Sphaerularia vespae sp. nov. (Nematoda, Tylenchomorpha, Sphaerularioidea), an Endoparasite of a Common Japanese Hornet, Vespa simillima Smith (Insecta, Hymenoptera, Vespidae)

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Sphaerularia vespae sp. nov. (Nematoda, Tylenchomorpha, Sphaerularioidea), an Endoparasite of a Common Japanese Hornet, Vespa simillima Smith (Insecta, Hymenoptera, Vespidae)

Natsumi Kanzaki1*, Hajime Kosaka2, Katsuhiko Sayama2, Jun-ichi Takahashi3,4 and Shun’ichi Makino5

1Forest Pathology Laboratory, Department of Forest Microbiology, Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan
2Hokkaido Research Center, Forestry and Forest Products Research Institute, Sapporo, Hokkaido 062-8516, Japan
3Honeybee Science Research Center, Research Institute, Tamagawa University, Machida, Tokyo 194-8610, Japan
4Present address: Center for Ecological Research, Kyoto University, 2-509-3, Hano, Otsu, Shiga 520-2113, Japan
5Department of Forest Entomology, Forestry and Forest Products Research Institute, Tsukuba, Ibaraki 305-8687, Japan

Sphaerularia vespae sp. nov., an endoparasite of a common Japanese hornet, Vespa simillima is described from Hokkaido, Japan, and its molecular sequence profiles are given. This newly discovered nematode appears to belong to the genus Sphaerularia, judging from its characteristic parasiatic form, the uterium, which looks like a sausage with many verrucae on its surface. Sphaerularia vespae sp. nov. is distinguished from S. bombi, the only other nominal species of the genus, by the morphology of the male bursa, female tail, and anterior end of parasitic juveniles. SSU, ITS, and D2/D3 (LSU) DNA sequences were determined for S. vespae sp. nov. and compared with those from related nematodes obtained from the GenBank database. The sequences from S. vespae sp. nov. were close to those of S. bombi and several another tylenchid entomoparasitic nematodes. Sphaerularia vespae sp. nov. parasitizes overwintering gynes of the hornet and practically sterilizes them, as S. bombi does for bumblebee gynes.

Key words: hornet, Japan, new species, Sphaerularia, taxonomy

INTRODUCTION

The genus Sphaerularia was established by Dufour (1837), as an extraordinary and unusual parasite of bumblebees, and is currently a monospecific genus comprised of only S. bombi Dufour, 1837, after generic revisions (Siddiqi, 2000). However, 270 years after the first identification of sphaerularid nematodes (Réaumur, 1742), we have discovered another Sphaerularia that is an endoparasite of the overwintered gynes (potential queens) of the hornet, Vespa simillima Smith (Sayama et al., 2007). The new species clearly belongs to the genus Sphaerularia, based on its characteristic morphology of the “uterium” female, the parasitic form, but is distinguished from S. bombi by several morphological features and its molecular profiles using SSU, ITS, and D2/D3 (LSU) rRNA gene sequences. The nematode is described and figured herein as Sphaerularia vespae sp. nov. Preliminary observations on its biological features are also given.

MATERIALS AND METHODS

Collection of hornets

Overwintered gynes of V. simillima were caught using transparent plastic traps baited with clear liquor (distilled spirit) and orange juice from May to August 2005 at Hitumigaoka, Sapporo, Hokkaido, Japan (E 141°23’, N 42°59’). Most trapped hornets were fixed in Carmon’s solution (ethanol : chloroform : glacial acetic acid=6 : 3 : 1) and preserved in 80% ethanol, and were later dissected for examination of parasitism, though some individuals found alive in the traps were immediately dissected to obtain living nematodes.

Rearing of the nematodes and morphological observation

Parasitic juveniles and uteria of the nematode were isolated from the haemocoel of a gyne of V. simillima caught on 21 July 2005. A water suspension containing the juvenile nematodes was pipetted onto autoclaved sawdust in a Petri dish (diameter 6.5 cm, height 9.0 cm). Infective adults of the nematode obtained from a 6-month-old culture and parasitic juveniles isolated from a gyne hor-
net caught on 20 July 2005 were heat-relaxed at 65°C, fixed in TAF (triethanolamine-formalin), and processed through a glycerol-ethanol series by using Seinhorst’s method (see Hooper, 1986). The glycerol specimens of the parasitic juveniles and infective adults were mounted in glycerin following the method of Maeseneer and d’Herde (see Hooper, 1986), and the uteri were stored in a small glass vial.

Molecular profiles
The molecular profiles, i.e., nearly full-length SSU, ITS (ITS 1, 5.8S, and ITS 2) and D2D3 (expansion segment of the LSU) rRNA gene sequences, of the new species were determined from a single free-living female, obtained from the sawdust medium. We prepared a DNA sample following the methods described in Ye et al. (2007), and DNA fragments were amplified with the primer sets SSU_F4 (5'-GCT TGT CTC AAA GAT TAA GCC -3') and SSU_R81 (5'-TGA TCC WKC YGC AGG TTC AC -3') (SSU: provided at Dr. M. Blaxter’s website, http://www.nematodes.org/barcoding/sourhope/nemoprimers.html), 18SF (5'-CGT AAC AAG GTA GCT GTA G -3') and 28SR (5'-TTT CAC TCG CCG TTA CTA AGG -3') (ITS: Ferris et al., 1993; Vrain, 1993), and D2a (5'-ACA AGT ACC GTG AGG GAA GGA ACC AGC TAC TA -3') and D3b (5'-TCG GAA GGA ACC AGC TAC TA -3') (D2D3: Nunn, 1992). The amplified fragments were sequenced by PCR direct sequencing by using a Big Dye Table 1. Morphometric values of Sphaeralaria vespae sp. nov. All measurements are in micrometers. The abbreviations are defined as: V=vulval position relative to body length (%); T=testis length relative to body length (%).

<table>
<thead>
<tr>
<th></th>
<th>Holotype (female)</th>
<th>Patatypes (females)</th>
<th>Patatypes (males)</th>
<th>Parasitic juveniles</th>
</tr>
</thead>
<tbody>
<tr>
<td>n (number of specimens)</td>
<td>–</td>
<td>12</td>
<td>2</td>
<td>10</td>
</tr>
<tr>
<td>L (body length)</td>
<td>1338</td>
<td>1392 ± 61</td>
<td>1162, 905</td>
<td>959 ± 54</td>
</tr>
<tr>
<td>a (body length / maximum body width)</td>
<td>55.6</td>
<td>52.7 ± 6.9</td>
<td>43.3, 39.1</td>
<td>26.8 ± 3.4</td>
</tr>
<tr>
<td>c (body length / tail length)</td>
<td>8.2</td>
<td>8.2 ± 0.4</td>
<td>21.5, 18.8</td>
<td>14.8 ± 0.7</td>
</tr>
<tr>
<td>c' (tail length / anal body width)</td>
<td>5.0</td>
<td>5.2 ± 0.5</td>
<td>3.3, 3.2</td>
<td>2.7 ± 0.3</td>
</tr>
<tr>
<td>V or T</td>
<td>84.2</td>
<td>83.9 ± 0.7</td>
<td>68.0, 57.2</td>
<td>–</td>
</tr>
<tr>
<td>M (conus length relative to stylet length (%))</td>
<td>25.6</td>
<td>27.9 ± 1.6</td>
<td>30.0, 26.7</td>
<td>–</td>
</tr>
<tr>
<td>Lip width</td>
<td>10.5</td>
<td>10.5 ± 0.4</td>
<td>9.0, 8.0</td>
<td>–</td>
</tr>
<tr>
<td>Lip height</td>
<td>4.5</td>
<td>4.5 ± 0.4</td>
<td>4.0, 3.0</td>
<td>–</td>
</tr>
<tr>
<td>Stylet cone</td>
<td>4.5</td>
<td>4.5 ± 0.2</td>
<td>4.0, 4.0</td>
<td>–</td>
</tr>
<tr>
<td>Stylet length</td>
<td>18.0</td>
<td>16.5 ± 0.8</td>
<td>14.0, 14.0</td>
<td>6.5 ± 0.6</td>
</tr>
<tr>
<td>Nerve ring</td>
<td>100</td>
<td>118 ± 7.7</td>
<td>108, 94</td>
<td>101 ± 3.8</td>
</tr>
<tr>
<td>Excretory pore</td>
<td>135</td>
<td>147 ± 7.4</td>
<td>122, 107</td>
<td>114 ± 4.2</td>
</tr>
<tr>
<td>Maximum body width</td>
<td>24.0</td>
<td>26.5 ± 3.8</td>
<td>27.0, 23.0</td>
<td>36.0 ± 3.4</td>
</tr>
<tr>
<td>Ovary+oviduct or testis length</td>
<td>158</td>
<td>165 ± 20</td>
<td>790, 517</td>
<td>–</td>
</tr>
<tr>
<td>Spermapheteca</td>
<td>198</td>
<td>412 ± 141</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Uterus+ quadricolumella</td>
<td>115</td>
<td>94 ± 24</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Post uterine sac</td>
<td>11.5</td>
<td>14 ± 5.9</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Testis reflection</td>
<td>–</td>
<td>–</td>
<td>0.41 ± 0.0</td>
<td>–</td>
</tr>
<tr>
<td>Vulva-anus length</td>
<td>136.0</td>
<td>147 ± 17</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Anal body width</td>
<td>15.0</td>
<td>15.0 ± 1.8</td>
<td>16.5, 15.0</td>
<td>23.5 ± 2.9</td>
</tr>
<tr>
<td>Tail length</td>
<td>76</td>
<td>79 ± 4.8</td>
<td>54.8, 48</td>
<td>64 ± 2.9</td>
</tr>
<tr>
<td>Spicule length</td>
<td>–</td>
<td>–</td>
<td>24.0 ± 0.5, 27.0</td>
<td>–</td>
</tr>
<tr>
<td>Gubernaculum length</td>
<td>–</td>
<td>–</td>
<td>6.0 ± 0.5, 8.5</td>
<td>–</td>
</tr>
</tbody>
</table>

aAverage ± SD (range).
bFirst and second individual, respectively.
cSubventral view.
Terminator Cycle Sequencing Kit v. 3.0® (PE Applied Biosystems, Foster City, CA).

The SSU and D2D3 sequences from a uterium were also determined and compared with those obtained from a single female to confirm species identification. A DNA sample was prepared from an ethanol-fixed uterium using a DNeasy Mini Kit® (Qiagen Japan, Tokyo) following the manufacturer’s instructions. PCR amplification was conducted as above. To separate the nematode’s amplicons from the host’s amplicons, the PCR fragments were cloned with a pCR8/GW/TOPO TA cloning Kit® (Invitrogen, Tokyo), and sequenced using M13 sequencing primers 5' - GTA AAA CGA CGG CCA G -3' and 5' - GTA AAA CGA CGG CCA G -3', following the manufacturer’s manual.

**TAXONOMY**

*Sphaerularia vespa* sp. nov. (Figs. 1–6)

**Measurements.** See Table 1.

**Description. Female** (Figs. 1, 3). Body slender, annulated, relaxed or slightly ventrally bent when killed by heat. Lateral field with four conspicuous incisures, originating in the region of procorpus extending to close to the tail tip. Lip fused, smooth, slightly constricted, difficult to distinguish. Stylet conspicuous, conus and shaft separated. Stylet conus short, stout, triangular. Stylet shaft long, slightly curved, basal thickening absent. Procorpus tube-like, about two body diameters long. Two esophageal glands observed, but their openings very obscure. Esophageal glands approx. 5–6 body diameters long, constricted by a nerve ring at about anterior 1/4 position, posterior part overlapping intestine. Esophageal-intestinal junction not observed. Nerve ring conspicuous, about 120 μm behind nerve ring. Hemizonid just anterior to excretory pore. Rectum present but very obscure. Approx. 1/2 body diameter long, not muscular. Anus present, not protuberant, sometimes very difficult to observe. Rectum and anus may be nonfunctional. Tail short, conical, possessing one to three constrictions. Tail tip has a rounded, finger-like shape.

**Uterium (mature parasitic female)** (Figs. 5, 6). Found in haemocoel of the host insect. Consists of the female reproductive organ. Anfractuous and sausage-shaped, sometime growing to more than 15 mm in length. Female body atrophied, sometimes found as an appendage of uterus, but usually not visible. Uterus ejected from nematode body, enlarged, possessing many verrucae, which are derived from uterine cell nuclei, on its surface. The other parts of the reproductive organs invaginate the everted uterus. Quadriloculamella and spermatheca sac-like, difficult to distinguish from each other. Oviduct containing well-developed eggs. Ovary well-developed, elongated, with many well-developed oocytes present.

**Diagnosis and relationships.** *Sphaerularia vespa* sp. nov. is characterized by the rounded and finger-like tail tip of females and the conspicuous male bursa. Only one species, *S. bombi* Dufour was previously known in the genus *Sphaerularia*. The new species is distinguished from *S. bombi* by the length and shape of the female tail and male bursa, i.e., *S. bombi* has a shorter (47–68 μm) tail with a bluntly pointed tail tip in females and an inconspicuous male bursa, while *S. vespa* sp. nov. has a longer (>74–89 μm) tail, with a finger-like and mostly rounded tail tip in females and a large, conspicuous male bursa. The head shape of parasitic juveniles also distinguishes the new species from *S. bombi*. The anterior end of *S. vespa* sp. nov. is square in lateral view, while that of *S. bombi* is rounded and dome-like.

**Type host and locality.** The culture from which the type specimens were obtained was made from parasitic juveniles of *Sphaerularia vespa* sp. nov. isolated from the body cavity of an overwintered gyne of *Vespa simulilla* Smith, caught with a bait trap at Hitsujiyagoka, Sapporo, Hokkaido, Japan (42°59’N, 141°23’E), 21 July 2005.

**Type material.** Type specimens were obtained from a 6-month-old culture on wet sawdust media on 10 February 2006. Holotype (female), slide number *Sphaerularia vespa* F-01 (USDANC Number: T-613t). Paratypes, slide numbers *Sphaerularia vespa* F-02-05 (USDANC Number: T-5635p-T-5638p) (four females); M-01(USDANC Number: T-5639p) (one male) and *Sphaerularia vespa* P-01-04 (USDANC Number: T-5640p-T-5643p) (four parasitic juveniles) deposited in the USDA Nematode Collection, Beltsville, MD, USA;
Fig. 1. *Sphaerularia vespa* sp. nov. (A) Lateral view of female. (B) Lateral view of male. (C) Lateral view of female anterior region. (D) Body surface of female excretory pore region. (E) Lateral field at mid-body. (F) Female reproductive organ (vulva to spermatheca). (G) Female reproductive organ (spermatheca to outstretched ovary). (H) Female reproductive organ (spermatheca to out-tangled ovary). (I–K) Lateral view of female tail. (L) Subventral view of male tail (internal structure). (M) Subventral view of male tail (bursa and lateral field). (N) Lateral view of male tail. (O) Male spicule and gubernacula. Abbreviations: ep, excretory pore; ut, uterus; qc, quadriloculmella; sp, spermatheca; od, oviduct; ov, ovary.
Fig. 2. Parasitic juvenile of *Sphaerularia vespae* sp. nov. (A) Lateral view. (B) Lateral view of anterior region. (C) Body annulation of anterior end. (D) Body annulation of mid-body. (E) Body annulation of posterior end. (F) Lateral view of tail. (G–O) Variety of tail tip (left lateral view). Arrowhead, constriction.
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slide numbers *Sphaerularia vespae* F-06-10 (five females) and *Sphaerularia vespae* P-05-08 (four parasitic juveniles), deposited in The Herbarium and Insect Museum of the National Institute of Agro-Environmental Science, Tsukuba, Ibaraki, Japan; slide number *Sphaerularia vespae* F-11-13 (three females), M-02 (one male) and P-09-10 (two parasitic
juveniles), deposited in the Forest Pathology Laboratory Collection, Forestry and Forest Product Research Institute, Tsukuba, Japan.

**Etymology.** Specific epithet derived from *Vespa*, the generic name of the host insect.

**Distribution.** Besides the type locality, *S. vespae* sp. nov. was found on Mt. Moiwa, Sapporo, Hokkaido, Japan; Shiraikawa, Sapporo, Hokkaido, Japan; and Nishi-Nopporo, Ebetsu, Hokkaido, Japan.

**Molecular profiles.** The profiles obtained from the uterus and those from a single infective female were identical to each other. The partial SSU+ITS and D2/D3 sequences of *S. vespae* sp. nov., which were obtained from the single female, were deposited in the GenBank database under accession numbers AB300595 and AB300596, respectively. The closest sequences to these three molecular regions were from *S. bombi* (AB250213) for SSU, *Tylenchorhynchus leviterminalis* (EF030984) for ITS, and *S. bombi* (DQ328726) for D2/D3. The sequence similarities in the SSU and D2/D3 regions between *S. vespae* sp. nov. and *S. bombi* are 99% (1,709 identical bases per 1,727 bp: 4 substitutions and 14 insertions/deletions) and 90% (639 identical bases per 708 bp).

**Fig. 4.** Parasitic juvenile of *Sphaerularia vespae* sp. nov. (A) Lateral view. (B) Lateral view of anterior region (arrowhead, excretory pore). (C) Body annulation of mid-body. (D) Lateral view of tail (arrowhead, anus). (E–G) Variety of tail tip (left lateral view). Bar=100 μm in A; 40 μm in B–G.
Fig. 5. Mature parasitic female (uterium) of *Sphaerularia vespae* sp. nov. (arrowhead) and eggs and juveniles (small graining and lines, respectively, sometimes appearing cloudy) found during dissection of abdomen of *Vespa simillima* gyne. Bar=5 mm.

Fig. 6. Glycerol-processed mature parasitic female (uterium) of *Sphaerularia vespae* sp. nov. (A) Entire uterium. (B) Genital pore (arrowhead) of uterium and eggs in the genital tract (close-up of left side A). (C) Body of *S. vespae* sp. nov. (arrowhead) attached to uterium (close-up of right side A). Bar=5 mm in A; 1 mm in B and C.
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