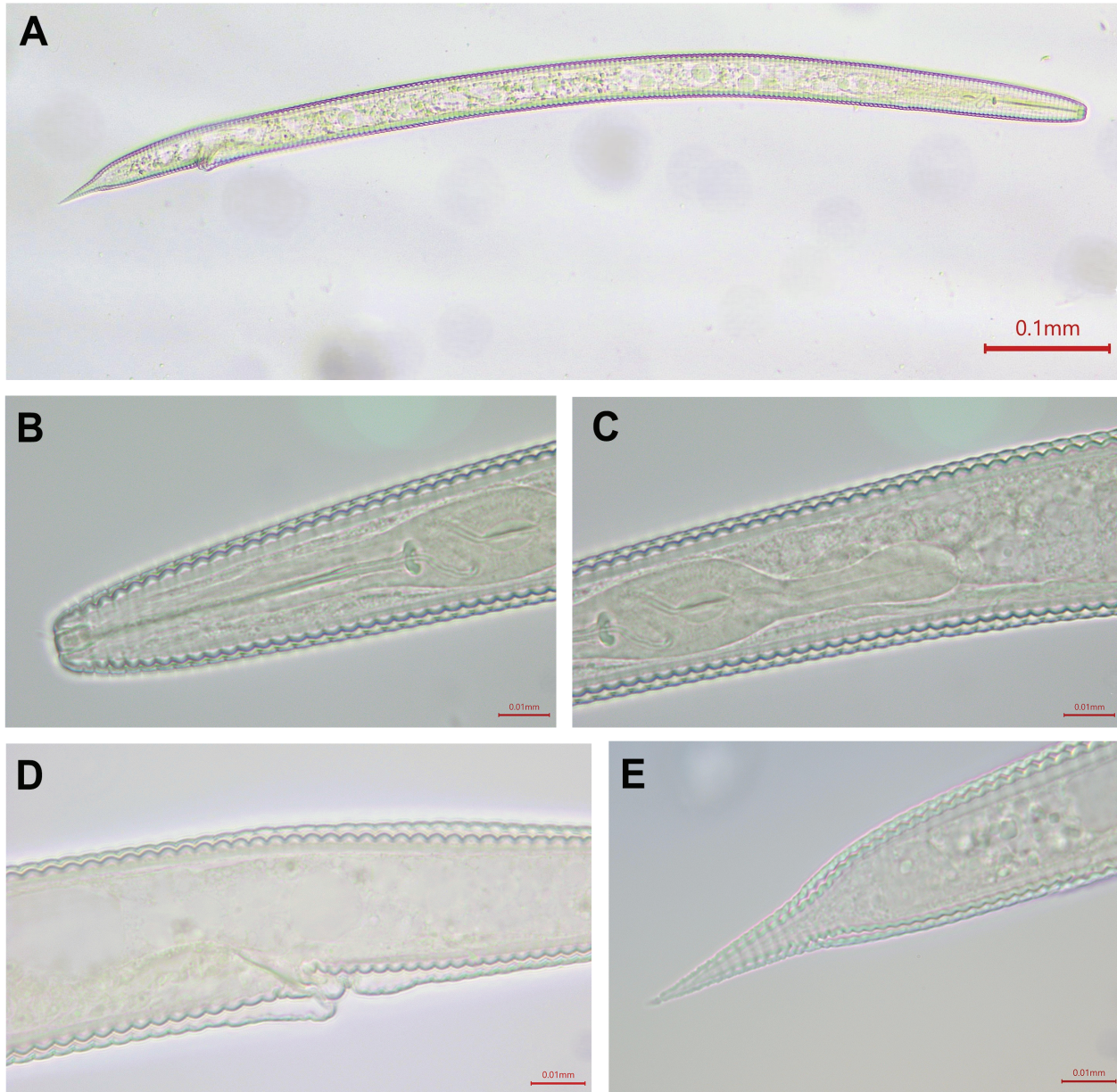


Fig. 1. *Hemicyclophora conida* female. A: Entire body; B-C: Anterior body region; D-E: Posterior body region.

GI8SU and the reverse R18Tyll amplify the partial 18S rRNA gene (Chizhov *et al.*, 2006). DNA was extracted using a modified proteinase K protocol (Chizhov *et al.*, 2006).

Ethical Approval and/or Informed Consent

The result of this work has not been published previously and is not under consideration elsewhere.

Results and Discussions

The morphological features of ten adult females are characterized by a slightly curved body ventrally; the cuticle outside the lateral field is divided into many small blocks by numerous longitudinal lines. Cuticular sheath is tightly adpressed to the body, the stylet is slightly curved, knobs rounded, backward sloping with distinct

cavity at base, lip region is rounded with two annuli, the excretory pore is situated slightly posterior to the pharyngeal bulb, vulval lips are slightly protruding but not elongated, the lateral field begins with a single line in the anterior end of the body, then transitions into two or three longitudinal lines, with the tail tapering gradually to a conoid terminus (Fig. 1). Body length = 801.4 μm (735 – 840 μm), greatest body diameter = 43.5 μm (36 – 54 μm), stylet length = 70.7 μm (63 – 77 μm), $a = 18.6$ (15 – 23), pharynx length = 150.1 μm (130 – 180 μm), $b = 5.3$ (4.5 – 6.2), $V (\%) = 84$ (78 – 87), $m (\%) = 69.4$ (50 – 86), $R = 216$ (192 – 240), $R_{ex} = 50$ (43 – 54), and $R_v = 39$ (35 – 45). The seven recovered adult males are characterized by a ventrally curved body. The lip region is rounded, not annulated, a stylet absent, a pharynx reduced, an excretory pore situated posterior to the base of the pharynx, a tail tapering gradually to a finely conoid pointed terminus, and a bursa well developed (Fig. 2). Body length = 678.9 μm (641 – 712 μm),

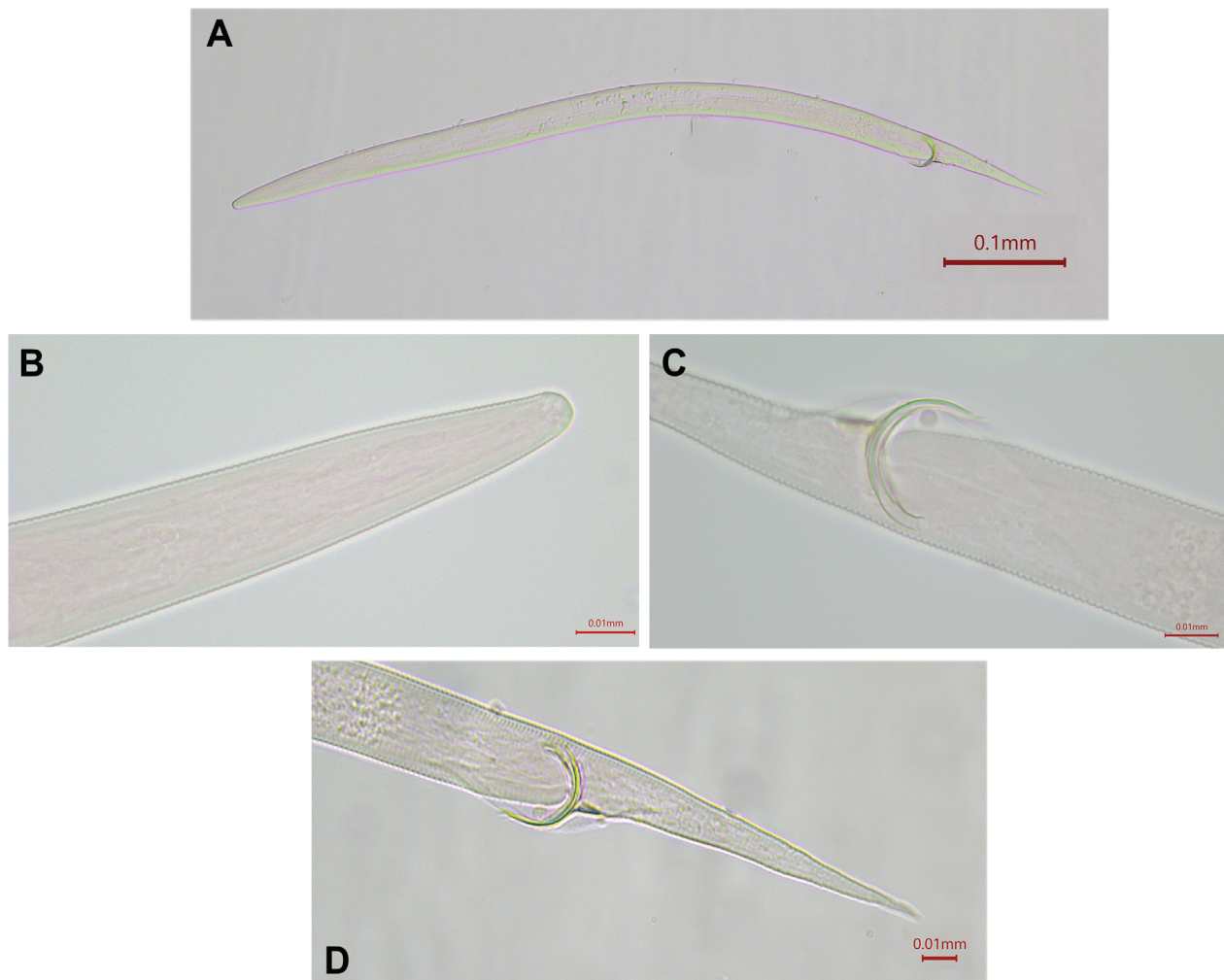


Fig. 2. *Hemicycliophora conida* male. **A:** Entire body; **B:** Anterior body region; **C-D:** Posterior body region.

greatest body diameter = 26.4 µm (21 – 32 µm), tail length = 113.6 µm (106 – 122 µm), Rv = 78 (70 – 84), spicules = 43.2 µm (36 – 49 µm), and gubernaculum = 8.6 µm (7 – 9.8 µm).

The recovered species of *Hemicycliophora* was molecularly characterized by sequencing two regions of rDNA (18S gene and D2/D3 expansion segments of the 28S rRNA gene). The sequences with accession numbers were deposited in GenBank. PQ776791 (18S rRNA: 411bp) and PQ776265 (28S rRNA: 687bp), and were compared by BLASTn on the NCBI website. BLASTn analysis of the 18S and D2-D3 regions showed 100 % similarity with two Iranian isolates of *Hemicycliophora conida* (= *H. typica* Raski & Luc, 1987) MW740208 and MN888470. These morphological and molecular data confirmed the first detection of *H. conida* in Jordan. To our knowledge, this is the first record of *H. conida* in Jordan. Its presence could harm plants like *J. maritimus*, a widespread aquatic species in the Zarqa River in Jordan, with medicinal, industrial, and economic values. It was also reported that *J. maritimus* controls salt accumulation in saline habitats and is considered an environmental quality indicator for high salinity and alkalinity environments (Suren *et al.*, 2000). The impact of *H. conida* on this and other aquatic plants in the Zarqa River needs further study.

Conflict of Interest

The authors state there is no conflict of interest.

Acknowledgments

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