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Meso- and bathy-pelagic fish parasites at the Mid-Atlantic Ridge (MAR): Low host specificity and restricted parasite diversity

Sven Klimpel^{a,b,*}, Markus Wilhelm Busch^a, Tracey Sutton^c, Harry Wilhelm Palm^a

^a Heinrich-Heine-University Düsseldorf, Institute of Zoomorphology, Cell Biology and Parasitology, Universitätsstr. 1, D-40225 Düsseldorf, Germany

^b Biodiversity and Climate Research Centre (BiK-F), Johann Wolfgang Goethe-University, Georg-Voigt-Str. 14-16, D-60325 Frankfurt am Main, Germany

^c Virginia Institute of Marine Science, College of William and Mary, PO Box 1346, Gloucester Point, VA 23062, USA

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ABSTRACT

Seven meso- and bathy-pelagic fish species from the Mid-Atlantic Ridge (MAR) were firstly studied for fish parasites and feeding ecology. With a total of seven parasite species, the 247 meso- and bathy-pelagic deep-sea fish specimens belonging to the families Melamphidae (3 spp.), Myctophidae (3 spp.) and Stomiidae (1 sp.) revealed low parasite diversity. The genetically identified nematodes *Anisakis simplex* (s.s.) and *Anisakis pegreffii* from the body cavity, liver and muscles of *Myctophum punctatum* were the most abundant parasites, reaching a prevalence of 91.4% and mean intensity of 3.1 (1–14). *Anisakis* sp. (unidentified) infected *Chauliodus sloani* and *Poromitra crassiceps*. Bothriocéphalidean and tetraphyllidean cestode larvae infected *Benthosema glaciale*, the latter also occurring in *C. sloani* and *Scopelogadus beanii*, at low prevalences. Adult parasites at low infection rates included the digenean *Lethadena* sp. (2.9%), and the two copepod species *Sarcotretes scopeli* (5.7%) and *Tautochondria dolichoura* (5.3–11.4%). The myctophid *Lampanyctus macdonaldi* and the melamphid *Scopelogadus mizolepis* were free of parasites. Analyses of the stomach contents revealed crustaceans, especially copepods and euphausiids for the myctophids and also amphipods for the melamphids as predominant prey items. While all stomachs showing distinct content comprising often unidentified 'tissue' (possibly gelatinous zooplankton), only *C. sloani* preyed upon fish. Though this feeding habit would enable transfer of a variety of crustacean-transmitted parasites into the fish, the parasite fauna in the meso- and bathy-pelagic fish was species poor. All observed parasites showed low host specificity, demonstrating no distinct pattern of host–parasite co-evolution. The MAR is no barrier for the parasite distribution in the North Atlantic meso- and bathy-pelagial.

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1. Introduction

Meso-pelagic fishes require various adaptations to cope with high pressure, cold temperatures, missing light and the immense space with an extremely scarce food supply. Consequently, their behaviour including extensive diurnal migration and characteristic feeding ecology affect the oceanic food web, and the pathways of parasite transmission in the deep sea. Meso-pelagic fishes represent a major component of the oceanic nekton community and are fundamental prey for piscivorous fish and commercially important species such as tunas and mackerels (e.g. Fock et al., 2004) or dolphins and other whales (Fiedler et al., 1998; Wang et al., 2003).

* Corresponding author at: Heinrich-Heine-University Düsseldorf, Institute of Zoomorphology, Cell Biology and Parasitology, Universitätsstr. 1, D-40225 Düsseldorf, Germany. Tel.: +49 211 8110521; fax: +49 211 8114499.

E-mail address: sklimpel@gmx.net (S. Klimpel).

First investigations on the parasite fauna of meso- and bathy-pelagic fish have been carried out e.g. by Noble (1973), Mauchline and Gordon (1984), Gartner and Zwerner (1989) and Campbell (1990). Klimpel et al. (2009) summarized the literature on fish parasites from deep-sea habitats and recorded over 789 parasite species in the so far studied 511 fish species (1.5 parasite species per fish species). With the existence of about 3800–4200 different deep-sea fishes (~10–12% of the known fish fauna, Froese and Pauly, 2009), only a fraction of deep-water fishes have been studied for parasites.

The Mid-Atlantic Ridge (MAR) is an extensive mountainous underwater system in the centre of the Atlantic Ocean, rising from the abyssal plains of about 4500–7500 m water depth up to several 100 m below or even above the sea surface (e.g. Iceland, Azores). It separates the North American and Eurasian Plates, and is divided at 52–53°N and 30–35°E by the Charlie-Gibbs Fracture Zone (CGFZ). The CGFZ consists of two main parallel deep rift valleys, 16–24 km wide, running perpendicular to the main ridge axis with a depth between 700 and 4500 m. The water masses are

the result of recirculation and mixing of northeastern and northwestern deep waters (Vinogradov, 2005). The CGFZ creates a north–south divide for benthic and pelagic fish species. This is caused in particular by the vicinity of the Sub-Polar Front, enhancing the turnover in the food web from planktonic organisms up to the whale and seabird consumers, and appears to be an important whale feeding area (e.g. Dotinga and Molenaar, 2008).

The MAR consequently might constitute a biogeographical barrier for east–west dispersal, limiting the distribution of deep-sea biota either to the eastern or western side. On the other hand, seamounts or mountainous structures may exhibit increased biological productivity, caused by unique currents and upwelling situations, bringing nutrient-rich deep water into the light-flooded productive surface layers (Sutton et al., 2008). Sutton et al. (2008) detected a maximum biomass in the bathy-pelagial at the MAR and connected this with the influence of the ridge. Usually it is assumed that biomass and species richness decline with depth in the pelagic environment and rise again towards the deep-sea floor (e.g. Marcogliese, 2002).

Recent biological surveys of the structure of the deep-sea fish assemblages at the MAR by Fock et al. (2004) and the Census of Marine Life Mar-Eco project (Bergstad et al., 2008; Sutton et al., 2008) revealed a diverse fish fauna and a high biomass. The authors, however, did not find any distinct differences on either side of the MAR. Studies on the vertical and horizontal structure, biomass and topographic association of zooplankton (e.g. copepods, decapods, amphipods, cnidarians) along the MAR also supported these results (Gaard et al., 2008; Stemmann et al., 2008). Multivariate analyses of the different physical and biological data that were sampled during the Mar-Eco surveys indicate that species composition and abundance along the ridge vary especially with the dominant water masses and more importantly with water depth.

Fish parasites on the MAR are largely unexplored, and we are just beginning to understand the marine parasite biodiversity in

the area. Recently, Busch et al. (2008), Kellermanns et al. (2009) and Klimpel et al. (2007, 2008a,b) analysed the fish parasite fauna, identifying several new species (Moravec and Klimpel, 2007, 2009; Kritsky and Klimpel, 2007) and speculating about the parasite composition of deep-sea macrourids at the MAR (Palm and Klimpel, 2008). The present study adds parasitological data on seven dominant meso- and bathy-pelagic fish species. Comments are made on the host specificity of the recorded parasites, and the ecology of the hosts and their importance for parasite transmission are analysed.

2. Material and methods

2.1. Sample collection

Fishes were sampled in June 2004 on board the Norwegian research vessel *G.O. Sars* along the MAR (Fig. 1). The stations were located on the MAR in the area 41°31′–53°05′N and 29°13′–36°43′W. The fish originated from different stations, because they were shared among different research groups prior examination and depending on catch composition. A total of 247 deep-sea fishes belonging to three families were examined for the parasite fauna and stomach contents. *Benthosema glaciale* (Reinhardt, 1837) (70 specimens caught at Super station 26, Local station 355), *Chauliodus sloani* Bloch & Schneider, 1801 (34 specimens caught at Super station 20, Local station 348), *Lampanyctus macdonaldi* (Goode & Bean, 1896) (34 specimens caught at Super station 12, Local station 339), *Myctophum punctatum* Rafinesque, 1810 (35 specimens caught at Super station 14, Local station 341), *Poromitra crassiceps* (Günther, 1878) (19 specimens caught at Super station 32, Local station 361), *Scopelogadus beanii* (Günther, 1887) (35 specimens caught at Super station 31, Local station 360) and *S. m. mizolepis* (Günther, 1878) (20 specimens caught at Super station 34, Local station 364) were caught with pelagic trawls in water depths between 340 and

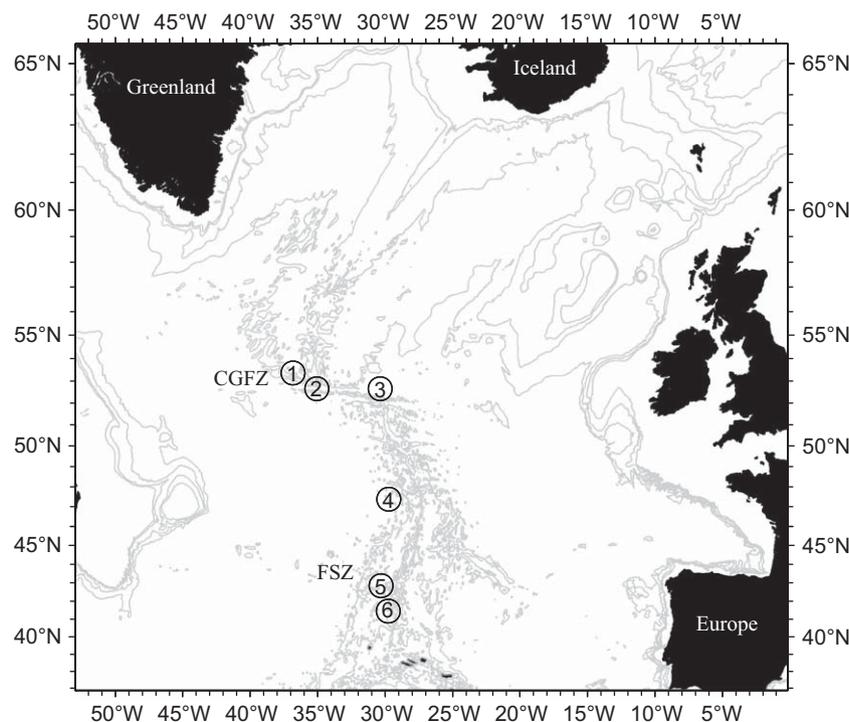


Fig. 1. Map of the area of investigation with sample stations 1–6 (Station 1. *Myctophum punctatum*, 2. *Lampanyctus macdonaldi*, 3. *Chauliodus sloani*, 4. *Benthosema glaciale*, 5. *Poromitra crassiceps*, *Scopelogadus beanii*, 6. *Scopelogadus mizolepis mizolepis*). CGFZ=Charlie-Gibbs Fracture Zone, FSZ=Faraday Seamount Zone.

2300 m as described by Wenneck et al. (2008). All fish specimens examined were deep frozen at -40°C immediately after catch. Prior to examination each fish was defrosted by $0-1^{\circ}\text{C}$. Morphometrical fish data, standard length (SL) and total weight (TW) were recorded to the nearest 0.1 cm and 0.1 g.

2.2. Parasitological examination

The eyes, skin, fins, gills, nostrils and buccal cavity of each fish were examined for ectoparasites. The body cavity was opened to examine the liver, stomach, pyloric caeca, intestine and gonads microscopically for endoparasites and the stomach contents were removed. The isolated parasites were fixed in 4% borax-buffered formalin and preserved in 70% ethanol/5% glycerine. For identification purposes, nematodes were dehydrated in a graduated ethanol series and transferred to 100% glycerine. Digenea and Cestoda were stained with acetic carmine, dehydrated, cleared with eugenol or creosote, and mounted in Canada balsam. Crustacea were dehydrated and transferred into Canada balsam. Parasite identification literature included original descriptions as well as Bray (pers. com.) for Digenea, Euzet (1994) and Kuchta et al. (2008) for Cestoda, Anderson (2000) for Nematoda and Boxshall (pers. com.) for Crustacea. The terms prevalence (P), mean intensity (mI), intensity (I) and mean abundance (mA) follow the recommendations of Bush et al. (1997). Host specificity at the species level was assessed using the specificity index (HSs) of Caira et al. (2003). Host specificity values ranging between 1 and ~ 10 and were calculated using the software available at <http://darwin.eeb.uconn.edu/specificity/specificity.html>.

2.3. Stomach content analysis

The stomach contents were sorted and food items were identified to the lowest possible taxon and grouped into taxonomic categories. The numerical percentage of prey N (%), the weight percentage of prey W (%) and the frequency of occurrence F (%) were determined from the stomach contents (Hyslop, 1980; Amundsen et al., 1996). Using these three indices, an index of relative importance IRI (Pinkas et al., 1971) was calculated. The importance of a specific prey item increases with higher values for N , W , F and IRI.

2.4. PCR amplification and sequencing of ITS-1, 5.8S and ITS-2 of *Anisakis simplex* (s.s.)

All nematodes were identified morphologically by existing keys and descriptions. Only nematodes isolated from the examined *M. punctatum* were identified genetically. After isolation and identification the anisakid nematodes were fixed and stored in absolute ethanol ($\sim 100\%$). Genomic DNA was isolated and purified from individual larvae by using a genomic DNA extraction kit (Peqlab Biotechnology GmbH, Erlangen, Germany) according to the instructions of the manufacturer. The rDNA region comprising the ITS-1, 5.8S, ITS-2 and flanking sequences (=ITS+) was amplified by using the previously described primers NC5 (5'-GTA GGT GAA CCT GCG GAA GGA TCA TT-3') and NC2 (5'-TTA GTT TCT TTT CCT CCG CT-3') (Zhu et al., 2000). PCR-reactions (26 μl) included 13 μl Master-Mix (Peqlab Biotechnology GmbH, Erlangen, Germany) containing dNTP, MgCl_2 , Buffer and Taq-Polymerase, 3 μl of each primer, 2 μl dest. water and 5 μl genomic DNA. Each PCR reaction was performed in a thermocycler (Biometra, Germany) under the following conditions: after initial denaturation at 95°C for 15 min, 30 cycles of 94°C for 1 min (denaturation), 55°C for 1 min (annealing), 72°C for 1 min (extension), followed by a final extension at 72°C for

5 min. Samples without DNA were included in each PCR run. PCR products were checked on 1% Agarose gels. A 100-bp ladder marker (peqGOLD, Erlangen, Germany) was used to estimate the size of the PCR products. In order to identify the anisakid nematodes, the PCR products were purified with E.Z.N.A. Cycle-Pure Kit (Peqlab Biotechnology GmbH, Erlangen, Germany). Afterwards a total volume of 7 μl , including 2 μl primer (individually) and 5 μl of the PCR product (250 ng/ μl) was sequenced by SeqLab (Goettingen GmbH, Germany). Both spacers and the 5.8S gene were sequenced in both directions from each PCR product, using primers NC5, NC13 (forward; 5'-ATC GAT GAA GAA CGC AGC-3'), NC13R (reverse; 5'-GCT GCG TTC TTC ATC GAT-3'), XZ1R (reverse; 5'-GGA ATG AAC CCG ATG GCG CAA T-3') and NC2. The obtained sequences were identified via GenBank and aligned with previously characterized sequences of the *A. simplex* complex, using CLUSTAL W (1.83) Multiple Sequence Alignments (Thompson et al., 1994).

3. Results

The analysis of the 247 meso- and bathy-pelagic fishes belonging to three different families from the deep sea along the MAR revealed low parasite diversity. Seven parasite species including three new locality records could be established, adding to the known number of fish parasites around the MAR. Including the present study, 34 parasite species have been collected so far from deep-sea fish species of different trophic levels at the MAR. Nine groups of prey items were identified, belonging to Mollusca, Crustacea and Teleostei.

3.1. Parasite composition and stomach contents

3.1.1. Myctophidae (Tables 1 and 2)

The studied myctophids showed low parasite richness, with three, three and no parasite species in *B. glaciale*, *M. punctatum* and *Lampanyctus macdonaldi*, respectively. Only the anisakid nematodes *A. simplex* (s.s.) and *Anisakis pegreffii* occurred in high numbers, while the other parasites had low infestation rates.

Three parasite species were isolated from *B. glaciale*. A single tetraphyllidean cestode larva was located in the pyloric caecum, and a single bothriocephalidean cestode larva was detected in the stomach lumen. Specimens of the mesoparasitic copepod *Sarcozetes scopeli* were isolated from the skin and musculature. All prey items in *B. glaciale* belonged to the Crustacea. The frequency of occurrence (F %) was highest for 'tissue', followed by Crustacea indet., Copepoda and Euphausiacea. In wet weight (W %) Euphausiacea were followed by 'tissue', Crustacea indet. and Copepoda. Numerically (N %) 'tissue' was dominant, followed by Crustacea indet., Copepoda and Euphausiacea. The proportion of empty stomachs was 67.1%.

Three parasite species were isolated from *M. punctatum*. A single specimen of the hemiurid digenean *Lethadena* sp. occurred in the stomach lumen. Third-stage larvae (L3) of the nematodes *A. simplex* (s.s.) and *A. pegreffii* (genetic identification see below) were detected in the body cavity, liver and muscles. The stomach contents varied, consisting of Mollusca, Crustacea and 'tissue'. The frequently (F %) dominant prey group was Crustacea, followed by 'tissue' and Gastropoda. Regarding the wet weight (W %) Copepoda and Hyperiididae exceeded 'tissue', Crustacea indet. and Gastropoda. Numerically (N %) Copepoda and Hyperiididae were the most consumed food items, while Gastropoda, Euphausiacea, Decapoda, Crustacea indet. and 'tissue' were of minor importance. All examined stomachs contained food.

Lampanyctus macdonaldi was free of parasites. Three prey groups could be identified: 'tissue', Mysidacea and Crustacea

Table 2
Number (no. examined), mean standard lengths (SL in cm) and total weights (TW in g) (range in parentheses) and food items of the studied deep-sea fish species. *F* %: frequency of occurrence, *W* %: weight percentage of prey, *N* %: numerical percentage of prey, *IRI*: index of relative importance.

| Fish family | <i>Myctophidae</i> | | | | | | | | | | | | <i>Stomiidae</i> | | | | <i>Melamphaidae</i> | | | | | | | | | | | |
|------------------|-----------------------------|------------|------------|------------|-------------------------------|------------|------------|------------|----------------------------|------------|------------|------------|--------------------------|------------|------------|------------|-----------------------------|------------|------------|------------|----------------------------|------------|------------|------------|----------------------------------|------------|------------|------------|
| Fish species | <i>Benthoosema glaciale</i> | | | | <i>Lampanyctus macdonaldi</i> | | | | <i>Myctophum punctatum</i> | | | | <i>Chauliodus sloani</i> | | | | <i>Poromitra crassiceps</i> | | | | <i>Scopelogadus beanii</i> | | | | <i>Scopelogadus m. mizolepis</i> | | | |
| No. examined | 70 | | | | 34 | | | | 35 | | | | 34 | | | | 19 | | | | 35 | | | | 20 | | | |
| SL mean (range) | 6.0 (4.3–7.4) cm | | | | 11.6 (7.5–15.3) cm | | | | 7.6 (6.3–9.5) cm | | | | 17.6 (11.4–25.0) cm | | | | 14.2 (13.2–15.3) cm | | | | 10.8 (10.0–11.7) cm | | | | 10.8 (9.7–12.7) cm | | | |
| TW mean (range) | 2.6 (1.0–4.9) g | | | | 16.9 (3.3–36.5) g | | | | 6.5 (3.4–14.5) g | | | | 12.0 (3.1–32.9) g | | | | 44.1 (30.3–61.8) g | | | | 22.5 (19.0–27.1) g | | | | 20.2 (17.3–25.1) g | | | |
| Prey category | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> | <i>F</i> % | <i>W</i> % | <i>N</i> % | <i>IRI</i> |
| Mollusca | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Gastropoda | | | | | | | | | 5.7 | 0.4 | 0.3 | 4 | | | | | | | | | | | | | | | | |
| Crustacea | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Copepoda | 4.4 | 0.2 | 4.2 | 19 | | | | | 91.4 | 30.8 | 55.7 | 7906 | | | | | | | | | | | | | | | | |
| Euphausiacea | 4.4 | 55.2 | 4.2 | 244 | | | | | 28.6 | 9.0 | 1.2 | 292 | | | | | | | | | | | | | | | | |
| Decapoda | | | | | | | | | 5.7 | 2.4 | 0.2 | 15 | | | | | | | | | | | | | | | | |
| Hyperiididae | | | | | | | | | 94.3 | 28.5 | 41.6 | 6610 | | | | | | | | | | | | | | | | |
| Amphipoda | | | | | | | | | | | | | | | | | | 6.7 | 3.6 | 6.7 | 69 | | | | | | | |
| Mysidacea | | | | | 11.8 | 39.4 | 10.0 | 583 | | | | | | | | | | | | | | | | | | | | |
| Crustacea indet. | 34.8 | 17.0 | 33.3 | 1751 | 35.2 | 42.8 | 30.0 | 2563 | 25.7 | 9.7 | 0.3 | 257 | | | | | | 6.7 | 4.7 | 6.7 | 76 | 30.8 | 42.9 | 30.8 | 2270 | | | |
| Teleostei | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Teleostei indet. | | | | | | | | | | | | | 3.6 | 34.2 | 3.6 | 136 | | | | | | | | | | | | |
| Tissue | 60.9 | 27.6 | 58.3 | 1737 | 70.6 | 17.8 | 60.0 | 5493 | 62.9 | 19.2 | 0.7 | 1252 | 96.4 | 65.8 | 96.4 | 15636 | 100 | 100 | 100 | 20000 | 86.7 | 91.7 | 86.6 | 15459 | 69.2 | 57.1 | 69.2 | 8740 |
| Empty stomachs | | 47 (67.1%) | | | | 17 (50.0%) | | | | | 0 (0.0%) | | | 6 (17.6%) | | | | 0 (0.0%) | | | 20 (57.1%) | | | | 7 (35.0%) | | | |

2009) in order to characterize the fish parasite fauna at this deep-sea ecosystem in the mid-Atlantic Ocean.

4.1. Myctophidae

4.1.1. *Benthosema glaciale*

The examined specimens of *B. glaciale* contained three parasite species. Two cestode larvae, one tetraphyllidean and a bothrioccephalidean, occurred with low infestation rates. The synonym 'Scolex pleuronectis' combines larvae of different final hosts. However, typical for marine cestodes, these larvae probably use crustaceans (Copepoda) as first intermediate host. Final hosts are elasmobranchs such as sharks and rays where they mature in the spiral valve (Euzet, 1994). Larger invertebrates and marine fishes harbour the plerocercoids and act as second intermediate or paratenic hosts (e.g. Euzet, 1994).

Sarcotretes scopeli belongs to a group of two parasitic copepod species that has been recorded from deep-sea pelagic fishes (Cherel and Boxshall, 2004). It utilizes only one host during its life cycle, different from most other members of the family Penellidae. Boxshall (1998) reported 11 deep-sea fish hosts, primarily from the Atlantic Ocean, and stated low host specificity for this species. Regarding the size of the midwater habitat, this adaptation enhances the chance to find a suitable host (Boxshall, 1998). The low infestation rate in the present study seems to be common for this parasite. Hogans (1988) reported low infestation rates from deep-sea fishes from the northwest Atlantic ($P=2.82\%$, $I=1$ on *B. glaciale*). Studies from the Norfolk Submarine Canyon showed a prevalence of 8.3% for *S. scopeli* (Gartner and Zwerner, 1989). Myctophid fishes get infected in the upper water column during their diel migrations (Boxshall, 1998). *B. glaciale* enters the epi-pelagic layer (< 200 m) during the night.

According to Froese and Pauly (2009), *B. glaciale* frequently preys upon calanoid copepods and euphausiids. Examinations of Sameoto (1989) off the subarctic region detected prey selectivity for copepods, especially *Calanus finmarchicus* and *Calanus hyperboreus*, which they hunt in the epi-pelagic zone during night. In this study two fish specimens contained calanoid copepods and euphausiids within their stomachs, together with unidentifiable crustacean fragments. Copepods serve as intermediate host for the tetraphyllidean cestode larvae and presumably for the bothrioccephalidean cestode larvae, but regarding the low number of copepods and also a low prevalence of infection, *B. glaciale* seems to have minor importance within their life cycle.

4.1.2. *Lampanyctus macdonaldi*

Lampanyctus macdonaldi is a typical diurnal migration fish species, and Sutton et al. (2008) captured *L. macdonaldi* frequently between 1500 and 2300 m at the MAR. The examined specimens had no parasites. Parasite infestation is generally low in *L. macdonaldi*. Mauchline and Gordon (1984) recorded a single unidentified nematode in the stomach of 23 specimens at the Rockall Trough, while Gartner and Zwerner (1989) documented only one parasitic cyst in *L. macdonaldi* from the Norfolk Submarine Canyon. Klimpel et al. (2006) studied *L. macdonaldi* from the Irminger Sea and detected larval cestodes (Tetraphyllidae) and nematodes with low infestation rates. The absence of fish parasites in the specimens during the present study might be caused by the smaller size of our studied specimens from the MAR (11.6 cm mean SL) compared with those from the Irminger Sea (13.0 cm mean SL) and by a less diverse prey spectrum (e.g. Klimpel et al., 2006). This myctophid is an offshore species that is less exposed to fish parasites either from the shelf or from the sea floor (Klimpel et al., 2006).

4.1.3. *Myctophum punctatum*

Parasitological studies on the meso-pelagic *M. punctatum* are scarce (Klimpel et al., 2009). Hogans (1988) isolated the copepod *S. scopeli* on *M. punctatum* from Newfoundland waters. Recently, Klimpel et al. (2008b) investigated the parasite fauna of *M. punctatum* from the MAR and recorded four parasite species. The digenean genus *Lethadena* (Hemiuridae) occurred in the present study with only a single specimen. The life cycle of *Lethadena* species is entirely unknown. However, a heteroxenous life cycle with gastropods (molluscs) as first intermediate and pelagic invertebrates (e.g. copepods, euphausiids, chaetognaths) as second intermediate hosts is most common in the family Hemiuridae (Gibson, 2002).

Anisakis simplex (s.s.) and *A. pegreffii*, both *A. simplex*-complex, have been earlier recorded from northern and central parts of the MAR. Kellermanns et al. (2007) and Klimpel et al. (2007) found *A. simplex* (s.s.) in the deep-sea fishes *Macrourus berglax* (Fam. Macrouridae) and *Maurolicus muelleri* (Fam. Sternoptychidae), respectively. Mattiucci and Nascetti (2008) listed *A. pegreffii* and *A. simplex* (s.s.) from *Trachurus* spp. (Fam. Carangidae) and *Scomber* spp. (Fam. Scombridae) at the Azores and north-eastern Atlantic. Final hosts for both anisakids are cetaceans, seldom pinnipeds. *Anisakis simplex* (s.s.) parasitizes in the whale families Delphinidae, Monodontidae, Phocoenidae and Balaenopteridae, and has been genetically identified mainly in the North Atlantic and Pacific Oceans. *Anisakis pegreffii* utilizes the families Delphinidae, Ziphiidae, Physeteridae and Neobalaenidae as final hosts, with the main zoogeographical distribution in the entire Atlantic Ocean and Mediterranean Sea (Klimpel et al., 2008b; Mattiucci and Nascetti, 2008). These cetacean families frequently occur at the MAR during the studied sampling period (Doksæter et al., 2008; Skov et al., 2008).

4.2. Stomiidae

4.2.1. *Chauliodus sloani*

At the MAR *C. sloani* is frequently caught at a depth range between 750 and 2300 m (Sutton et al., 2008). Only a single larval tetraphyllidean cestode and one larval nematode *Anisakis* sp. (possibly *A. simplex* (s.s.) or *A. pegreffii*, see above) were found in the examined *C. sloani*. Gartner and Zwerner (1989) (Norfolk Submarine Canyon) and Klimpel et al. (2006) (Irminger Sea) documented also tetraphyllidean larvae, but with higher prevalences and intensities of infestation. The prevalence of 8.3% by Gartner and Zwerner (1989) for the Nematoda genus *Anisakis* is similar to our findings.

Chauliodus sloani prefers a piscivorous diet (Sutton and Hopkins, 1996). Williams et al. (2001) recorded Myctophiformes and Stomiiformes in the stomachs of *C. sloani* from the Sargasso Sea and adjacent waters, while Klimpel et al. (2006) found unidentified teleosts and cephalopods. Hopkins et al. (1996) concluded that juveniles of the genus *Chauliodus* feeds also on crustaceans. In the present study teleosts occurred with minor importance. Nearly all stomachs with prey ($F=96.4\%$) contained unidentifiable 'tissue'. *Chauliodus sloani* might get infected with tetraphyllideans and *Anisakis* sp. as a paratenic host through preying upon fish.

4.3. Melamphidae

4.3.1. *Poromitra crassiceps*

At the MAR this melamphid species occurred with a high biomass in depths between 750 and 2300 m (Sutton et al., 2008). Parasitological records from *P. crassiceps* are still missing (Klimpel et al., 2009). Noble (1984) studied 17 specimens from the

Southern Ocean and could not detect any parasites. Our results also record a poor infection with metazoan parasites.

Hopkins et al. (1996) stated for the congener *Poromitra gibbsi* a mostly non-crustacean invertebrate prey preference. This corresponds with our data, because all stomachs contained unidentifiable 'tissue'. Following our record of L3 *Anisakis* sp. larvae (possibly *A. simplex* (s.s.) or *A. pegreffii*, see above) we can assume that *P. crassiceps* ingested Crustacea (e.g. calanoid copepods, euphausiids) that serve as obligatory intermediate hosts (Klimpel et al., 2004). The low infection rate indicates only minor importance of *P. crassiceps* for the life cycle of this nematode.

4.3.2. *Scopelogadus beanii*

Gartner and Zwerner (1989) examined 69 specimens from the western North Atlantic and detected seven different parasite species, including fungi, digeneans and nematodes. They isolated tetraphyllidean plerocercoid cestodes with a prevalence of 4.3%. Compared with the data from *S. beanii* from the MAR, tetraphyllidean larvae occurred at a similar low infestation rate. *S. beanii* gets infected with tetraphyllidean larvae while preying upon Crustacea and serves as intermediate host.

Gartner and Musick (1989) examined the stomach content of *S. beanii* from the western North Atlantic and found no evidence for vertical migration or ontogenetic difference in diet. The prey consisted mostly of Amphipoda and gelatinous zooplankton. Studies from the eastern North Atlantic (Rockall Trough) had been done by Mauchline and Gordon (1984). They found besides Crustacea (mainly Copepoda and Amphipoda) unidentifiable 'soft tissue' ($F=88.9\%$), which they assumed to be gelatinous zooplankton, such as salps. Our area of investigation (MAR) lies between these sample stations. Besides a small proportion of Amphipoda and unidentified Crustacea, unidentified 'tissue' occurred with a frequency of occurrence of 86.7% and supports the results of Mauchline and Gordon (1984) and Gartner and Musick (1989).

4.3.3. *Scopelogadus mizolepis mizolepis*

In the eastern Gulf of Mexico *S. m. mizolepis* preys on crustaceans (amphipods) and gelatinous zooplankton (e.g. tunicates, siphonophores). While smaller specimens mainly prefer crustaceans, this proportion shifts to gelatinous prey in the adult stage (Hopkins et al., 1996). *Scopelogadus m. mizolepis* from the MAR confirmed these results. While our examined specimens are larger than those of Hopkins et al. (1996) the stomach content consists mainly of unidentifiable 'tissue', maybe remains of gelatinous zooplankton, and to a smaller part of well digested crustaceans. Interestingly, in contrast to the related *S. beanii*, no parasites were found within the present study.

5. Conclusion

The host specificity of the recorded seven parasites from meso- and bathy-pelagic fishes was low, ranging from 5.574 (still metastenoxenous) to 9.485 (highly euryxenous). The only fish significant for accountable numbers of parasites was the myctophid *M. punctatum*, with a high prevalence of infestation for the both anisakid nematode species *A. simplex* (s.s.) and *A. pegreffii*. All other recorded fish helminths occurred only at very low numbers, appearing to be cases of accidental infection at the studied deep-sea locality. Consequently, while *M. punctatum* might play an important role for the completion of the life cycle of both *Anisakis* species in the mid-Atlantic, all other studied fish species have only a minor role for the existence of oceanic mid- and deep-water helminths at the MAR.

In general this result confirms earlier studies from other deep-sea localities on meso- and bathy-pelagic fishes, revealing only

low numbers of parasites and species. So far, the MAR has not generated a specific parasite fauna within these hosts. One of the important questions to ask for fish parasitological studies within the region was the importance of the MAR for the distribution and possibly evolution of fish-specific parasites (see Palm and Klimpel, 2008). According to our results from the meso-/bathy-pelagic realm, the fishes from these environments harbour low host-specific parasites, without any distinct pattern of host-parasite co-evolution. Consequently, these fishes become accidentally infected through their extensive diel migrations.

Similar to recent results concerning invertebrate and fish distribution surrounding the MAR (e.g. Bergstad et al., 2008; Sutton et al., 2008), the possession of only low host specific parasites seems to be a common pattern in the deep Atlantic (compare Klimpel et al., 2009), and thus not locally restricted. Larvae of generalist parasite species can penetrate from the oceanic epi-pelagial into the deep-sea environment, not necessarily enhancing their success to complete their natural cycles (see Palm and Klimpel, 2008). Consequently, the MAR does not appear to be a barrier for the recorded parasite distribution within the meso- and bathy-pelagial of the North Atlantic, and parasitism seems to be more dependent on chance and accident than local biomass distribution. However, in the case of *M. punctatum* and both *Anisakis* species of the *A. simplex*-complex, this meso-pelagic fish might contribute to the parasite transfer of these nematodes into the cetacean final hosts, reflecting its uptake of the first intermediate host as well as its importance as prey organism (for cetaceans) in the central Atlantic Ocean. Consequently, the combination of fish feeding ecology, depth zonation and respective water masses still might play a significant role for specific meso- or bathy-pelagic fish parasite species distribution.

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