1	First record of a mermithid nematode (Nematoda: Mermithidae) parasitizing
2	winged females of gall-forming aphids (Hemiptera: Aphididae: Eriosomatinae)
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17 Abstract

18	Juvenile mermithid nematodes were found to parasitize winged females (sexuparae) of
19	Erisoma auratum and Tetraneura radicicola. The morphological characteristics of
20	mermithid nematodes are briefly described. The 18S rDNA and 28S rDNA extracted from
21	one nematode were sequenced and used to construct a Bayesian phylogenetic tree, on
22	which the host ranges of mermithid nematodes were represented. Our study indicated that
23	mermithid parasitism of sexuparae led to fewer and smaller sexual female embryos. This
24	is the first record of a mermithid in relation to eriosomatine aphids and the fourth record
25	with respect to Aphididae.
26	
27	Key words: Mermithidae, nematode, aphid, parasite, Eriosomatinae

found in many invertebrates (Poinar 1975; Yeates & Buckley 2009; Kubo *et al.* 2016; Watanabe *et al.* 2021). As with other parasitic nematodes, free-living mermithid nematodes parasitize the hosts by actively penetrating the cuticles, either through natural openings of the host body, or through ingestion of their eggs by host insects (Hajek 2004). During our biological survey of eriosomatine aphids, a species of unidentified mermithid nematode was found in the abdomens of aphids collected in Hokkaido, Japan.

36 Aphids of Eriosomatinae (Insecta: Hemiptera: Aphididae) induce leaf galls on the 37 primary host plants and parthenogenetically produce second-generation aphids within the 38 gall from early May to mid-June in Hokkaido, Japan, a cool temperate zone. Second-39 generation aphids develop into winged adults, which migrate to the roots of secondary 40 host plants to form colonies. In autumn, winged females (sexuparae) appear on the roots 41 and migrate back to the primary host plants to produce sexual offspring. These offspring 42 (male and female embryos) develop inside the abdomens of the females at their nymphal 43 stage and are viviparously born on the trunk of the primary host plant. Sexual offspring 44 experience both underground and aboveground environments along with their mothers 45 from the embryonic stage until they are delivered.

After colonizing the roots of the secondary host plants, eriosomatine aphids live in the soil environment from early summer to autumn, making them susceptible to infection by soil-living parasites, such as nematodes and microbes. In the present study, we examined the rate of parasitism of the unidentified mermithid and attempted to molecularly characterize the species by employing the sequences of two ribosomal RNA genes, 18S and 28S. Thereafter, the phylogenetic status of the species in the available mermithid sequences was inferred based on the rDNA sequences.

On October 9, 2017, in Yoichi, Hokkaido, Japan (43°12'9" N, 140°45'52" E), 53 54 autumnal winged females (sexuparae) were collected using forceps just after their 55 alighting on the branches of Ulmus davidiana and maintained in 80% ethanol. Sexuparae 56 were dissected and slide-mounted with their embryonic sexual offspring in Hoyer's 57 mountant for morphological observation (Tong & Akimoto 2019). When a parasite was 58 found inside the sexuparae, it was isolated for later morphological and molecular 59 identification. Aphids were identified morphologically, and all specimens were deposited 60 in the Laboratory of Systematic Entomology, Hokkaido University, Sapporo, Japan.

61 The wing lengths of sexuparae and the body area of sexual offspring (female and 62 male embryos) after mountant were measured and used as an index of body size (Tong & 63 Akimoto 2019). All images were captured using a microscope eyepiece camera (Dino-64 Eye, AnMo Electronic Corporation, Taipei) and measurement was carried out using 65 IMAGEJ software (http://rsbweb.nih.gov/ij/). Statistical analysis was performed using 66 JMP software ver. Pro 14.

The isolated nematodes in mounted specimens with the host aphids were observed using light microscopy (Eclipse 80i, Nikon, Tokyo) with DIC optics and photographed with a digital camera system (MC170 HD, Leica, Wetzlar) attached to the microscope. The digital photographs were edited to enhance brightness and contrast in order to construct a micrographic figure (Fig. 1) using PhotoShop 2019 (Adobe).

72 One parasite found in an *Eriosoma auratum* sexupara was isolated, and its genomic 73 DNA was extracted and purified using the DNeasy Blood and Tissue Kit (QIAGEN, 74 Venlo, the Netherlands). The 18S ribosomal gene and the gene fragment of the large 75 ribosomal subunit (LSU) 28S rDNA sequence were amplified and polymerase chain 76 reaction (PCR) was performed according to Kobylinski et al. (2012) and Shih et al. (2019). 77 The following primers were used: 18S, 18S-F: 5'-CAAGGAC GAAAGTTAGAGGTTC-3' and 18S-R: 5'-GG AAACCTTGTTACGACTTTTA-3', and for 28S, LSU-F: 50-78 79 50-ACAAGTACCGTGAGGGAAAGTTG-30 and LSU-R:

TCGGAAGGAACCAGCTACTA-30 (Shih *et al.* 2019). The resulting templates were purified using a QIAquick PCR purification kit (QIAGEN Inc.) and sequenced in both directions using an ABI 3730xl Analyzer (Applied Biosystems). The resulting sequences were deposited in GenBank, and the BLASTn algorithm (Altschul *et al.* 1990) was applied to confirm the identity of the sequences.

The dataset of partial sequences of the nuclear 18S rDNA of mermithid nematodes 85 86 in GenBank was searched and aligned using the MEGA X software package (Kumar et 87 al. 2018). Host species were referenced to related publications and GenBank after 88 obtaining 18S rDNA sequences of the parasitic mermithid nematodes (Table S1). 89 Phylogenetic trees were constructed using Bayesian inference (BI) (Larget & Simon 1999) 90 and maximum likelihood (ML) (Felsenstein 1981). The best-fit evolutionary model K2 + 91 G + I was adopted by Mega X and used for all model-based methods (BI and ML). The Bayesian tree was constructed by MrBayes 3.2.7 (Ronquist et al. 2012) using a Markov 92 93 chain Monte Carlo (MCMC) approach with 2 million generations, with tree sampling 94 every 500 generations. The 1000 replicates were run for maximum likelihood (ML) 95 bootstrap sampling using Mega X.

In total, 418 eriosomatine sexuparae, consisting of eight species of two genera, *Tetraneura* and *Eriosoma*, were available for examination of parasitism. Five sexuparae of *E. auratum* and one of *T. radicicola* out of the 418 individuals were found to be parasitized by a slender worm (Table 1). One parasite coexisted with embryonic sexual offspring inside the abdomen of each parasitized aphid. One of the parasites was isolated for molecular identification. The others were individually maintained with the host sexuparae in the mounted specimens for morphological observation.

103 No significant difference was found in body size between adult mermithid-104 parasitized and uninfected *E. auratum* sexuparae (ANOVA, df = 1,32, F = 0.935, P =105 0.34). However, the number and body size of sexual female embryos were significantly 106 reduced in mermithid-parasitized sexuparae (df = 1,32, F = 9.93, P = 0.0035; and df =

107 1,32, F = 16.87, P = 0.0003, respectively) compared to uninfected sexuparae, whereas no 108 such significant associations were found in male embryos (df = 1,32, F = 0.15, P = 0.70; 109 and df = 1,32, F = 0.26, P = 0.61, respectively).

All nematodes were post-parasitic juveniles. One specimen that emerged from a *T*.
 radicicola sexupara was in relatively good condition and was examined under a stereo
 microscope for typological characters (Figure 1).

113 All isolated nematodes were juveniles without generic or species-specific 114 characters, and some parts of the morphological structures were vague, likely because of 115 the Hoyer fixation. Some morphological characteristics were confirmed in the specimens. 116 The body was slender, approximately 1.5 cm long, with a smooth surface. Anterior end 117 dome-shaped cephalic or labial papillae were not observed, possibly because of material 118 conditions. Stoma was conspicuous, and a stylet-like well-sclerotized stoma reached the 119 anterior end; the pharyngeal tube possessed a conspicuous lumen, connecting the stoma 120 and cardia, and at least two gland-like structures were observed on both sides of the stoma 121 and the anterior part of the pharyngeal tube. The cardia was funnel-shaped. Genital anlage 122 was not confirmed, possibly because of the material conditions. The posterior end of the 123 intestine was inconspicuous, and the anus and rectum were not observed, also likely due 124 to the material condition. A short and bluntly pointed spike-like projection was observed 125 at the tail tip.

126 The 18S rDNA and 28S rDNA gene fragments of the isolated parasite were 127 successfully sequenced from one individual, and the sequences were deposited in 128 GenBank under accession numbers MW649131 and MW653323. After alignment, 18S 129 rDNA of 42 taxa and 563 base pairs were available for phylogenetic analysis. The BLAST 130 search in GenBank indicated that the amplified sequence had the closest match and 131 formed a clade with a previously sequenced mermithid juvenile 18S sequence 132 (AY919185), which was collected from a grassland soil sample from Lincoln, Nebraska 133 (Posers, pers. comm.).

Although GenBank reference sequences are limited for mermithid nematodes, here, the Bayesian-based phylogeny was constructed using currently available 18S rDNA sequences with information on the host range. Mermithid nematodes have broad host ranges, including 12 invertebrate genera, mainly Diptera and Hemiptera (Fig. 2). The mermithid sp., which was isolated from an aphid (Insecta: Hemiptera) in the present study, formed a clade with an environmental sample and was clearly separated from neighboring hemipteran associates (Fig. 2).

For aphids and other herbivorous hemipteran insects that share a common arrangement of sucking mouthparts, mermithid nematodes cannot enter host bodies through mouthparts. In the present study, the unidentified mermithid nematode likely parasitized the aphid by penetrating the cuticle or gaining entry through a natural opening such as the anus. Root aphids are sedentary and susceptible to infection by nematodes and other pathogens.

147 Mermithid parasitism of aphids is not commonly known and only three cases have 148 been reported (Guercio 1899; Davis 1916; Poinar 2017), although this could be due to 149 undersampling of the aphids for this condition. The most remarkable record is the 150 parasitism of an extinct aphid, Caulinus burmitis (Hemiptera: Burmitaphididae) by a 151 fossil mermithid, which was found in mid-Cretaceous Myanmar amber (Poinar 2017). 152 This example implies that the parasitic association between aphids and mermithid 153 nematodes has continued for more than 100-million years. In Italy, nymphs and winged 154 adults of the root aphid Trama radices Kaltenbach were found to be parasitized by an 155 unidentified mermithid in April and May 1899, which was dispersed and embedded in 156 the winged aphid (Guercio 1899). Davis (1916) conducted fieldwork to collect 157 mermithid-parasitized aphids in Indiana, USA between mid-September and October 1911, 158 and found mermithid-parasitized apterous viviparous and oviparous aphids of an Anoecia 159 sp. on October 16th and 19th on the roots of Muhlenbergia. This is also the first record of 160 mermithid parasitism in oviparous aphids.

161 The unidentified mermithid found in the present study was closest to a species 162 collected from grassland soil around the root system of Leadplant, Amorpha canescens 163 Pursh in the USA (Powers, pers. comm., also described in 164 https://nematode.unl.edu/mermissp.htm), which possibly contained herbivorous insects, 165 including aphids. However, the taxonomic status of the nematodes is unknown in both 166 cases since the samples were juveniles not closely aligned to any identified species. In 167 addition, although these two species formed a well-supported clade in the phylogenetic 168 analysis (Fig. 2), they were clearly separated from each other considering the branch 169 length between them. Therefore, they possibly represent separate, undersampled clades. 170 Further collections followed by phylogenetic analyses are required to understand their 171 relationships and taxonomic status.

172 The survival and performance of parasites can be largely affected by their hosts. 173 Nematodes receive nutrition from the host tissues and hemolymph, competing with the 174 host for nutrients that are important for its physiological development and reproduction 175 (Smith et al. 1985; Mcrae et al. 2015). Once mermithid nematodes parasitize host insects, 176 they can manipulate host behavior for their own benefits. For example, Allahverdipour et 177 al. (2019) reported that mermithid-parasitized female mosquitoes seek water three times 178 more than a blood source, whereas uninfected females were twice as likely to seek blood 179 than water. Moreover, parasitizing adult hosts could be a dispersal strategy for mermithid 180 nematodes (Campos & Sy 2003; Di Battista et al. 2015). In the present study, obvious 181 morphological or behavioral alterations were not confirmed in parasitized aphids and 182 parasitism was not detected until dissection. Nevertheless, our study indicated that 183 mermithid parasitism in sexuparae led to fewer and smaller female sexual embryos. It is 184 not clear whether the parasites negatively affect offspring fitness by competing for 185 nutritious resources directly or whether maternal investment changes in response to 186 parasitism. Thus, it is necessary to increase the sample size to investigate host 187 manipulation by mermithid nematodes in future studies.

188 Mermithid nematodes can infect a broad range of aquatic and terrestrial 189 invertebrates. However, because nematodes are often collected as juveniles, their 190 identification and host specificity are difficult to evaluate. Mermis nigrescens, a parasite 191 of grasshoppers, is reported to be found in other insect orders, such as Dermaptera, 192 Coleoptera, and Lepidoptera (Poinar 1979). However, because of the difficulty in 193 morphological identification, information on the host range needs to be confirmed by 194 molecular barcoding analyses. In the present study, although the species status is still 195 unknown, the molecular sequences can be regarded as a species-specific barcode for 196 taxonomic identification and evaluation of the host range in future studies.

197

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199

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- 335

336 SUPPORTING INFORMATION

337

338 Additional Supporting Information may be found online in the Supporting Information

- 339 section at the end of the article.
- 340 **Table S1.** List of GenBank accession numbers, sample species, and references for host
- information included in the phylogenetic tree. DS: direct submission to GenBank.

343 Figure legends

344

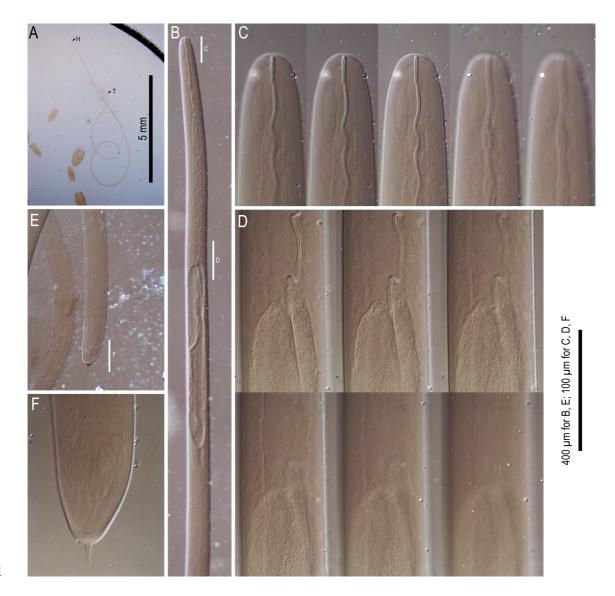
345	Figure 1 Typological characters of nematode isolated from <i>T. radicicola</i> . A: Whole body;
346	B: Anterior region; C: Close-up of anterior end ("C" in subfigure B) in five different focal
347	planes showing stoma and glands; D : Close-up of pharynx-intestional junction region ("D"
348	in subfigure B) in six different focal planes showing funnel-shaped cardia and body
349	surface structure; E: Posterior end of body; F: Close-up of tail tip ("F" in subfigure F)
350	showing tail spike (appendage).
351	
352	Figure 2 Bayesian phylogenetic tree inferred from the 18S rDNA sequences of mermithid
353	nematodes. Values on nodes represent posterior probabilities for Bayesian inference and
354	bootstrap support for maximum likelihood, respectively. The orders of the hosts
355	parasitized by mermithid nematodes are listed on the right of the tree in accordance with
356	the record of parasites.
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368	Table 1 Proportion of n	nermithid parasitism in en	eriosomatine aphids collected in 2017	
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	Τ.	Т.	Τ.	Т.	Ε.	Ε.	Е.	Е.	Total
	sorini	radicicola	triangula	nigriabdominalis	harunire	auratum	yangi	parasiticum	
No. examined	273	49	15	8	29	41	2	15	432
No. parasitized	0	1	0	0	0	5	0	0	6
Parasitized rate (%)	0	2.04	0	0	0	12.20	0	0	1.39

369

Figure 1



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373 Figure 2

