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***Heth impalutiensis* n. sp. (Nematoda: Ransomnematodea: Hethidae) a millipede parasite from Central Mindanao, Philippines**

SVETLANA V. MALYSHEVA^{1,3}, ALMA B. MOHAGAN² & SERGEI E. SPIRIDONOV¹

¹Center of Parasitology, A.N. Severtsov's Institute of Ecology and Evolution, Russian Academy of Sciences, Leninskii prospect, 33, Moscow, 119071, Russian Federation. E-mail: malysheva24@gmail.com, sergeiedwardspiridonov@gmail.com

²Center for Biodiversity Research and Extension in Mindanao, Central Mindanao University, University Town, Musuan, Maramag, Bukidnon, 8710, Philippines. E-mail: almohagan@gmail.com

³Corresponding author

Abstract

The nematode *Heth impalutiensis* n. sp. is described from an unidentified spirostreptid millipede (Harpagophoridae) from the Bukidnon Province of Mindanao, the Philippines. Based on morphological characters, *H. impalutiensis* n. sp. is closest to Asian-Pacific representatives of the genus. Females of *H. impalutiensis* n. sp. are close to *H. dimorphum* and *H. vietnamensis* in body size and form of the lateral lappets, but can be distinguished by the significantly longer tail. Males of *H. impalutiensis* n. sp. strongly resemble that of *H. xaniophora* by the presence of such a rare character combinations as mammiform papillae and a bursa-like cuticular fold, but can be easily differentiated by the numbers of genital papillae (7 vs 6 pairs, respectively). *Heth impalutiensis* n. sp. can be distinguished from all nominal species by hypertrophy of the anterior anal lip in females which overlaps the anal aperture. Phylogenetic analysis based on the newly obtained set of sequences did not provide an evidence of infraorder Rhigonematomorpha monophyly as two superfamilies Ransomnematodea and Rhigonematodea formed independent clades in the frames of ascaridid-spirurid-oxyurid super clade (Clade III of Nadler *et al.*, 2007).

Key words: description, *Heth impalutiensis* n. sp., millipede, morphology, nematode, phylogeny, SEM, Spirostreptida, taxonomy

Introduction

The type genus of the Hethidae family, *Heth* Cobb, 1898 (Nematoda: Ransomnematodea) is the most numerous in species composition among all other Ransomnematodea genera. To date, 49 species have been described from South and Central America (Brazil, Panama, Paraguay, Venezuela and Mexico), the Caribbean (Puerto Rico, Martinique, Dominican Republic and Cuba) and the Asia-Pacific region (Vietnam, Philippines, Sumatra, Papua New Guinea, Australia and New Zealand). The only representative of the genus previously recorded from the Philippines was *Heth dimorphum* Chitwood, 1935. This species was described by Chitwood (1935) from *Spirostreptus* sp. collected at Sumatra, which was noted as the type locality, while Mt. Makiling on the Luzon Island (Philippines) was mentioned by the author as an additional collection site. *Heth impalutiensis* n. sp. from Mindanao Island is described together with a molecular phylogenetic analysis.

Material and methods

Nematode material. Specimens of *Heth impalutiensis* n. sp. were recovered from two females of spirostreptid millipedes collected by Mohagan A.B. and Spiridonov S.E. in disturbed natural habitats (woodland, bush) near Dila Falls place and Mountain View College of Bukidnon Province, Central Mindanao, Philippines. Millipedes were identified by Dr Golovatch S.I. as representatives of Spirostreptida (Harpagophoridae), a more precise definition being hampered by the fact that only the female sex was recovered.

rDNA sequences can only really demonstrate that the Philippine species is not 'identical' to those three. As might be expected, the level of nucleotide differences in 18S rDNA is lower than in 28S rDNA (4 bp and 19 bp from the closest species, correspondingly), and more data needed to estimate the level of intrageneric and interspecific diversity of ribosomal nucleotide sequences within Ransomnematodea. Nevertheless, revealed molecular and morphological differences clearly indicate the independence of described species.

All known and sequenced *Heth* species form a well-supported clade both in 18S and 28S phylogenetic trees, with sister relationships with the clade of several Carnoyidae (*Brumptaemilius* Dollfus, 1952, *Cattiena* Hunt & Spiridonov, 2001 and *Insulanema* Malysheva, Luc & Spiridonov, 2012 genera). At the same time both 18S and 28S sequences of *Carnoya filipjevi* Malysheva, 2014 (JX982120 and JX946703, respectively) are not included in this latter clade, but demonstrate weakly-supported clustering with *Heth* representatives. It is important to note that the addition of new sequence data into the phylogenetic analysis did not change what is perhaps the most surprising pattern of Ransomnematodea phylogeny—the absence of monophyly in the Rhigonematomorpha which currently comprises two superfamilies, the Ransomnematodea and Rhigonematodea (Malysheva, Luc & Spiridonov, 2012; Malysheva & Spiridonov, 2013).

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