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Paratylenchus shenzhenensis n. sp. (Nematoda: Paratylenchinae) from the rhizosphere soil of *Anthurium andraeanum* in China

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Abstract

Paratylenchus shenzhenensis **n. sp.** was collected from the rhizosphere soil of *Anthurium andraeanum* in Shenzhen, Guangdong Province, China. The new species is characterized by having a female with a small body (249–302 μm), well developed stylet (17–21 μm), rounded head with four submedian lobes and lip-region with a slight depression at the oral area, small post-vulval uterine sac with a few vestigial cells; male with body dorsally curved behind the cloacal opening, stylet absent, pharynx degenerate, prominent penial sheath; and juveniles with a stylet. It is morphologically similar to *P. minutus*. The internal transcribed spacer sequences of ribosomal DNA (ITS-rDNA) of the new species only have 72–73% identity with *P. minutus*, confirming its status as a separate species. The D2/D3 region of 28S ribosomal DNA (28S rDNA) and 18S small subunit ribosomal DNA (18S rDNA) from *P. shenzhenensis* **n. sp.** were also amplified and sequenced in this study.

Key words: new species, morphology, molecular, taxonomy

Introduction

The pin nematodes, *Paratylenchus* Micoletzky, 1922 are root ectoparasites of various plants, such as grasses, crops, trees, ornamentals, perennial plants, etc and are found world-wide (Raski 1991). They are especially common in orchard soils and can reach huge numbers (Siddiqi 2000). At present, the taxonomy of *Paratylenchus* is based on morphological characterization only, and molecular data has rarely been explored for identification of species of this genus. More than 100 species have been described (Brzeski & Háněl 2000; Siddiqi 2000), and many are known pathogens of their hosts (Brzeski 1995). For example, *P. bukowinensis* parasitizes parsley and carrot and causes malformed, shorter or forked roots (Brzeski 1976, 1995). *Paratylenchus microdorus* inhibits the growth of red clover and lettuce, causing smaller leaves and fewer lateral roots (Andrássy 1985).

In China, a survey of plant nematodes around the roots of ornamental plants was carried out in 2012. A *Paratylenchus* population was collected from rhizosphere soil of *Anthurium andraeanum,* and is here described as a new species, *Paratylenchus shenzhenensis* **n. sp.** The internal transcribed spacer sequences of ribosomal DNA (ITS-rDNA), D2/D3 region of 28S ribosomal DNA (28S rDNA) and 18S small subunit ribosomal DNA (18S rDNA) from *P. shenzhenensis* **n. sp.** were amplified and sequenced. Scanning electron micrographs of it are presented in this study.

Material and methods

Nematode population. Soil samples were obtained from the rhizosphere of *Anthurium andraeanum* growing in a nursery in Shenzhen, Guangdong Province. Nematodes were extracted using the modified Baermann funnel method and the pin nematodes were picked out by hand for examination.

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Nine sequences were obtained from the D2/D3 region of 28S rDNA of *Paratylenchus shenzhenensis* **n. sp.** Intraspecific variation of the sequences from the D2/D3 region (GenBank KF668516–KF668524) for *P. shenzhenensis* **n. sp.** was 0–6 bp. There was at least 145 bp difference between the new species and two other sequenced *Paratylenchus* species, *P. bukowinensis* Micoletzky, 1922 and *P. nanus* Cobb, 1923 (GenBank AY780943 and AY780946) in D2/D3 region of 28S rDNA and the sequence identity was 73–74%.

Eleven newly obtained 18S rDNA sequences of *Paratylenchus shenzhenensis* **n. sp.** were 1731 bp in length and the intraspecific variation for this species was 0–10 bp. At present, only six 18S rDNA sequences from other *Paratylenchus* species are available: one from *P. neoamblycephalus* Geraert, 1965 (GenBank AY284634), two from *P. microdorus* (GenBank AY284632 and AY284633), two from *P. straeleni* (de Coninck, 1931) Oostenbrink, 1960 (GenBank AY284630 and AY284631) and one from *P. dianthus* Jenkins & Taylor, 1956 (GenBank AJ966496). The 18S rDNA sequences of *P. shenzhenensis* **n. sp.** (GenBank KF668494–KF668504) differed from other sequenced *Paratylenchus* species by 119–148 bp and the sequence identity between the new species and the morphologically similar species *P. microdorus* was 92–93%.

Discussion

It is a challenging task to identify species of the genus *Paratylenchus* accurately, given their small size and the overlap of many measurements and characters between different species (Raski 1975b). Over the past 20 years, many studies have suggested that sequences of rDNA are a valuable marker for the taxonomy of nematodes (Powers *et al*. 1997; Uehara *et al*. 1998; Gasser & Newton 2000; Holterman *et al*. 2006; Meldal *et al.* 2007). Based on morphological features and morphometrics, *P. shenzhenensis* **n. sp.** is closest to *P. minutus*. However, there are big differences in the ITS sequences of *P. shenzhenensis* **n. sp.** and *P. minutus*. The sequence identity between the two species was only 72–73% and there was at least 347 bp difference between the two species in ITS region, while the intraspecific sequence identity for *P. shenzhenensis* **n. sp.** was at least 97% and at least 99.6% in *P. minutus* (Chen *et al*. 2009). Thus, both the morphological and molecular data support *P. shenzhenensis* **n. sp.** as a new species.

In addition, molecular sequence data is useful in the identification of closely similar species or cryptic species (Chilton *et al*. 1995). However, little molecular data for *Paratylenchus* is available and there are not enough sequenced species of *Paratylenchus* to support a phylogenetic analysis. Molecular data should be included in future species descriptions and may be invaluable for identification of *Paratylenchus* species.

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