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METAZOAN PARASITES OF TWO STICKLEBACK SPECIES AT THE SOLOVETSKY ARCHIPELAGO (WHITE SEA)

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The Solovetsky Archipelago, situated in the White Sea, comprises six large islands. Out of them, the two largest ones, Bolshoy Solovetsky and Anzersky islands, possess an extensive system of lakes, streams, and canals, which are connected with each other and with the sea. The study of hydrobionts, including fish, from freshwater bodies of the Solovetsky Archipelago is of great importance for understanding historical processes of fauna formation. The freshwater ichthyofauna of the Solovetsky Islands has been monitored for almost 30 years. As a result of these long-term observations, two sticklebacks were recognized as the most abundant native fish species of the Solovetsky Archipelago: the three-spined stickleback *Gasterosteus aculeatus* and the nine-spined stickleback *Pungitius pungitius*. These fish play an important role in inshore and offshore communities of the White Sea, being a common prey of predatory fish species and marine mammals. There have been few parasitological studies of the White Sea sticklebacks. Most parasitological data available on sticklebacks from the White Sea concern its marine forms from various areas and sticklebacks from the river mouth areas at the White Sea coast. So far, there is no information on parasites of sticklebacks of the Solovetsky Archipelago. In this paper, we present data on parasites of two stickleback species, *P. pungitius* (freshwater and marine forms) and *G. aculeatus* (marine form), caught in the Solovetsky Archipelago waters (the White Sea). Standard parasitological investigation methods were implemented. *Diplostomum spathaceum* metacercariae were additionally identified with the use of mitochondrial marker *cox*1. The parasitic fauna of both stickleback species from two study sites at the Solovetsky Archipelago was poor. Ten parasite species belonging to Copepoda, Monogenea, Nematoda, Cestoda, and Trematoda were found. The marine three-spined stickleback caught off the coast of the archipelago was infected with 6 helminth species. The parasitic fauna of the nine-spined stickleback from a freshwater stream on Bolshoy Solovetsky Island comprised 4 helminth species, while the marine form harbored 5 species. *Cryptocotyle* sp. metacercariae were the most abundant and widespread parasites recorded during our study. Most of the parasite species were acquired by sticklebacks through various invertebrate food items. Zoonotic species (nematodes *Eustrongylides excisus*, cestodes *Diphyllobothrium* spp., and trematodes *Cryptocotyle* spp.) were revealed in fish analyzed. Further research is needed on the parasites of various fish species of the Solovetsky Archipelago, *inter alia* applying molecular methods.

Keywords: Bolshoy Solovetsky Island, Anzersky Island, *Gasterosteus aculeatus*, *Pungitius pungitius*, parasites, *Diplostomum*, *cox*1

The Solovetsky Archipelago, situated in the White Sea, comprises 6 large islands with a total area of 295.23 km^2 and more than 110 small islands. The largest 2 islands, Bolshoy Solovetsky and Anzersky, possess an extensive system of lakes connected by streams and canals with each other and with the sea [Prirodnaya sreda Solovetskogo arkhipelaga, 2007].

The study of hydrobionts, including fish, from freshwater bodies of the Solovetsky Archipelago is of certain interest for understanding historical processes of fauna formation [Bolotov, 2014]. Firstly, the freshwater ichthyofauna of the Solovetsky Islands was investigated by A. Zakhvatkin [1927a]. Then, it was monitored in 1989–2016, and 40 lakes located on these islands were examined. As a result of this long-term monitoring, 15 fish species have been classified into two groups: aboriginal and introduced ones (see the review of Ja. Alekseeva *et al.*, 2014). The changes in the condition of lake ichthyofauna have been identified and shown to be associated mainly with natural factors [Alekseeva, Makhrov, 2018; Alekseeva et al., 2014].

The most numerous aboriginal fish species on the Solovetsky Archipelago are the perch (*Perca fluviatilis* Linnaeus, 1758) and two sticklebacks: the three-spined stickleback *Gasterosteus aculeatus* (Linnaeus, 1758) and the nine-spined stickleback *Pungitius pungitius* (Linnaeus, 1758) [Alekseeva et al., 2014]. The three-spined stickleback is also the most abundant fish species in the White Sea in general, playing a significant role in inshore and offshore communities and being a common prey of predatory fish species [Lajus et al., 2020]. Moreover, both sticklebacks are a common component of the diet of marine mammals in the White Sea [Svetochev, Svetocheva, 2010; Svetocheva, Svetochev, 2015].

Recent genetic data indicate that the three-spined stickleback arrived in the White Sea basin from both Europe and North America after glacial recession [Artamonova et al., 2022]. Therefore, one may expect it to harbor a diverse parasitic fauna. However, there have been few parasitological studies of sticklebacks in the White Sea. Most parasitological information available on stickleback from the White Sea concerns its marine forms from various areas [Isakov, 1970, 1974; Rybkina et al., 2016; Shulman, Shulman-Albova, 1953]. There are also some parasitological data on sticklebacks from the river mouth areas at the White Sea coast [Lumme et al., 2016; Mitenev, Shulman, 2005]. So far, there is no information on the parasites of sticklebacks of the Solovetsky Archipelago.

In this study, we present the first data on the parasites of freshwater and marine forms of *Pungitius pungitius* and marine form of *Gasterosteus aculeatus* from the Solovetsky Archipelago.

MATERIAL AND METHODS

The material for the study was sampled in July 2016 and 2022 in two sampling sites situated on the watershed of Bolshoy Solovetsky Island of the Solovetsky Archipelago (Fig. 1).

The first sampling site was the so-called Filippovskie cages (N65.03°, E35.68°), a narrow bay separated from the sea by an artificial dam. It is thought to have served as enclosure for keeping marine fish in cages. Three-spined sticklebacks (14 specimens on 3 July, 2016, and 6 specimens on 3 July, 2022) and nine-spined sticklebacks (5 specimens on 3 July, 2022) were caught in the bay with a dip net. Three-spined sticklebacks were 60–70 mm long, while nine-spined sticklebacks were 40–60 mm.

The second sampling site was a small freshwater stream near the Solovetsky Settlement (N65.03°, E35.71°) flowing into the White Sea. Nine-spined sticklebacks were caught in the stream with a dip net on 2 July, 2016 (14 specimens), and on 3 July, 2022 (11 specimens). Their length ranged from 25 to 65 mm.

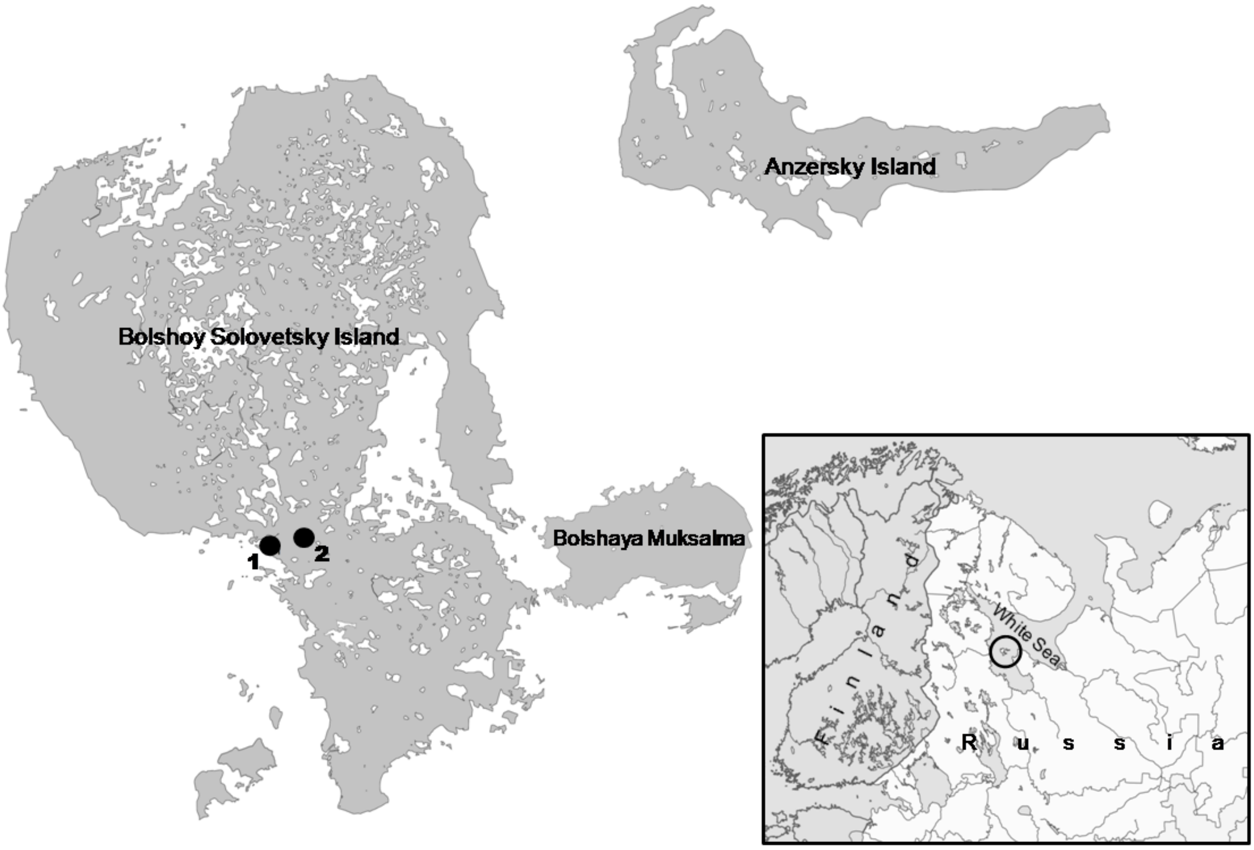

Fig. 1. Sampling sites: 1, Filippovskie cages; 2, a stream near the Solovetsky Settlement

All specimens were examined macroscopically for the presence of ectoparasites immediately after capture and then dissected and studied for endoparasitic helminths and other metazoan parasites using a standard parasitological method [Bykhovskaya-Pavlovskaya, 1985]. All parasites were preserved in 70% and 96% ethanol. Nematodes were cleared in 80% lactic acid, and temporary glycerol preparations were made. Parasitic copepods were fixed in 70% alcohol and mounted on slides with Faure–Berlese mounting medium. Monogeneans were cut into two parts. The opisthaptors were prepared for morphological examination, and then partially digested by proteinase K in a final concentration of 60 $\mu g \cdot mL^{-1}$ *prior* to their preservation in ammonium picrate-glycerin [Zietara, 2004]. Cestodes were stained with iron acetocarmine, dehydrated through a graded ethanol series, clarified in clove oil, and finally mounted in Canada balsam [Georgiev et al., 1986].

Trematodes were stained with acetocarmine, dehydrated, contrasted (cleared) with dimethyl phthalate, and finally mounted in Canada balsam. Trematodes of the genus *Diplostomum* von Nordmann, 1832 were sampled for an integrative study with the use of both molecular and morphological approach. Several metacercariae were stained with acetocarmine and mounted in Canada balsam. Measurements and morphological identification of parasites were made under an Olympus CX41 microscope according to the keys of S. Delyamure *et al.* [1985]; A. Shigin [1986]; A. Gusev [1987]; R. Bray and R. Campbell [1996]; F. Moravec [1994]; T. Scholz *et al.* [2007]; and O. Pugachev *et al.* [2010].

Ecological parameters characterizing fish infection, prevalence, and mean abundance were calculated according to A. Bush *et al.* [1997].

Diplostomum metacercariae were investigated applying molecular method. Genomic DNA was isolated from an ethanol-fixed specimen (in total, two metacercaria from two different fish species were studied this way) using DNA-Extran kits (Syntol, Russia). The fragment of the mtDNA *cox*1 gene was amplified using the primers Cox1_schist_5' (5'-TCTTTRGATCATAAGCG-3') and Cox1_schist_3' (5'-TAATGCATMGGAAAAAAACA-3') of A. Lockyer *et al.* [2003]. PCR assay was carried out in 25 µL of reaction mixture containing 10 ng of total DNA, 75 mM of Tris-HCl (pH 8.8), 20 mM of $(NH_4)_2SO_4$, 0.01% Tween 20, 5 mM of $MgCl_2$, 0.25 mM of each dNTP, 1.5 pmol of each primer, and 0.6–0.7 U of Taq DNA polymerase. Cycling parameters of PCR amplification followed those of [Lockyer et al., 2003].

PCR products were purified using ColGen Extraction Kit (Syntol) following the manufacturer's instructions and then sequenced directly using the same primers of PCR reactions with MegaBACE 1000 DNA Analysis System (Beagle, Saint Petersburg, Russia) (https://biobeagle.com/). Consensus sequences (404 bp) were assembled in MEGA v. 10 [Kumar et al., 2018]. The sequences were deposited in GenBank with accession numbers ON995624 and ON995625.

Identity of newly-generated sequences was checked with the Basic Local Alignment Search Tool (BLAST, https://blast.ncbi.nlm.nih.gov/Blast.cgi). The novel sequences were aligned with the representative sequences of *Diplostomum* spp. previously reported from different places with MUSCLE algorithms implemented in MEGA v. 10 [Kumar et al., 2018] and edited manually. The *cox*1 alignment (353 nt) comprised 2 novel and 44 sequences of *Diplostomum* spp. from GenBank. *Tylodelphys clavata* (JX986908) were used as an outgroup.

Bayesian Inference analysis was conducted using MrBayes software (v. 3.2.3) [Ronquist et al., 2012] with TN93 + I + G model assigned in jModelTest 2.1.2 [Darriba et al., 2012]. Markov chain Monte Carlo (MCMC) simulations were run for 3,000,000 generations, log-likelihood scores were plotted, and only the final 75% of trees were used to produce the consensus trees by setting the "burn in" parameter at 7,500. FigTree v. 1.4 software [Rambaut, 2018] was used to visualize the trees.

RESULTS

The parasitic fauna of the two stickleback species examined in our study was represented by 10 species (Tables 1, 2) from 5 systematic groups: Copepoda, Monogenea, Nematoda, Cestoda, and Trematoda. Six of these species were found in sticklebacks caught in the sea: *Thersitina gasterostei* (Pagenstecher, 1861); *Bothriocephalus scorpii* (Müller, 1776) Cooper, 1917; *Diphyllobothrium* sp.; *Hysterothylacium aduncum* (Rudolphi, 1802) Deardorff & Overstreet, 1981; *Podocotyle reflexa* (Creplin, 1825) Odhner, 1905; and *Cryptocotyle* sp. The monogenean *Gyrodactylus arcuatus* Bychowsky, 1933 was registered in both marine and freshwater sticklebacks. Three species were recorded in sticklebacks caught in the freshwater stream: *Eustrongylides excisus* Jägerskiöld, 1909; *Proteocephalus ambiguus* (Dujardin, 1845) Weinland, 1858; and *Diplostomum spathaceum* (Rudolphi, 1819) Olsson, 1876.

The morphological taxonomy of the genus *Diplostomum* is rather complex; so, we barcoded the metacercariae with the mitochondrial marker *cox*1 (Fig. 2). The sequences formed a well-supported clade with representatives of *D. spathaceum* from different host species and geographical locations, with the *p*-distance values ranging from −0.2 to 1.1%. The *p*-distance value for metacercariae sequences from *P. pungitius* and *G. aculeatus* was 0.2%.

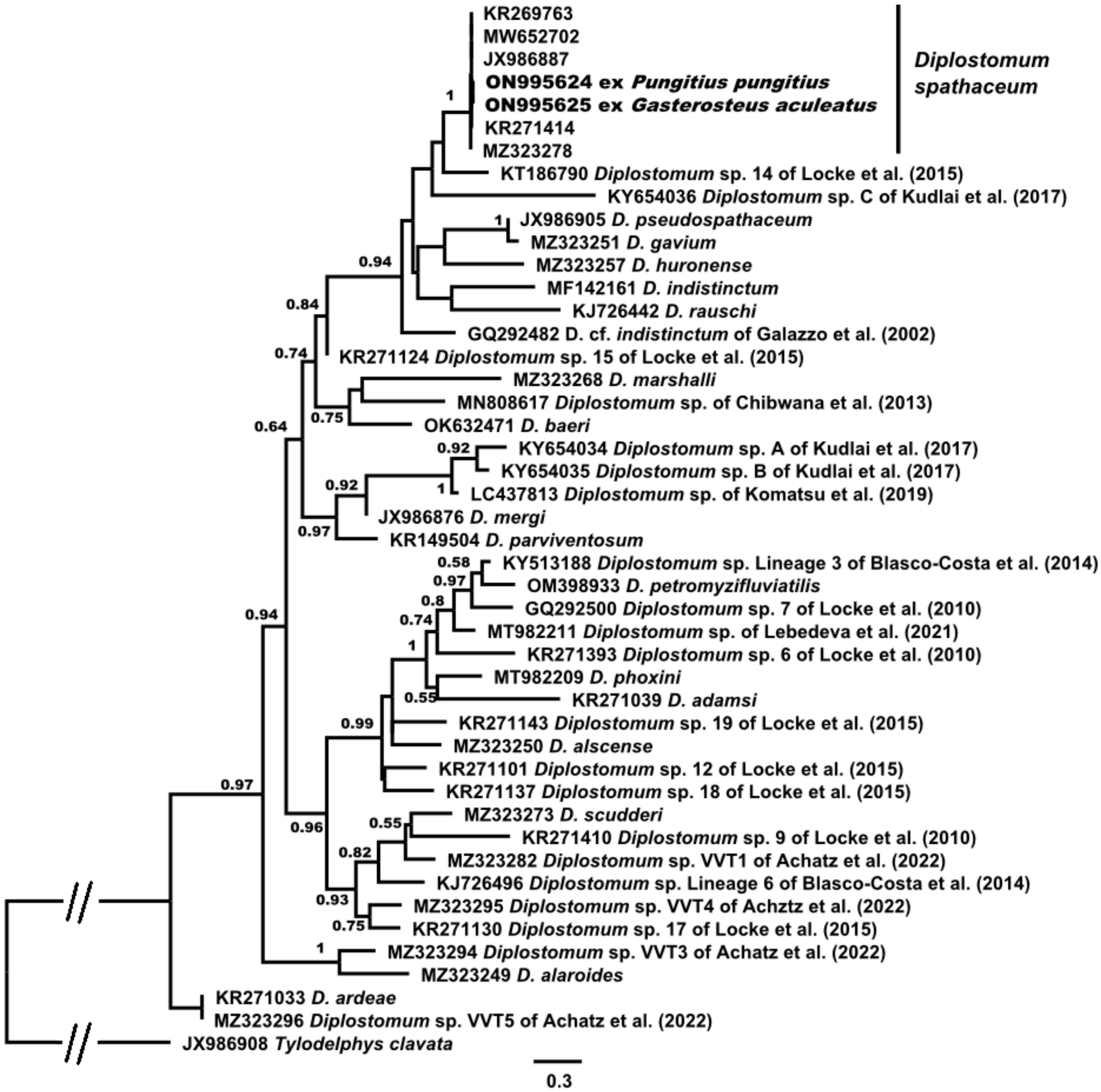

Fig. 2. Phylogenetic tree of *Diplostomum* spp. based on the partial *cox*1 mtDNA sequences (353 bp) inferred using Bayesian Inference analysis. Values lower than 0.5 are not shown. New sequences are in bold

The nine-spined stickleback harbored representatives of all 5 systematic groups recorded in our study (Table 1). Ectoparasites were represented by the crustacean *T. gasterostei* and the monogenean *G. arcuatus*. The latter parasite was the most common, although not numerous. The most species-rich group of endoparasites were cestodes: 3 species, each represented by 1 individual, were found (see Table 1). The cestode *P. ambiguus* was observed in the intestines of *P. pungitius* freshwater form, while *B. scorpii* was noted in the intestines of the marine form. Several plerocercoids of *Diphyllobothrium* sp. were registered on the intestinal wall of two marine nine-spined sticklebacks. The larvae of nematodes *E. excisus* were found on the intestinal wall in almost half of the fish specimens from the stream, though only 1 larva *per* fish was recorded in all the cases. Speaking about trematodes, *Cryptocotyle* spp. metacercariae infected all individuals of the marine stickleback, and the infection was high. In contrast, *D. spathaceum* larvae were found only in several individuals of the freshwater fish (Table 1).

Table 1. Parasites of the nine-spined stickleback *Pungitius pungitius* of Bolshoy Solovetsky Island

Parasite species	Freshwater locality				Marine locality	
	2016		2022		2022	
	P, %	M (min–max)	P, %	M (min–max)	P, %	M (min–max)
Copepoda						
Thersitina gasterostei (Pagenstecher, 1861)	–	–	–	–	4 / 5*	1.4 (1–3)
Monogenea						
Gyrodactylus arcuatus Bychowskiy, 1933	14	1.3 (8–10)	82	4.7 (1–18)	4 / 5	1.5 (1–3)
Nematoda						
Eustrongylides excisus Jägerskiöld, 1909, l.	43	0.5 (1–2)	–	–	–	–
Cestoda						
Bothriocephalus scorpii (Müller, 1776) Cooper, 1917	–	–	–	–	1 / 5	0.4 (2)
Proteocephalus ambiguus (Dujardin, 1845) Weinland, 1858	–	–	27	0.45 (1–3)	–	–
Diphyllobothrium sp., pl.	–	–	–	–	2 / 5	1.0 (1–4)
Trematoda						
Diplostomum spathaceum (Rudolphi, 1819) Olsson, 1876, mtc	29	0.5 (1–3)	–	–	–	–
Cryptocotyle sp., l.	–	–	–	–	5 / 5	4.6 (1–9)
Number of fish examined	14		11		5	
Number of parasite species	4		2		5	

Note: P, prevalence; M, mean abundance; min–max, minimum and maximum number of parasite individuals *per* fish; l., larva; pl., plerocercoid; mtc, metacercaria; *, number of invaded hosts / number of investigated hosts.

The parasitic fauna of three-spined sticklebacks, all of which were caught in the sea, was represented by 6 species belonging to 4 systematic groups: Copepoda, Monogenea, Nematoda, and Trematoda. In contrast with the nine-spined stickleback, no Cestoda species were found in the three-spined stickleback (Table 2).

Metacercariae of *Cryptocotyle* sp., the most numerous and widespread parasites of marine *G. aculeatus*, were found on the skin, fins, and gills. Ectoparasites *T. gasterostei* from the gills and operculum were less numerous. Single specimens of *G. arcuatus* were observed on the gills of several fish. Larvae of nematodes *H. aduncum* were detected on the intestinal wall in 4 out of 6 fish examined. A metacercaria recorded in the lens of one stickleback belonged to *D. spathaceum*, which was also confirmed by molecular methods (Fig. 2). One specimen of the trematode *P. reflexa* was registered in the intestine. In our study, all the parasite species found in the three-spined stickleback were parasites of marine fish, except for *D. spathaceum*.

Table 2. Parasites of *Gasterosteus aculeatus* of Bolshoy Solovetsky Island

Parasite species	Marine locality			
	2016		2022	
	P, %	M (min–max)	P, %	M (min–max)
Copepoda				
Thersitina gasterostei (Pagenstecher, 1861)	93	5.9 (1–31)	5 / 6*	4.2 (1–9)
Monogenea				
Gyrodactylus arcuatus Bychowskiy, 1933	14	1.3 (8–10)	6 / 6	3.8 (1–8)
Nematoda				
Hysterothylacium aduncum (Rudolphi, 1802) Deardorff & Overstreet, 1981, l.	–	–	4 / 6	2.5 (2–6)
Trematoda				
Diplostomum spathaceum (Rudolphi, 1819) Olsson, 1876, mtc	7	0.1 (1)	–	–
Podocotyle reflexa (Creplin, 1825) Odhner, 1905	–	–	1 / 6	0.2 (1)
Cryptocotyle spp., mtc	100	3.1 (1–5)	6 / 6	5.4 (3–12)
Number of fish examined	14		6	
Number of parasite species	4		5	

Note: P, prevalence; M, mean abundance; min–max, minimum and maximum number of parasite individuals *per* fish; l., larva; mtc, metacercaria; *, number of invaded hosts / number of investigated hosts.

DISCUSSION

The parasitic fauna of *G. aculeatus* (marine form) and *P. pungitius* (marine and freshwater forms) obtained from two study sites at the Solovetsky Archipelago comprised 10 species. Marine forms of these two sticklebacks had only 3 parasite species in common: *T. gasterostei*, *G. arcuatus*, and *Cryptocotyle* sp. (see Tables 1, 2). Their other helminths were different, which reflected the differences in their life styles.

Two parasites, *G. arcuatus* and *D. spathaceum*, were recorded both in marine and freshwater sticklebacks. This finding agrees with the literature data. According to L. Isakov [1970] and J. Lumme *et al.* [2016], *G. arcuatus* can parasitize both marine and freshwater fish. *D. spathaceum* metacercariae have been found in fish from brackish waters [Karvonen, Marcogliese, 2020].

The finding of the trematode *P. reflexa* in *G. aculeatus* intestines is very interesting, even though only 1 specimen was recorded. This species has never been registered in the sticklebacks of the White Sea before, while a close species, *Podocotyle atomon* (Rudolphi, 1802) Odhner, 1905, has been observed [Rybkina et al., 2016; Shulman, Shulman-Albova, 1953].

Sticklebacks become infected with various parasites found in our study in several ways. Only 2 species, *G. arcuatus* and *T. gasterostei*, have direct life cycles. Those are transmitted from one host to another or reproduce on the same host. This infection mode suggests that there is a constant source of infection in both marine and freshwater fish populations.

Other parasite species were acquired by the sticklebacks through various invertebrate food objects. We found chitinous odds of insects and crustaceans, small gastropod, and bivalves in the intestines of freshwater nine-spined stickleback. The gut of marine nine-spined sticklebacks contained only amorphous contents. In the intestines of marine three-spined stickleback, odds of insect larvae, crustaceans, small bivalves, and algae were recorded.

The presence of large number of helminths registered in our study indicates that sticklebacks feed on benthos. We found the larvae of nematodes *E. excises*, whose development is associated with benthic oligochaetes *Lumbriculus* Grube, 1844, *Tubifex* Lamarck, 1816, and *Limnodrilus* Claparède, 1862 [Baruš et al., 1978]. Species of these 3 genera have been recorded in the Solovetsky Islands waters [Popchenko, 1972].

The same fish was infected with *D. spathaceum* metacercariae, whose larvae leave their first intermediate host and actively penetrate the second intermediate host through the skin [Shigin, 1986]. In all probability, while feeding on benthos, the sticklebacks were infected with diplostomes from *Lymnaea* spp. These molluscs were noted in water bodies of the Solovetsky Archipelago, in particular, in the small lake, through which the stream where we caught sticklebacks flows [Bespalaya et al., 2021; Zakhvatkin, 1927b]. The nematode *H. aduncum* infects fish feeding on marine invertebrates, such as polychaetes, amphipods, copepods, and chaetognaths. The trematode *P. reflexa* infects fish through various crustaceans [Køie, 1981; Moravec, 1994].

Marine forms of both stickleback species were infected by *Cryptocotyle* spp. metacercariae that actively penetrated the host after they left their intermediate host, the mudsnail *Peringia ulvae* (Pennant, 1777) [Golovin et al., 2021; Gonchar, 2020]. This finding indicates that the fish keep close to the littoral shallows.

The nine-spined sticklebacks from the stream examined in 2022 mostly fed on plankton. It is evidenced by the infection with the cestode *P. ambiguus*, which occurs through eating planktonic crustaceans *Eudiaptomus gracilis* (Sars G. O., 1863) and *Cyclops strenuus* Fischer, 1851 [Scholz, 1999], common on Bolshoy Solovetsky Island [Zakhvatkin, 1927a]. Moreover, these fish were not infested with diplostomids (see Table 1).

In the sea, the nine-spined stickleback is also more likely to feed on plankton, as evidenced by infection with the cestodes *B. scorpii* and *Diphyllobothrium* sp. The fish become infected with the former parasite by eating planktonic crustaceans *Acartia* (*Acartiura*) *longiremis* (Lilljeborg, 1853), which was described for the White Sea as an intermediate host of *B. scorpii* [Grozdilova, Makrushin, 1985].

The parasitic fauna of both stickleback species from two study sites at the Solovetsky Archipelago included parasites common for these fish in nearby northern ecosystems of the White and Barents seas [Isakov, 1974; Mitenev, Shulman, 2005; Rybkina et al., 2016; Shulman, Shulman-Albova, 1953] but was poorer in general. It was also poorer than the parasitic fauna of sticklebacks from Onega and Ladoga, large lakes situated further to the south [Rumyantsev, 2007]. Some of the helminths found in all the above-mentioned water bodies, such as *Schistocephalus solidus* (Müller, 1776) Steenstrup, 1857 and *Diplostomum pungitii* Shigin, 1965, are absent in the sticklebacks from the Solovetsky Archipelago. Apparently, this is due to the absence of the first intermediate hosts necessary for the helminth development or due to a local habitat separation from definitive hosts, fish-eating birds, though the latter ones are numerous and diverse at the Solovetsky Archipelago [Cherenkov et al., 2014]. To the north, V. Mitenev and B. Shulman [2005] recorded only *Schistocephalus pungitii* Dubinina, 1959 in *P. pungitius*, and the closest locality of *S. solidus* in *G. aculeatus* is Mashinnoe Lake, Karelian coast of the White Sea [Borvinskaya et al., 2021]. Besides, the parasitic fauna of freshwater sticklebacks of the Solovetsky Archipelago does not include numerous nonspecific species, especially larval forms of trematodes

Ichthyocotylurus Odening, 1969, *Apatemon* Szidat, 1928, *Tylodelphys* Diesing, 1850, and *Diplostomum*, noted in many northern water bodies [Kuhn et al., 2015; Mitenev, Shulman, 2005; Rumyantsev, 2007; Soldánová et al., 2017].

Zoonotic species found in our material deserve special mention. Those were represented by larvae of the nematode *E. excisus* in freshwater *P. pungitius*, plerocercoids of *Diphyllobothrium* spp. in marine *P. pungitius*, and metacercariae of *Cryptocotyle* spp. in all marine fish. These parasites may cause diseases of birds and mammals, possibly including humans [Duflot et al., 2021; Guardone et al., 2021; Waeschenbach et al., 2017]. Their presence in our material is a consequence of the fact that both stickleback species are an integral part of the diet of ringed seal [Svetochev, Svetocheva, 2010; Svetocheva, Svetochev, 2015], which probably promotes the abundance and dispersal of these parasites.

Nematodes *Eustrongylides* spp. are cosmopolitan parasites using several freshwater fish species as intermediate or paratenic hosts. These nematodes have not been found in either of the two stickleback species before [Moravec, 1994]. In all likelihood, their invasion is related to their ubiquitous distribution and temporary contact with the final host, the cormorant *Phalacrocorax carbo* (Linnaeus, 1758), which forms large colonies on the Solovetsky Archipelago [Cherenkov et al., 2014]. Similarly, *E. excisus* was shown to infect the large-scale sand smelt (*Atherina boyeri* A. Risso, 1810) in the lake Massaciuccoli (Italy) [Guardone et al., 2021].

Another exciting finding is the discovery on the intestinal wall of the marine nine-spined stickleback of plerocercoids of the genus *Diphyllobothrium* Cobbold, 1921. According to A. Waeschenbach et al. [2017], this genus now includes only the worms whose development ends in marine mammals and, probably, in humans. Those are a threat to human health, and their investigation is very important. The larvae found in our study presumably belong to 1 of 4 *Diphyllobothrium* spp. previously noted in marine mammals in the White Sea: *Diphyllobothrium cordatum* (Leuckart, 1863) Gedoelst, 1911; *D. lanceolatum* (Krabbe, 1865) Cooper, 1921; *D. roemeri* (Zschokke, 1903) Meggitt, 1924; and *D. tetrapterum* (von Siebold, 1848) [Delyamure et al., 1985]. However, taking into account the species composition and migratory pathways of marine mammals from the White Sea to the Barents Sea and back [Lukin, Ognetov, 2009; Stenson et al., 2020; Svetochev et al., 2017], it cannot be ruled out that we found *Diphyllobothrium schistochilos* (Germanos, 1895) Cooper, 1858, which has been identified in the Barents Sea, but has never been recorded in the White Sea before [Schaeffner et al., 2018].

High infection levels of sticklebacks by *Cryptocotyle* spp. metacercariae, which were noted during our study and in different spots of the White Sea [Golovin et al., 2021; Rybkina et al., 2016], are associated with favorable conditions for the implementation of the life cycle of this trematode. Its first intermediate hosts are mudsnails *P. ulvae*, and its final hosts are fish-eating birds or marine mammals [Duflot et al., 2021]. *P. ulvae* are numerous in the White Sea [Golovin et al., 2021; Gonchar, 2020]; moreover, fish-eating birds (for example, the cormorant) and marine mammals (including the ringed seal) are widespread in the White Sea and around the Solovetsky Islands [Cherenkov et al., 2014; Chernetsky et al., 2011; Lukin et al., 2006; Surkov, 1957].

Future research of the fish parasites from the Solovetsky Archipelago, *inter alia* molecular studies, will be expanded for several reasons. Firstly, the data on parasites of various freshwater fish species of the Solovetsky Islands, which are now lacking, would be useful to explore the historical processes of formation of the islands' fauna. Secondly, the systematics of many parasite groups (e. g., *Diphyllobothrium* and *Diplostomum*) is currently being revised with the use of the integrative method, and any information on these helminths is in demand. Finally, fish play a significant role in maintaining populations of epizootically important species (*Eustrongylides excisus*, *Cryptocotyle* spp., and *Diphyllobothrium* sp.).

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МНОГОКЛЕТОЧНЫЕ ПАРАЗИТЫ ДВУХ ВИДОВ КОЛЮШЕК СОЛОВЕЦКОГО АРХИПЕЛАГА (БЕЛОЕ МОРЕ)

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Соловецкий архипелаг, расположенный в Белом море, состоит из шести крупных островов. Среди них два самых больших острова, Большой Соловецкий и Анзерский, характеризуются наличием обширной системы озёр, ручьёв и каналов, которые связаны между собой и с морем. Изучение гидробионтов, в том числе рыб, из пресноводных водоёмов Соловецкого архипелага необходимо для понимания исторических процессов формирования фауны. Мониторинг пресноводной ихтиофауны Соловецких островов ведётся более 30 лет. В результате этих наблюдений наиболее многочисленными аборигенными видами рыб на Соловецком архипелаге были признаны два вида колюшек — трёхиглая *Gasterosteus aculeatus* и девятииглая *Pungitius pungitius*. Эти рыбы играют важную роль в прибрежных и морских сообществах Белого моря, являясь обычной добычей хищных видов рыб и морских млекопитающих. Паразитологических исследований колюшек в Белом море проведено немного. Большинство имеющихся паразитологических сведений по колюшке из Белого моря касаются её морских форм из разных районов и колюшки из устьев рек на побережье Белого моря. До настоящего времени не было данных о паразитах колюшки Соловецкого архипелага. Нами получены первые сведения по паразитам двух видов колюшек, *P. pungitius* (пресноводная и морская форма) и *G. aculeatus* (морская форма), выловленных в водах Соловецкого архипелага (Белое море). Были применены стандартные методы паразитологического исследования. Метацеркарии *Diplostomum spathaceum* были дополнительно молекулярно идентифицированы с использованием митохондриального маркера *cox*1. Паразитофауна обоих видов колюшек из двух мест исследования на Соловецком архипелаге была бедной. Обнаружено 10 видов паразитов, относящихся к группам Copepoda, Monogenea, Nematoda, Cestoda и Trematoda. Морская трёхиглая колюшка, выловленная у береговой зоны архипелага, была заражена 6 видами гельминтов. Паразитофауна пресноводной девятииглой колюшки из ручья на Большом Соловецком острове включала 4 вида гельминтов; морская форма была инвазирована 5 видами. Метацеркарии *Cryptocotyle* sp. были самыми многочисленными и широко распространёнными паразитами, зарегистрированными в нашем исследовании. Большинство видов паразитов приобретаются колюшками через различных беспозвоночных как объектов питания. У проанализированных рыб выявлены имеющие важное значение зоонозные виды паразитов (нематоды *Eustrongylides excisus*, цестоды *Diphyllobothrium* spp. и трематоды *Cryptocotyle* spp.). Необходимы дальнейшие исследования паразитов различных видов рыб Соловецкого архипелага, в том числе с использованием молекулярных методов.

Ключевые слова: остров Большой Соловецкий, остров Анзерский, *Gasterosteus aculeatus*, *Pungitius pungitius*, паразиты, *Diplostomum*, *cox*1