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## New Host Record (*Gobiosoma bosc*, Teleostei), for *Homalometron* sp. (Digenea: Apocreadiidae) in the Charleston Harbor, South Carolina, U.S.A.

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**ABSTRACT:** During a dietary study of the naked goby, *Gobiosoma bosc*, collected from Charleston Harbor, South Carolina, in 2011–2012, gut content analyses showed the presence of several digenean species. The identity of one of the digenean species was investigated using molecular and morphological techniques. A comparison of 374 base pairs of an internal transcribed spacer region of ribosomal DNA (ITS2) with the GenBank database revealed that the digenean was a *Homalometron* sp., most likely *Homalometron palmeri* or an undescribed sister taxon. Specimens examined for morphology were immature, less than 1 mm in length, and had an oral to ventral sucker width ratio of 1:1.15–1.29. This is the first record of *Homalometron* sp. parasitizing a *Gobiosoma bosc* host, and it represents the first potential occurrence of *H. palmeri* outside of the Gulf of Mexico.

**KEY WORDS:** *Homalometron*, *Gobiosoma bosc*, naked goby, Digenea, ITS2, rDNA, phylogeny, western Atlantic, life cycle.

In estuarine ecosystems, parasites make up a large portion of standing biomass, and their key roles in both ecosystem productivity and the regulation of trophic relationships are now broadly recognized (Kuris et al., 2008). Despite the importance of parasites, the life cycles of many of these organisms remain uncharacterized or unknown (Dobson et al., 2008), a fact that is especially true for parasites of noneconomically important hosts. The ability to describe complex life cycles and to ultimately understand the role of parasites in food webs requires the identification of all hosts that connect their different life history stages, a phenomenon that often arises from unplanned opportunities related to host studies performed for other reasons (Macnish et al., 2003).

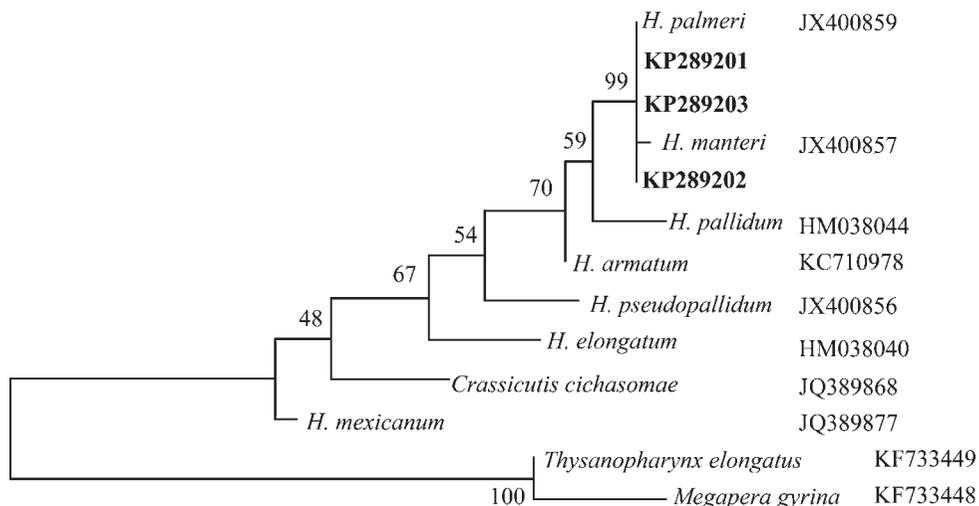
As such, a dietary study of the naked goby, *Gobiosoma bosc* (Lacepède, 1800), from Charleston Harbor, South Carolina, documented that 61.2% of 178 gobies examined were infected with various digeneans in the digestive tract (D'Aguillo et al., 2014). Although *G. bosc* is widespread and abundant in estuaries from Connecticut to the Gulf of Mexico (Dawson, 1969; Ross and Rohde, 2004), to our knowledge, no parasites other than myxozoans (Whipps and Font, 2013) have been reported in this fish to date. Significantly, there is evidence that trophically transmitted parasites may be more common in hosts, such as the naked goby, that are involved in a large number of predator-prey links in

food webs (e.g., generalist predators) (Chen et al., 2008; Amundsen et al., 2009; Hatcher and Dunn, 2011). The naked goby is a generalist predator, and juveniles and adults feed primarily on polychaetes, gammarid amphipods, and harpacticoid copepods (Longenecker, 1993; unpublished thesis, University of South Florida, Tampa, FL, U.S.A.; D'Aguillo et al., 2014). In turn, the naked goby serves as food for larger estuarine piscivores, including red drum, *Sciaenops ocellatus* (Linnaeus, 1766) (see Facendola and Scharf, 2012); Atlantic croaker *Micropogonias undulatus* (Linnaeus, 1766) (see Overstreet and Heard, 1978); and striped bass *Morone saxatilis* (Walbaum, 1792) (see Rudershausen et al., 2005). Taken together, the high numerical abundance of this fish in estuaries, its generalist diet, and prior observations of the presence of helminths in its digestive tract are in compliance with the hypothesis that naked gobies have the potential to act as hosts for trophically transmitted parasites. The purpose of this study was to identify some of the digeneans that infect the digestive tract of the naked goby. Because digenean specimens observed were immature, we used molecular techniques and then verified our results using a subset of morphological criteria of the species identified.

### MATERIALS AND METHODS

Fish examined during the initial diet study were fixed in formalin and were not usable for molecular or morphological identification of their parasites. Thus, additional fish specimens were collected in November 2012 ( $n = 15$ ) and April 2013 ( $n = 17$ ) from a single tidal creek in the

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**Figure 1.** Phylogenetic tree of representatives of *Homalometron*, 3 other genera of Apocreadiidae, and samples from the present study (KP289201–KP289203) produced by maximum likelihood. Numbers at nodes estimate phylogenetic accuracy using 1,000 bootstrap replications. GenBank accessions are listed to the right of each species.

Charleston Harbor (32°44'58"N; 79°53'49"W) using the submerged rubble shell tray method (Lehnert and Allen, 2002). Fish were transferred to the laboratory and euthanized one at a time by overdose of MS222. The digestive tract was resected, and fresh digeneans were isolated and transferred to saline before being immediately processed for either molecular or morphological study.

For the molecular study, 3 samples of genomic DNA were isolated from specimens pooled in pairs using an Epicenter Kit (Epicenter, Madison, WI). The internal transcribed spacer II (ITS2) region of rDNA was amplified using universal trematode primers, as modified by Tandon et al. (2007): forward (5'-GGTACCGGTGGATCACTCGGCTC GTG-3') and reverse (5'GGGATCCTGGTTAGTTTCTTT TCCTCCGC-3'). Amplifications occurred in a 20 µl solution consisting of 5 µl template DNA, 3.75 mM MgCl<sub>2</sub>, 0.5 mM dNTP, 0.5 µM of each primer, 0.5X BSA, 5X GoTaq buffer, and GoTaq DNA polymerase. Amplification cycles consisted of 4 min of denaturing at 95°C, followed by 35 cycles of 30 sec denaturation at 95°C, 30 sec annealing at 45°C, and 30 sec of extension at 72°C. Amplified products were cleaned with an ExoSap Clean-Up kit (United States Biochemical), and Quickstart (Beckman) sequencing reactions were performed in the forward and reverse directions and processed using capillary electrophoresis on a Beckman CEQ8000. Chromatograms and their base calls were edited in FinchTV (Geospiza, Inc.) to produce a consensus sequence. For 2 of the samples, small stretches of the DNA sequences (2 and 5 bps, respectively) that were of low quality and that did not produce an identical read for the forward and reverse were coded as "n" (i.e., missing data). During phylogenetic tree construction, these missing data, along with gaps, were treated using pairwise deletion. During calculations of percentage divergence between sequences, missing data were treated by eliminating sites containing missing data (complete deletion).

Sequences (GenBank accession numbers KP289201 to KP289203) were compared to the GenBank database using

BLAST, and 10 closely aligned taxa obtained via BLAST (the 7 most closely aligned species within the *Homalometron* Stafford, 1904 genus and the 3 most closely aligned species outside of *Homalometron*), were downloaded and aligned via ClustalX 2.1 (Larkin et al., 2007) using default settings. We used jModelTest 2.1.3 (Darriba et al., 2012) to select the Jukes Cantor as the best model of DNA substitution, as determined via the Akaike Information Criterion. We generated a maximum likelihood phylogeny and its statistical support using 1,000 bootstrap replicates in MEGA 5.05 (Tamura et al., 2011).

For morphological work, isolated digeneans were heat killed in saline, fixed in alcohol formalin acetic acid, stained with Mayer's hematoxylin, and mounted in Cytoseal XYL (Richard-Allan Scientific). A voucher specimen (USNM 1281915) was deposited in the National Museum of Natural History.

Two specimens were measured and compared with museum specimens representing *Homalometron palmeri* Curran, Tkach, and Overstreet, 2013 and *Homalometron manteri* (Overstreet, 1970) (USNPC 105799–105804 and USNPC 105804, respectively). Measurements provided are ranges given in micrometers.

## RESULTS

The maximum likelihood tree indicated that the digeneans collected from the naked gobies studied were members of the genus *Homalometron*, with 99% bootstrap support for both *H. palmeri* and *H. manteri* (Fig. 1). Excluding missing base pairs, all 3 samples were identical and showed 0% divergence from *H. palmeri*, 0.5% divergence from *H. manteri*, and 3.2% divergence from *Homalometron pallidum* Stafford, 1904 (Table 1).

**Table 1.** Number of variable sites based on pairwise comparisons between each sample of digenean (KP289201, KP289202, and KP289203) collected from the naked goby in South Carolina and *Homalometron palmeri*, *Homalometron manteri*, and *Homalometron pallidum* sequences from the GenBank database for the 372 bp segment examined (ITS2 marker and adjacent regions).

Species	GenBank Accession No.	KP289201	KP289202	KP289203
<i>H. palmeri</i>	JX400859	0	0	0
<i>H. manteri</i>	JX400857	2	2	2
<i>H. pallidum</i>	HM038044	12	12	12
Number of nucleotide sites interpreted as missing data		0	5	2

Morphological examination of the collected specimens could not be thorough because both individuals were immature and much smaller (740 long by 300 wide,  $n = 1$ ) than any USNPC specimens as well as the described specimens in Curran et al. (2013) of either *H. palmeri* or *H. manteri* (minimum size reported 1,780 and 2,250, respectively). However, molecular identification of *Homalometron* sp. was consistent with the presence of robust spines covering the entire body, the oral to ventral sucker width ratios (1:1.15–1.29), and the size of both the subterminal oral suckers (97–127 long by 80–112 wide) and ventral suckers (97–130 long by 92–145 wide).

## DISCUSSION

These findings document the presence of individuals of *Homalometron* sp., most likely *H. palmeri*, in the digestive tract of the naked goby and a new locality for *H. palmeri*. *Homalometron* is a cosmopolitan genus, and several species in the southeastern United States have been reported to parasitize economically important and/or numerically abundant teleost fishes (Cribb and Bray, 1999; Curran et al., 2013). In the western Atlantic and Gulf of Mexico, marine species include *H. pallidum*, which is most likely restricted to the northwest Atlantic from Maine to Massachusetts (Linton, 1901; Curran et al., 2013), *H. manteri*, which was reported from the Gulf of Mexico and along the Atlantic coast from Massachusetts to North Carolina (Linton, 1940; Thoney, 1991; 1993), and *H. palmeri*, which is known only from the Gulf of Mexico (Curran et al., 2013). According to Curran et al. (2013), it is likely that multiple additional undescribed *Homalometron* species exist along the Atlantic coast and in the Gulf of Mexico.

The identification of the naked goby as a host for *Homalometron* sp. was made using a single genetic marker. In general, the ITS regions are extremely useful markers for species delineation in trematodes because sister taxa with identical sequences are very rare (Blair et al., 1997; Nolan and Cribb, 2005).

Moreover, the presence of true intraspecific variability is questionable and usually absent in high-quality, well-replicated studies (Nolan and Cribb, 2005). Thus, considering our ITS2 sequence data, combined with morphological and ecological information, we can exclude the identity of our samples as *H. pallidum* based on 3.2% divergence at ITS2 and a geographic restriction of *H. pallidum* to the northern Atlantic (Curran et al., 2013).

Whereas we cannot conclusively identify our specimens as being either *H. palmeri* or *H. manteri*, the combination of molecular, morphological, and ecological data strongly support the conclusion that our specimens are either *H. palmeri* or an undescribed sister species. Regarding the molecular data, the specimens examined in the present study showed 0% divergence from *H. palmeri* at ITS2, in comparison to 0.5% divergence (2 nucleotide substitutions) from *H. manteri*. Although very few morphological features could be analyzed in our specimens, the oral to ventral sucker width ratio recorded (1:1.15–1.29) is more similar to that of *H. palmeri* (1:1.2–1.3) than to that of *H. manteri* (1:1.3–1.5). Whereas the specimens observed were immature, which likely contributed to their small body size, *H. palmeri* demonstrates host-specific variation in body size: mature individuals are approximately half as large in both black drum, *Pogonias cromis* (Linnaeus, 1766), and silver mojarra *Eucinostomus argenteus* Baird and Girard, 1855, than in their 5 other definitive hosts (Curran et al., 2013). Lastly, *H. palmeri* is considered a generalist and has been documented in 7 host species from 3 families (Curran et al., 2013). In contrast, *H. manteri* is considered more of a specialist and was documented only in the spot, *Leiostomus xanthurus* Lacepède, 1802 (see Thoney 1991; 1993; Curran et al., 2013), and occurs at very low abundance (<0.1 worm per host) in the Atlantic croaker (Thoney, 1991).

Concerning the role of the naked goby in the *Homalometron* sp. life cycle, there are 4 possibilities:

the naked goby may serve as a definitive host, a second intermediate host, a paratenic host, or a dead-end host. Because the individuals of *Homalometron* sp. examined in this study were found in the digestive tract, *G. bosc* may be a definitive host for this digenean. However, all worms initially isolated for molecular and morphological analysis in the present study ( $n = 32$ ) were immature. Although maturation of individuals of *Homalometron* sp. may be seasonal in the western Atlantic, there is no direct evidence to support the notion that individuals of *Homalometron* sp. reach maturity in *G. bosc* because the specimens we examined in April and November may have fallen outside of the seasonal periods when they would reach maturity. It is, however, possible that the immature individuals of *Homalometron* observed in the naked goby were nonencysted metacercariae. In this case, the naked goby may then serve as either a second intermediate host or as a paratenic host. In support of these potential roles for the naked goby in the life cycle of *Homalometron* sp. and our identification of these worms as *H. palmeri*, the naked goby is a known prey item of 2 of the definitive hosts of *H. palmeri*: the Atlantic croaker and the red drum (Overstreet and Heard, 1978; Facendola and Scharf, 2012, respectively). Such transmission of intestinal nonencysted metacercariae to their serranid definitive hosts is thought to occur for bivesiculids in labrid fish (Cribb et al., 1998). Given that predation and cannibalism are known ways for some parasites, including helminths (Buron and Maillard, 1987; Pizzatto and Shine, 2011), to be transmitted to animals otherwise less accessible to intermediate hosts, that postcyclic transmission via predation may be underestimated in some enteric worms (Nickol, 2003), and that trophically transmitted parasites appear to be more common in generalist members of food webs (Chen et al., 2008; Amundsen et al., 2009; Hatcher and Dunn, 2011), the naked goby may thus be serving as a trophic link to the definitive hosts of *H. palmeri*.

Stunkard (1964) performed experimental infection using individuals of *H. pallidum* and demonstrated that cercariae of *H. pallidum* were released by a mollusk (first intermediate host) and that they then encysted in annelids, which he suggested could be second intermediate hosts for this parasite. Thus, the naked goby could possibly serve as a second intermediate host for *Homalometron* sp. after infection by cercariae released from one of the many molluscs present in the oyster reef habitat (Dame, 1979). Alternatively, the naked goby may also serve as

a paratenic host after ingestion of infected annelid prey, which are dominant elements of their diet (in particular *Polydora cornuta*, *Streblospio benedicti*, and nereidid species; see D'Aguillo et al., 2014).

In a final scenario, if the naked goby is not a definitive host or does not effectively transmit immature individuals of *Homalometron* sp. to their definitive host, it may then be a dead-end host for the parasite. Such dead-end hosts in parasite life cycles are occasionally documented in wildlife (Hernandez and Muzzall, 1998; Costa et al., 2014) and whether the impacts of such sinks on the population dynamics of parasites is anything but negligible remains unclear (Hanelt and Janovy, 2003; Leung and Poulin, 2008; Koppel et al., 2011). Considering the present study, the generalist diet of the host, its high numerical abundance, the high incidence of digenean infection of the naked goby, and the documented presence of the naked goby in the diet of known definitive hosts for *H. palmeri*, this fourth scenario is possible but unlikely.

In summary, the results of the present study document a new locality for *H. palmeri* or an undescribed digenean with no genetic divergence from *H. palmeri* at ITS2 outside of the Gulf of Mexico. Whereas the naked goby may serve as a definitive or dead-end host for *Homalometron* sp., the fact that trophically transmitted parasites appear to be more common in generalist members of food webs (Chen et al., 2008; Amundsen et al., 2009; Hatcher and Dunn, 2011) leads us to suspect that the naked goby is either a second intermediate host or a paratenic host carrying nonencysted metacercariae.

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