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First report and molecular characterisation of *Rhabdochona hospeti* Thapar, 1950 (Thelazioidea: Rhabdochonidae) from tor barb, *Tor tor* (Hamilton) (Cyprinidae), in Assam, India

Keisham Lebanan[1], **Phougeishangbam Rolish Singh**[2] and **Naorem Mohilal**[1]

[1] Department of Zoology, Manipur University, Manipur, India;

[2] Nematology Research Unit, Department of Biology, Ghent University, Belgium

Abstract: Tor barbs, *Tor tor* (Hamilton), a cyprinid fish collected from Barak Valley, Assam, India were examined for helminth parasites. A nematode species of the genus *Rhabdochona* Railliet, 1916 (Rhabdochonidae) was found in the intestine of the fish specimens. The morphology of these nematodes was characterised by the presence of a funnel shaped prostom, head with four submedian sublabia, four cephalic papillae, long and slender posterior glandular oesophagus in both sexes, presence of 14 caudal papillae and two unequal spicules with pointed proximal tips in male specimens, and prominent post-equatorial vulval position, posteriorly directed vagina, uterus with fully scattered eggs in female specimens, and a tail pointed with a small mucron in both sexes. This nematode species was subsequently identified as *Rhabdochona hospeti* Thapar, 1950, reported herein for the first time in the northeastern India. In addition to its morphological description based on light microscopy, partial 18S and 28S rDNA sequences were generated to assess phylogenetic relationships of *R. hospeti* with other species of *Rhabdochona.*

Keywords: 18S rDNA, 28S rDNA, Barak Valley, phylogeny, taxonomy, Nematode

The nematode genus *Rhabdochona* Railliet, 1916, belonging to the superfamily Thelazioidea Skrjabin, 1915 and the family Rhabdochonidae Travassos, Artigas et Pereira, 1928, consists of a large number of species parasitic exclusively in the digestive tract of freshwater fishes from all zoogeographical regions (Moravec 2007, 2010, Moravec and Jirků 2014, Caspeta-Mandujano et al. 2020). The wide distribution of this nematode group is attributed to the fact that they utilise aquatic insects as intermediate hosts and sometimes they are brought into brackish or seawater by their migratory hosts (Moravec 2010).

The host specificity of these parasites in definitive hosts is mostly manifested at the level of fish families, subfamilies or genera (Moravec 2010). However, adult forms of some species of *Rhabdochona*, such as *R. denudata* (Dujardin, 1845) and *R. hellichi* (Šrámek, 1901), are also known to mature in invertebrate hosts (precocious development) (Moravec 2010, Moravec and Nagasawa 2021).

Many new species of *Rhabdochona* are continually being described from previously less-explored regions in the Americas, Africa and Asia, including India, thereby increasing the number of the nominal species of *Rhabdochona* quickly. As many as 103 species are now known from diverse geographic regions within this genus (Caspeta-Mandujano et al. 2020). However, even though some species described recently included scanning electron microscopy (SEM) images, the majority of the existing species of *Rhabdochona* were inadequately described (Moravec 2007).

This is well illustrated by the South-Asian species of *Rhabdochona* representing a perplexing group and a serious taxonomic problem in this genus. Furthermore, many of the known species of *Rhabdochona* are also not yet linked to their molecular information and the existing few molecular information on this genus belongs to populations originated from limited geographical locations.

Our recent helminthological investigations on freshwater fish of Barak Valley, Assam, India revealed the presence of *Rhabdochona hospeti* Thapar, 1950 infecting the intestine of the cyprinid fish *Tor tor* (Hamilton). The parasite species was studied with the objective to provide its description using an integrated taxonomic approach by including morphological, molecular and phylogenetic analysis data. Herein, the light microscopy images, illustrations, partial sequences of 18S and 28S rRNA gene sequences are presented and phylogenetic relationships of *R. hospeti* with other species of *Rhabdochona* based on these new sequences assessed.

Address for correspondence: Keisham Lebanan, Department of Zoology, Manipur University, Canchipur, Imphal-795003, Manipur, India. E-mail: lebanank@manipuruniv.ac.in

MATERIALS AND METHODS

Nematode collection and morphological characterisation

Seven specimens of *Tor tor* were caught from the Barak River (24.5227 N, 92.3443 E), Karimganj, Assam (India) in September 2020. The fish were identified following Vishwanath (2002). Nematodes were collected from the host's intestine using 'wash' method (Justine et al. 2012). The recovered nematodes were washed in 0.9% physiological saline and fixed in hot 70% ethanol. Thereafter, the nematodes were cleared in glycerine alcohol (GA) (95 part 70% ethanol + 5 part glycerine) by allowing the ethanol and water to evaporate until the specimens remained in pure glycerin. The nematodes were then mounted in pure glycerin on glass slides for light microscopic examination. Measurements and photomicrographs of the mounted specimens were prepared using a camera mounted microscope Nikon Eclipse E200.

All measurements are in micrometres unless otherwise stated and presented as range, with mean and standard deviation in parentheses. Vouchers were stored in GA in a properly sealed glass vial and deposited at the Parasitology section, Department of Zoology, Manipur University, Canchipur, Imphal, Manipur (Coll. No. MUPS-NS13-RH1-7). These are accessible to other researchers on request. Prevalence, abundance, and mean density were determined according to Bush et al. (1997).

Molecular characterisation

For extraction of genomic DNA, two nematode specimens previously stored in GA were first transferred to distilled water in a glass cavity block for washing and rehydration. The water in the glass cavity block was changed every hour for six to seven times and the specimens were left in the water overnight at room temperature. The following day, individual specimen was transferred in a drop of distilled water on glass slide and cut into pieces using a blade.

The nematode pieces were transferred to polymerase chain reaction (PCR) tubes, each containing 40 µl of worm lysis buffer (50 mM KCl, 10 mM Tris at pH 8.3, 2.5 mM $MgCl_2$, 0.45% NP 40 (Tergitol Sigma, Hoeilaart, Belgium), 0.45% Tween 20). The PCR tubes were frozen at −20°C (15 min) followed by adding 2 µl proteinase K (1.2 mg/ml), incubation at 65°C (1 h) and 95°C (10 min) and ending by centrifuging the lysate at 14,000 g for 1 min (Singh et al. 2022). The extracted genomic DNA was used for PCR amplification of ribosomal RNA (rRNA) gene regions and cytochrome c oxidase sub-unit 1 region of mitochondrial genome (mtCOI). For amplification of the D2–D3 region of the 28S rRNA gene, the primer pair D2A: 5′-ACA AGT ACC GTG AGG GAA AGT TG-3′ / D3B: 5′-TCC TCG GAA GGA ACC AGC TAC TA-3′ (Nunn 1992) was used with thermal profile of 94°C for 4 min, 35 cycles of (94°C for 1 min, 55°C for 1.5 min and 72°C for 2 min), 72°C for 10 min and a final hold at 12°C.

Amplification of partial sequence of the 18S rRNA gene was done using the primer pair, SSU18A: 5′-AAA GAT TAA GCC ATG CAT G-3′/SSU26R: 5′-CAT TCT TGG CAA ATG CTT TCG-3′ (Mayer et al. 2007) with thermal profile of 95°C for 5 min, 35 cycles of (94°C for 1 min, 52°C for 1.5 min and 68°C for 2 min), 68°C for 10 min and a final hold at 4°C. Finally, amplification of mtCOI regions were also attempted using the primer pairs COI-F1: 5′-CCT ACT ATG ATT GGT GGT TTT GGT AAT TG-3′/COI-R2: 5′-GTA GCA GCA GTA AAA TAA GCA CG-3′ (Gulcu et al. 2008) and LCO1490: 5′-GGT CAA CAA ATC ATA AAG ATA TTG G-3′/HCO2198: 5′-TAA ACT TCA GGG TGA CCA AAA AAT CA-3′ (Folmer et al.1994) using the thermal profile of 94°C for 5 min, 40 cycles of (94°C for 30 s, 51°C for 30 s and 68°C for 2 min), 68°C for 10 min and a final hold at 10°C.

Phylogenetic analysis

The phylogenetic relationships of *Rhabdochona hospeti* with other species of *Rhabdochona* were analysed based on the 28S and 18S rDNA sequences. For this, all available 18S and 28S rDNA sequences of species of *Rhabdochona* in GenBank and two sequences of a selected outgroup species, *Spinitectus mexicanus* Caspeta-Mandujano, Moravec et Salgado-Maldonado, 2000 (MK353497 & MK353469), were retrieved. The outgroup was selected following Lagunas-Calvo et al. (2019).

The 18S rDNA sequences alignment and the 28S rDNA sequences alignment were made using MUSCLE alignment of Geneious Prime 2020.0.5 using default parameters, followed by manually trimming off of the poorly aligned ends in the two alignments. Bayesian phylogenetic analysis (MrBayes 3.2.6) was carried out using the GTR + I + G nucleotide substitution model as recommended by Abadi et al. (2019). Analyses were run under 1 × 10^6 generations (4 runs), and Markov chains were sampled every 200 generations, and 20% of the converged runs were regarded as burn-in (Huelsenbeck and Ronquist 2001).

RESULTS

Rhabdochona (*Rhabdochona*) *hospeti* Thapar, 1950

Figs. 1, 2

Synonyms: *Rhabdochona barbi* Karve et Naik, 1951; *R. penangensis* Furtado, 1965; *R. bosei* Sahay, 1966; *R. ghaggari* Sood, 1972; *R. alii* Kalyankar, 1972; *R. labeonis* Kalyankar, 1972; *Comephronema* [sic] *mackiewiczi* Malhotra et Rautela, 1984; *R. moraveci* Duggal et Kaur, 1987; *R. bifidum* Kakar et Bilqees, 2007; *R. uvaginus* Kakar et Bilqees, 2007; *R. bolani* Kakar, Bilqees et Ahmad, 2008; *R. cephalodiverticula* Kakar, Bilqees et Ahmad, 2008.

Morphological characterisation (based on seven specimens)

Medium-sized whitish worms, cylindrical and thread-like in structure without transverse cuticular striations (Fig. 1). Head truncated and somewhat rounded at anterior end with four submedian cephalic papillae (Fig. 2A). Funnel-shaped prostom with four submedian sublabia (Fig. 2A,B). Prostom armed with 14 small anterior teeth. Vestibule straight, connected to anterior muscular oesophagus. Posterior glandular oesophagus long and slender, runs towards intestine. Deirids small, bifurcated, situated posterior to midline of vestibule. Entire length of anterior and glandular oesophagus representing 25–38% and 25–33% of total body length of males and females, respectively. Tail of both sexes tapering, slender and sharply pointed with a small mucron (Fig. 1D,F).

Male (n = 3): Body 9.1–12.8 (11.1 ± 1.3) mm long, 110–164 (138 ± 19) µm wide. Prostom 14–16 (15 ± 1) µm long, 8–10 µm wide. Vestibule length including prostom 73–113 (92 ± 14) µm, 4–7 (6 ± 1) µm wide. Nerve ring

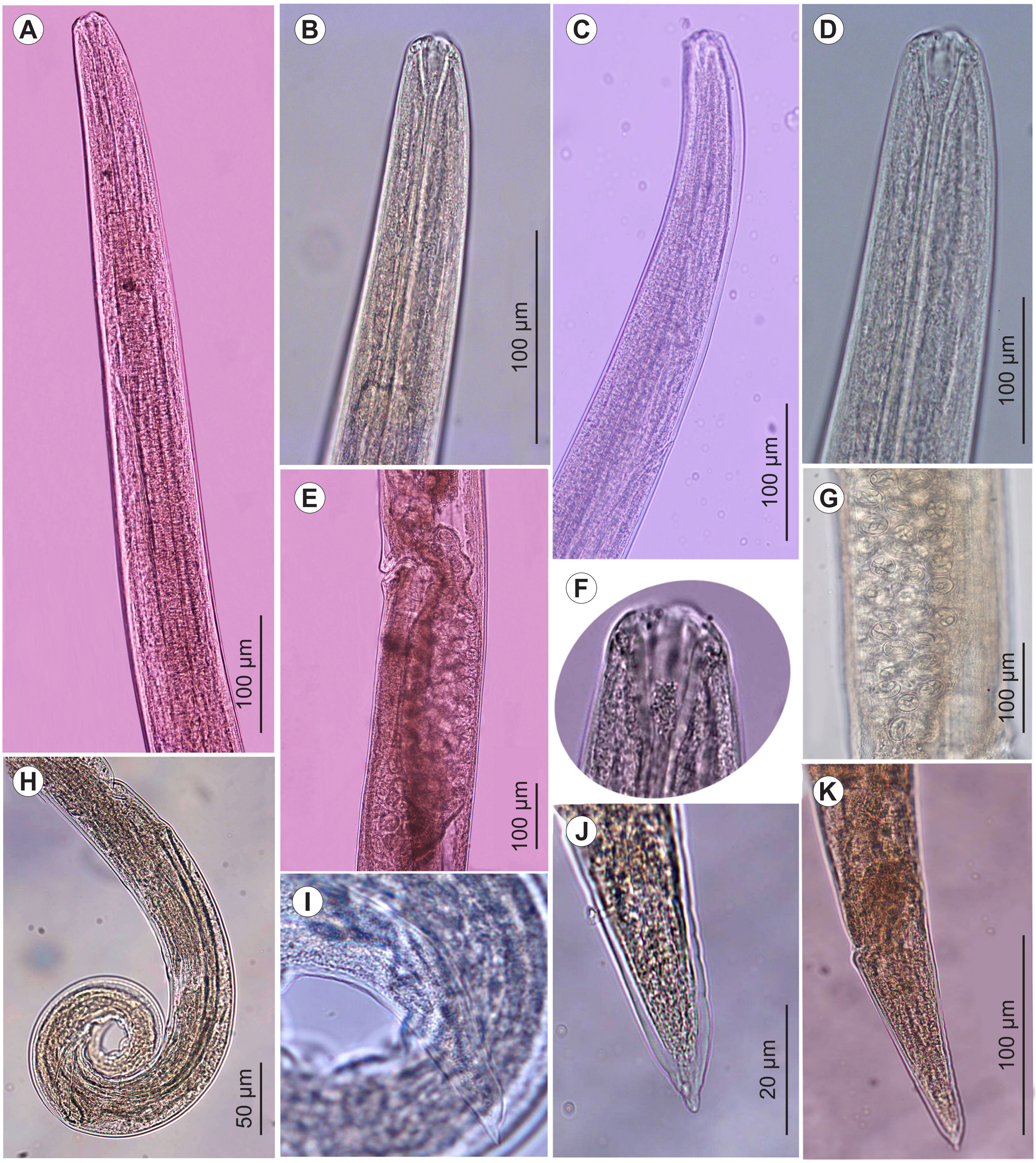

Fig. 1. *Rhabdochona hospeti* Thapar, 1950 from *Tor tor* (Hamilton), Assam, India. **A** – anterior part of male body, lateral view; **B**, **C** – anterior end of male (dorsoventral) and anterior end of female (lateral views), respectively; **D** – anterior end of male showing deirids; **E**, **G** – vulva (lateral view) and eggs near vulval region; **F** – cephalic end of male, lateral view; **H**, **I** – posterior end of male, lateral view showing spicules and tail tip, respectively; **J** – tail tip of female; **K** – female tail, lateral view.

and excretory pore 134–162 (148 ± 10) µm and 92–154 (118 ± 23) µm from anterior extremity, respectively. Muscular oesophagus 40–94 (68 ± 19) µm long, 10–14 (12 ± 2) µm wide; glandular oesophagus 2.8–3.8 (3.4 ± 0.4) mm long, 19–30 (24 ± 5) µm wide. Oesophagus length representing 25.2 to 38.3% of total body length (TBL). Posterior extremity with 14 pairs of papillae: 8 pairs precloacal, of which fourth pair (from cloaca to anterior extremity) is more lateral; 5 pairs postcloacal, of which second pair (from cloaca to posterior extremity) is more lateral. Unequal spicules, right one larger but shorter, 60.2–117 (93 ± 19) µm long, and slender & longer left spicule 301–593 (435 ± 114) µm long. Cloaca 98–186 (146 ± 37) µm from posterior extremity. Length of mucron 4–5 (5) µm.

Females (n = 4). Body 9.2–15.3 (12.2 ± 2.5) mm long, 110–210 (150 ± 4) wide. Prostom 14–22 (18 ± 3) µm long,

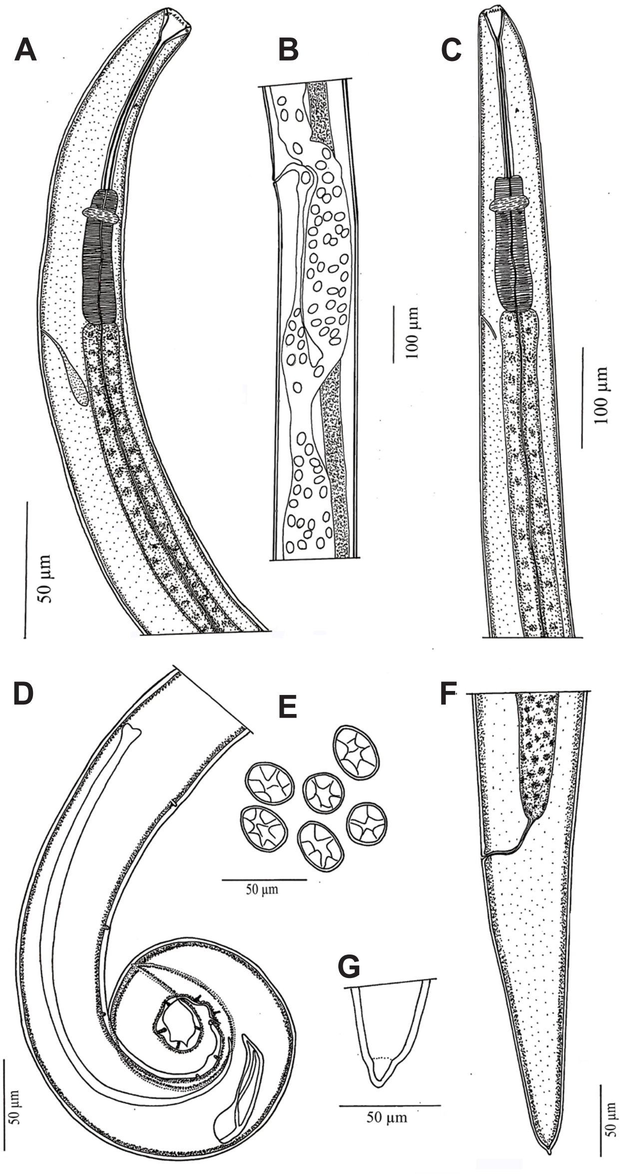

Fig. 2. *Rhabdochona hospeti* Thapar, 1950 from *Tor tor* (Hamilton), Assam, India. **A**, **C** – anterior end of male and female respectively, lateral view; **B** – vulval region, laterial view; **D**, **F** – posterior end of male and female respectively, lateral view; **G** – tail tip of female; **E** – immature eggs.

10–19 (13 ± 4) µm wide. Vestibule (including prostom) 85–150 (114 ± 27) µm long, 4–9 (7 ± 2) µm wide. Nerve ring and excretory pore 122–180 (150 ± 24) µm and 164–283 (210 ± 52) µm from anterior extremity, respectively. Muscular oesophagus 91–258 (163 ± 70) µm long, 13–25 (17.9 ± 5.1) µm wide; glandular oesophagus 2.8–3.8 (3.4 ± 0.5) mm long, 19.1–33.8 (25.7 ± 6.1) mm wide. Total oesophagus length representing 25 to 33% of TBL. Post equatorial vulva 5.2–10.6 (7.8 ± 2.2) mm from anterior extremity. Eggs smooth, non-filamentous and embryonated, 12–32 (21 ± 7) µm long, and 11–24 (18 ± 4.8) µm wide. Anus 107–221 (160 ± 47) µm from posterior extremity. Length of mucron 4–6 (5 ± 1) µm.

Table 1. Morphometric measurements of *Rhabdochona hospeti* Thapar, 1950 from *Tor tor* (Hamilton) (All measurements are in µm unless otherwise indicated).

Characters	Range (mean ± SD)	
	Females (n = 4)	**Males** (n = 3)
Prostom		
length	14–22 (18 ± 3)	14–16 (15 ± 1)
width	9.5–19 (13 ± 4)	8.0–10.0 (9.18 ± 0.86)
Vestibule		
length	84.9–150 (114 ± 27)	72.7 - 113 (92.2 ± 14.2)
width	4.49–9.20 (6.7 ± 1.9)	4.44–7.14 (6 ± 1.14)
Body		
length	9.2–15.3 (12.2 ± 2.5) mm	9.1–12.8 (11.1 ± 1.3) mm
width	110–210 (150 ± 4)	110–164 (138 ± 19)
Muscular oesophagus		
length	90.9–258 (163 ± 70)	40.3–93.7 (67.6 ± 18.9)
width	12.6–24.9 (17.9 ± 5.1)	10.4–13.9 (12.3 ± 1.5)
Glandular oesophagus		
length	2.78–3.80 (3.41 ± 0.45) mm	2.8–3.8 (3.4 ± 0.4) mm
width	19.1–33.8 (25.7 ± 6.1) mm	18.9–29.8 (24 ± 4.5) mm
Anterior end to nerve ring	122–180 (150 ± 24)	134–162 (148 ± 9.7)
Anterior end to excretory pore	164–283 (210 ± 51.6)	92–154 (118 ± 23.1)
Vulva position from anterior end	5.23–10.6 (7.84 ± 2.2) mm	-
Egg		
length	12–32.06 (20.7 ± 7.2)	-
width	11.0–24.2 (17.7 ± 4.75)	-
Tail length	107–221 (159 ± 47)	98–186 (146 ± 37)
Mucron length	4–5.6 (4.9 ± 0.5)	4–5 (5 ± 0.4)
Left spicule length	-	301–593 (435±114)
Right spicule length	-	60.2–117 (93±19)

Molecular characterisation

A sequence of the D2–D3 region of the 28S rRNA gene (OK486360, 753 bp) and a sequence of the partial 18S rRNA gene (OK483374, 882 bp) were generated. The D2–D3 sequence is presented for the first time for this species and was found closest to a sequence of *R. ictaluri* Aguilar-Aguilar, Rosas-Valdéz et Pérez-Ponce de León, 2010 (MK353493; 92% similarity) based on the BLAST similarity search. The 18S rRNA gene sequence was found identical to a *Rhabdochona hospeti* (JF803938) sequence originated from India; however, no morphological data are associated with this sequence for a comparison with our data. PCR amplifications of the partial mtCOI using the two primer pairs COI-F1/COI-R2 and HCO2198/LCO1490 were unsuccessful.

Taxonomic summary

Type host: *Tor tor* (Hamilton) (Cypriniformes: Cyprinidae).

Type locality: Hospet, Madras.

Distribution: Assam, India; new locality: Barak River (24.5227 N, 92.3443 E).

Site of infection: Small intestine (duodenum and jejunum)

Prevalence: 28% (2 fish hosts infected of 7 fish examined).

Mean intensity of infection: 3.5.

Mean abundance of infection: 1.0.

Type specimens: *Rhabdochona hospeti* Thapar, 1950.

Voucher specimens: Parasite Museum, Department of Zoology, Manipur University, India (MUPS-NS13-RH1-7).

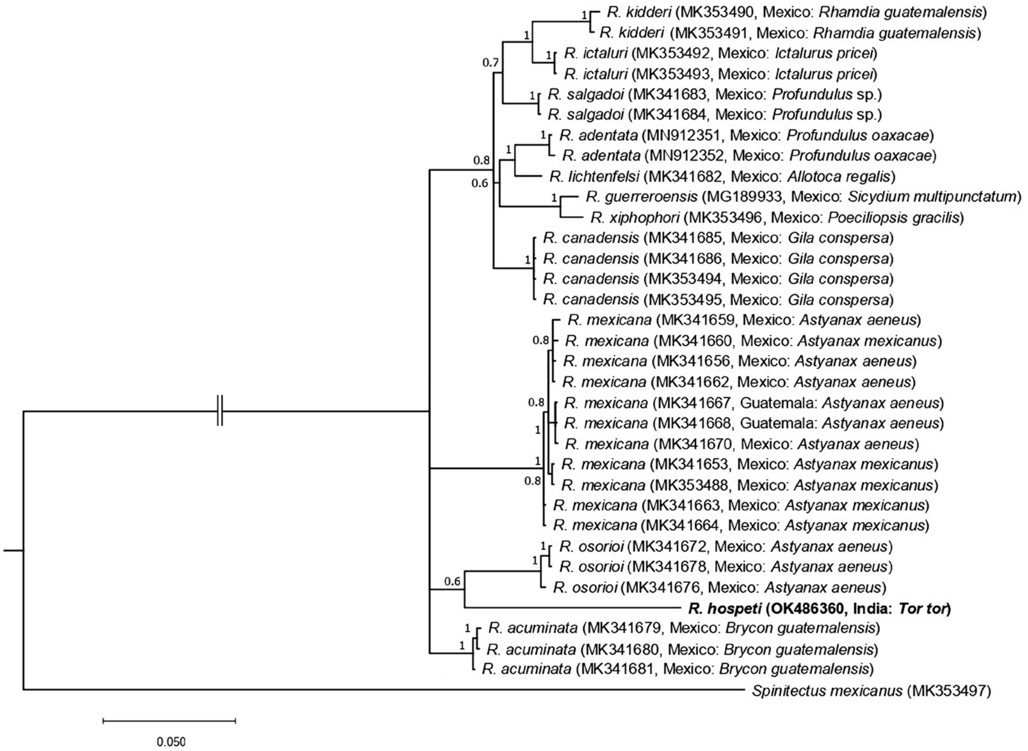

Fig. 3. Phylogenetic relationships of *Rhabdochona hospeti* Thapar, 1950 with other closely related species of *Rhabdochona* Railliet, 1916. Bayesian 50% majority rule consensus tree as inferred from the analysis of the D2–D3 region of 28S rRNA gene sequences using GTR + I + G nucleotide substitution model. Posterior probabilities of more than 0.5 are given for appropriate clades and GenBank accession number, country of sequence origin and the associated host of nematode parasite are also given for each sequence. A sequence of *Spinitectus mexicanus* Caspeta-Mandujano, Moravec, Salgado-Maldonado, 2000 (MK353497) was chosen as an outgroup.

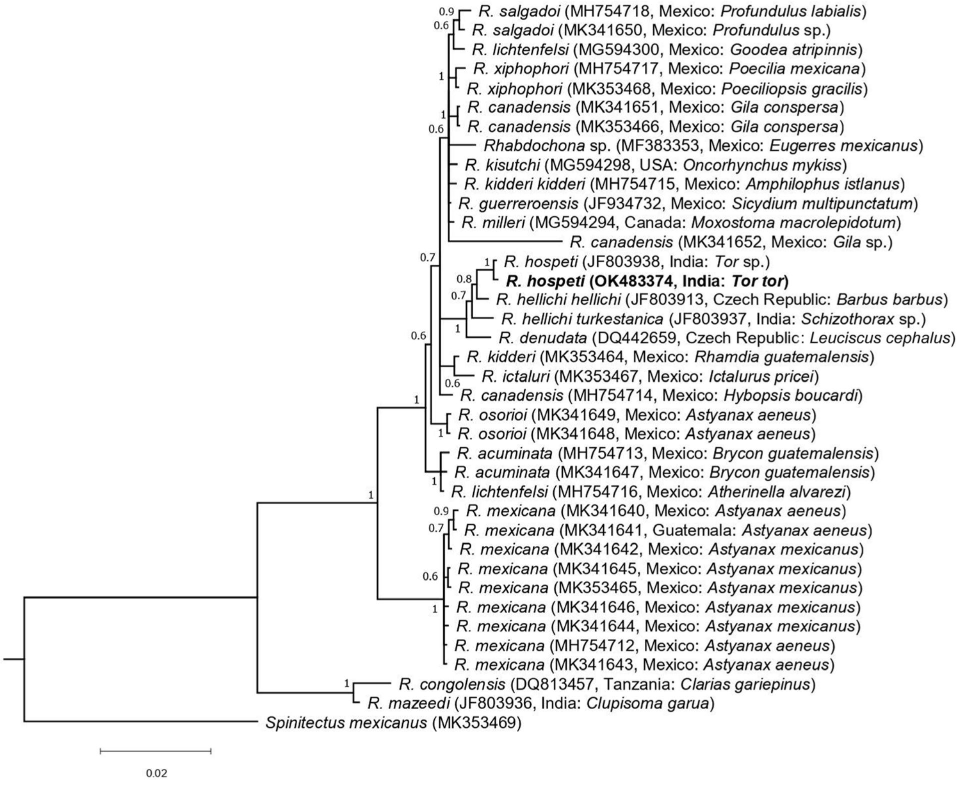

Fig. 4. Phylogenetic relationships of *Rhabdochona hospeti* Thapar, 1950 with other closely related species *Rhabdochona* Railliet, 1916. Bayesian 50% majority rule consensus tree as inferred from the analysis of partial 18S rRNA gene sequences using GTR + I + G nucleotide substitution model. Posterior probabilities of more than 0.5 are given for appropriate clades and GenBank accession number, country of sequence origin and the associated host of nematode parasite are also given for each sequence. A sequence of *Spinitectus mexicanus* Caspeta-Mandujano, Moravec, Salgado-Maldonado, 2000 (MK353469) was chosen as an outgroup.

Table 2. Measurements of *Rhabdochona hospeti* Thapar 1950 with similar congeneric species from cyprinoid fish. All measurements are in millimetres unless otherwise indicated.

Species		***R. hospeti***	***R. barbi***	***R. penangensis***	***R. ghaggari***	***R. labeonis***	***R. alii***	***R. hospeti***	***R. hospeti***	***R. hospeti***
Reference		Thapar (1950)	Karve and Naik (1951)	Furtado (1965)	Sood (1972)	Kalyankar (1972)	Kalyankar (1972)	Soota and Sarkar (1981)	Moravec (2010)	present study
Fish host		*Tor tor*	*Puntius kolus* and *Tor khudree*	*Puntius binotatus*	*Tor tor*	*Labeo rohita*	*Labeo rohita*	*Tor tor*	*Tor* sp.	*Tor tor*
Locality		Hospet, Madras, India	Poona, India	Malaysia	Chandigarh, India	Maharastra, India	Maharastra, India	Solan, India	Sikkim, India	Assam, India
Body length	♂♀	– 15.8	9.7–11.3 15.5–19.3	9.6 22.2	5.8–7.5 7.6–13.3	9.9 15.5	7.4–7.5 15.1–17.0	8.6 16.2	10.1–11.1 11.4–11.7	9.1–12.8 9.2–15.3
Body width	♂ ♀	– 0.16	0.11–0.15 0.12–0.17	0.15 0.25	0.09–0.13 0.13–0.22	0.15 0.22	0.13–0.14 0.22–0.23	0.11 0.22	0.14–0.15 0.15–0.16	0.11–0.16 0.11–0.21
Prostom length	♂♀	– 0.01	0.017–0.02 0.02–0.03	0.02 0.03	0.01–0.02 0.02–0.03	0.02 0.03	0.02 0.03	–	0.02 0.23	0.01–0.02 0.01–0.02
Anterior end to nerve ring	♂♀	– 0.22	0.16–0.18 0.18–0.23	0.30–0.33 0.41	0.12–0.14 0.15–0.21	0.17 0.18	0.13–0.14 0.11–0.14	–	0.20–0.21 0.20–0.21	0.13–0.16 0.12 –0.18
Excretory pore	♂♀	– 0.3	0.27–0.28 0.24–0.3	– –	0.21–0.25 0.27–0.29	– –	– –	–	0.25–0.26 0.26–0.28	0.09–0.15 0.16–0.28
Vulva position and length from anterior end	♀	post-equatorial 9.5	pre-equatorial 6.9–10.1	– –	4.5–7.6	8.9	8.5–9.7	post-equatorial 9.0	post-equatorial 7.0–7.3	post-equatorial 5.3–10.6
Egg type		filamentous	filamentous	– –	without filaments	without filaments	with cuticular projections	without filaments	filamentous	without filaments
Spicule Left	♂	–	tip expanded	–	broadened proximally and bifurcated at distal end	longer, tip with three spine like projections	with pointed tip	dissimilar and unequal, smaller 0.88	longer, distal tip narrowed, 0.7–0.72 long	long, narrow distal tip, 0.3–0.6 long
Right		–	truncated shaped with a small barb	–	scoop-shaped with reflexed barb	broad, anteriorly and shoe like posteriorly	distal end shoe shaped and broad	larger 0.53 long, both with bifurcated tips	without distinct dorsal barb at distal tip, 0.16–0.17 long	large, broadened proximally and pointed distal end, 0.6 –0.12 long
No. of caudal papillae		–	10+0+6=16	13+6+6=19	10+0+5=15	9+0+8=17	7+0+7=16	7+0+5=12	8+9+0+6=14–15	8+0+6=14

Phylogenetic analysis

For phylogenetic analysis based on the D2–D3 28S rDNA alignment, 33 sequences of species of *Rhabdochona* were aligned together with a sequence of *Spinitectus mexicanus* (MK353497) which was chosen as an outgroup. The alignment was 1,240 bp long. In the resultant tree, *R. hospeti* appeared to be sister species to *R. osorioi* Santacruz, Ornelas-García et Pérez-Ponce de León, 2019 with a weak branch support (PP = 0.62) and the relationship of this clade with other species remain unresolved (see Fig. 3). For phylogenetic analysis using 18S rDNA alignment, 37 sequences of species of *Rhabdochona* were aligned together with the outgroup, *S. mexicanus* (MK353469), and the alignment was 1790 bp long. In the resulted tree, *R. hospeti* forms a strongly supported clade with *R. hellichi hellichi* (Šrámek, 1901), *R. hellichi turkestanica* (Skryabin, 1917) and *R. denudata* (Fig. 4).

DISCUSSION

Rhabdochona hospeti was originally described by Thapar (1950) based on a single female specimen, detected from the host *Tor tor* collected in Hospet, Madras, India. This species was typified by filamented eggs, but Moravec (2007) later pointed out that only fully developed eggs show the presence of the filaments on both poles of the egg and such filaments are often less developed or absent in younger eggs.

In 1951, *Rhabdochona barbi* was described from *Puntius kolus* (Sykes) and *Tor khudree* (Sykes) from Pune, Maharashtra, India (Karve and Naik 1951), but showed many similar key characters with *R. hospeti* and was therefore subsequently synonymised with the latter by Rasheed (1965). Later, *Rhabdochona penangensis* was described from *Puntius binotatus* (Valenciennes) from Malaysia (Furtado 1965), *R. ghaggari* from *T. tor* from the Indus River basin, Chandigarh, India (Sood 1972), and *R. alii* and *R. labeonis* from *Labeo rohita* (Hamilton) from Maharashtra, India (Kalyankar 1972). However, Moravec (1975) considered these four inadequately described species as junior synonyms of *R. hospeti*.

Another species *R. bosei* (synonym of *R. garuai* Agrawal, 1965 according to Moravec 1975) from the catfish *Wallago attu* (Bloch et Schneider) from Lucknow, India was misidentified by Verma (1972) but later on considered as species conspecific with *R. hospeti* (Moravec 1975). Furthermore, authors such as Soota and Sarkar (1981), and Soota (1983) worked on nematode parasites of Indian vertebrates and reported a new locality of *R. hospeti* from *T. tor* in Himachal Pradesh, India. Meanwhile, the validity of *R. barbi*, *R. alii*, *R. ghaggari* and *R. labeonis* was argued for by Sood (1989). *Rhabdochona ghaggari* was reported from *T. tor* in Pakistan by Siddiqi and Khattak (1983). However, this revalidation of the mentioned four species was not considered acceptable by Moravec (2010).

Additionally, six species namely, *Comephronema* [sic] *mackiewiczi*, *R. moraveci*, *R. bifidum*, *R. uvaginus*, *R. bolani* and *R. cephalodiverticula*, all inadequately described from *T. tor* (type host of *R. hospeti*) or *Tor putitora* (Hamilton) in India and Pakistan, are considered junior synonyms of *R. hospeti* (see Malhotra and Rautela 1984, Duggal and Kaur 1987, Kakar and Bilqees 2007a,b, Kakar et al. 2008).

Despite the apparently wide distribution of *R. hospeti*, genetic data on this species are scarce. Before this study, a very limited molecular information on species of *Rhabdochona* from few restricted geographic regions was available, with a single partial 18S sequence of *R. hospeti* available in Genbank. This 18S sequence is not linked to the nematode morphology and also the exact location in India from where the nematode host was collected is not mentioned. Given the taxonomical complexities illustrated abundantly by the numerous synonyms of *R. hospeti*, the genus *Rhabdochona* is in urgent need of molecular characterisation of its species. Most importantly, linking molecular data with morphological data of the species will solve the many existing taxonomical discrepancies within this genus.

The morphological data of our studied population were found in good agreement with the original description of *R. hospeti*, and particularly to that of the *R. hospeti* population reported from the state of Sikkim in northeast India (Moravec 2010), which is over 500 km away from our currently studied location. Also, morphological comparison of our population with the records of other populations of *R. hospeti* from different locations has been presented in this study. Furthermore, this species is herein reported for the first time in Assam and first sequences of 18S and 28S rDNA are provided.

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Author contributions. K. Lebanan: sampling, data collection, analysis and drafting the manuscript. P. R. Singh: data collection, analysis and revision of the manuscript. N. Mohilal: conceptualisation of the work, supervision and revision of the manuscript.

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