

***Anisakis typica* (DIESING, 1860), DOMINANT ANISAKID NEMATODE PRESENT IN SHORTFIN SCAD, *Decapterus macrosoma* (BLEEKER, 1851) FROM TERENGGANU WATERS, MALAYSIA**

MING SHE SEE¹, FAIZAH SHAROM HARISON², HAZLINA AHAMAD ZAKERI^{1,3} AND NOR
OMAIMA HARUN^{1,3*}

¹Faculty of Science and Marine Environment, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia.

²Faculty of Fisheries and Food Science, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia.

³BIOSES Research Interest Group, Faculty of Science and Marine Environment, Universiti Malaysia Terengganu, 21030 Kuala Nerus, Terengganu, Malaysia.

*Corresponding author: omaima@umt.edu.my

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Abstract: Anisakid (*Anisakis* spp.) nematode is a fish-borne parasite that can cause zoonotic disease, Anisakiasis and IgE hypersensitivity in humans. Thus, the ecology and epidemiology of *Anisakis* nematode are important to control this zoonotic infection. Although *Anisakis* larvae have been reported in Malaysia, it has not been studied through morphological characteristics and molecular analyses. The objective of this study was to identify the *Anisakis* species and its infection status in *Decapterus macrosoma* from Terengganu waters, Malaysia. All *Anisakis* larvae found were morphologically similar to each other and identified as *Anisakis typica*. High infection level ($P = 100\%$, M.I. = 23.31 ± 17.26) of *A. typica* was found in *D. macrosoma*. There was a bioaccumulation of *A. typica* in *D. macrosoma*, showing significant correlation of body weight ($p = 0.05$) and total body length ($p = 0.02$) with the amount of *A. typica* present in *D. macrosoma*. Interestingly, the gonad was the specific site of infection of *A. typica* in *D. macrosoma*, where the intensity of *A. typica* was significantly ($p < 0.003$) higher than other visceral organs. Therefore, the migration of *A. typica* depended on the fatty tissue of the organ.

Keywords: *Anisakis typica*, *Decapterus macrosoma*, bioaccumulation, fatty tissue, Terengganu.

Introduction

Anisakiasis is a fish-borne zoonotic disease caused from consuming raw or undercooked *Anisakis* larvae (L3) of infected fish or seafood (Kim *et al.*, 2013; Lim *et al.*, 2015; Tsukui *et al.*, 2016; Mattiucci *et al.*, 2017; València, 2017). Common symptoms of anisakiasis include nausea, vomiting and epigastric pain (Mattiucci, 2015). In addition, there are 14 types of allergenic proteins found in anisakid nematodes which can cause IgE hypersensitivity to certain patients (Kobayashi *et al.*, 2007; Mattiucci *et al.*, 2018). It has been reported in Spain that one in every three fish are found to be infected with anisakid nematodes (València, 2017). In Malaysia, the first case of anisakiasis was reported in 2016, when a 64-year-old Chinese man was diagnosed having abdominal discomfort after consuming sushi and empurau fish from Sarawak which

was infected with *Anisakis simplex* larva (Amir *et al.*, 2016).

Anisakis simplex and *Anisakis pegreffii* commonly cause anisakiasis in Spain, Morocco, Japan, Indonesia and Taiwan (Chou *et al.*, 2011; Palm *et al.*, 2017; Shawket *et al.*, 2017; Cavallero, 2018; Cipriani *et al.*, 2018; Yamamoto, 2019; Roca-Geronès *et al.*, 2020). However, species such as *A. simplex* and *A. pegreffii* are rarely found in warm waters located along the equatorial (Mattiucci *et al.*, 2018). Instead, *A. typica*, a heterogeneous species of *A. simplex* and *A. pegreffii* is found in temperate and tropical waters (Mattiucci *et al.*, 2002; Cavallero *et al.*, 2012; Chen & Shih, 2015). Reports stated wide distribution of *A. typica* in the Indian Ocean (Mattiucci *et al.*, 2002), Atlantic Ocean (Hermida *et al.*, 2012), Central Pacific (Kuhn *et al.*, 2013), Red Sea (Kleinertz *et al.*, 2014)

and Taiwan Sea (Chen & Shih, 2015) since its definitive host, the oceanic dolphin, is present in the area (Mattiucci & Nascetti, 2008; Iñiguez *et al.*, 2011). Malaysia's neighbouring countries like Indonesia, Thailand and the Philippines have *A. typica* as the dominant species, followed by *A. pegreffii* (Eamsobhana *et al.*, 2018; Tunya *et al.*, 2020; Ayun *et al.*, 2021; Hien *et al.*, 2021). Australia and New Caledonia have the most diverse *Anisakis* such as *A. simplex*, *A. pegreffii*, *A. typica*, *Anisakis berlandi*, *Anisakis brevispiculata* and *Anisakis paggiae* (Shamsi *et al.*, 2018; Shamsi, 2021). Meanwhile, Taiwan and Japan have reported four species of *Anisakis* nematodes: The dominant species is *A. simplex*, followed by *A. pegreffii*, *A. typica* and *A. berlandi* (Gomes *et al.*, 2020; Sonko *et al.*, 2020). The larvae of *A. simplex*, *A. pegreffii* and *A. typica* are morphologically classified as *Anisakis* Type I larvae (Berland, 1961). *A. typica* larvae have a cylindrical mucron which can be differentiated from *A. simplex* larvae that have a cone-shape mucron (Tunya *et al.*, 2020).

Anisakid nematodes have an indirect life cycle, which are classified as heteroxenous parasites. Marine mammals such as delphinoids serve as definitive hosts of anisakid nematodes (Mattiucci & Nascetti, 2008). Adult anisakid nematodes are found in the stomach of the marine mammal: Cetaceans such as *Orcinus orca* and *Pontoporia blainvillei* and sea lion such as *Zalophus californianus* (Hrabar *et al.*, 2021; Irigoitia *et al.*, 2021). The female anisakid nematodes release their eggs into the host faeces, which are then excreted from host body into open water. After hatching, the first-stage larvae (L1) become the second-stage larvae (L2) in free living form (Mattiucci *et al.*, 2018). The L2 stage larvae (L2) are eaten by the first intermediate host (crustacean: *Crangon crangon*), becoming the third-stage larvae (L3) in hemocoel (Pawlak *et al.*, 2019). Following the food web, infected crustaceans are eaten by the cephalopods and fish and the third-stage (L3) larvae bore into the digestive tract to migrate into the visceral organ of the intermediate host. L3 larvae only develop into mature males and females in marine mammals, where the sexual life cycle

will take place (Mattiucci *et al.*, 2018). Starting from the 1950s, studies on *Anisakis* have not only been found in the marine environmental host. Other than marine animal hosts, animals such as amphibians, birds, reptiles and mammals including humans have been infected by the *Anisakis* nematodes (Measures, 2014). Shamsi *et al.* (2017) also observed that the pathogenicity of L3-stage *Anisakis* sp. depended on the species of *Anisakis* larvae that infected the unusual hosts (other than teleost fish). For example, *A. typica* (L3) were not encapsulated in the digestive system of Blue-lipped sea krait, *Carcharhinus brevipinna* and Spinner shark, *Laticauda laticauda* while *A. berlandi* (L3) and *A. pegreffii* (L3) were encapsulated in Grey petrel, *Procellaria cinereal* and Little penguin, *Eudyptula minor* (Shamsi *et al.*, 2017).

Decapterus is a pelagic coastal fish found throughout the year and is widely present in global waters, including western Indian Ocean and western Pacific Ocean (Saikliang, 1997) and East China Sea, Indo-Pacific and Taiwan coastal region until southern Japan (Shiraishi *et al.*, 2010). Three species of *Decapterus*: *Decapterus macrosoma*, *Decapterus macarellus* and *Decapterus russelli* have been identified in Southeast Asia including Indonesia and Malaysia, where they are widely consumed as local delicacies (Arnaud *et al.*, 1999; Borsa, 2003; Rohit & Shanbogue, 2005). In Malaysia, *D. macrosoma* or Shortfin Scad is also known as *selayang*, *basung* or sardine. It is commonly used as the main ingredient for fish crackers and canned fish products in Malaysia (Kang *et al.*, 2018; Nartasha & Sarbon, 2019). *Decapterus macrosoma* has a body length ranging from 11.5 cm to 31.5 cm (Afdhila *et al.*, 2019; Rada *et al.*, 2019) and the male *D. macrosoma* is more predominant than the female (Asni *et al.*, 2019; Ahmadi, 2020). However, cases where this fish was infected with *A. typica* have been reported in Indonesia, causing food-safety problems in the fisheries products (Palm *et al.*, 2008; Palm *et al.*, 2017). In addition, in Malaysia, the anisakid nematodes were found in eight brands of canned fish products in 2018 (ProMED, 2018; Ruxyn, 2018). Coincidentally, in Indonesia and Peru,

Anisakis nematodes were detected in canned fish products (News Desk, 2017; Marwati, 2018). These problems cause health concerns for consumers and affect the sales of canned fish products, with more studies on *Anisakis* infection having been done in ASEAN countries in recent years. Therefore, the aim of this study was to identify the *Anisakis* species, its prevalence (P), mean intensity (M.I.) and mean abundance (M.A.) in *D. macrosoma* from Terengganu waters, Malaysia.

Materials and Methods

Parasite Collection

A total of 30 Shortfin Scad, *Decapterus macrosoma* were purchased from the fish market of Kuala Terengganu Fisheries Department, Terengganu, Malaysia between February to April 2021. The fish samples were transported in a cool box filled with ice to the Histology Lab, Faculty of Science and Marine Environment, Universiti Malaysia Terengganu (UMT). The body weight and total body length of fish samples were recorded upon reaching the lab. The fish samples were dissected under a light dissecting microscope (Olympus SZX7). The *Anisakis* third stage larvae (L3) were identified and removed from the surface of the fish organs, such as gut, liver, pyloric cecum, intestine and gonad and washed with (0.95% NaCl) saline water. The amount of *Anisakis* nematodes found from each organ was record individually. *Anisakis* larvae were identified at the genus level using the diagnostic morphological keys from Berland (1961). The identification of *Anisakis* nematodes (L3) was based on the morphological characteristic of the lips surrounding the anterior end, the presence of boring tooth, the shape of ventriculus, the shape of the tail and the mucron at the posterior end. The ultrasonic cleanser machine (Sonic-P27) was used to remove the outer coat of the larvae to get a finer result for the genetic and morphological study. A total of 676 *Anisakis* larvae were isolated and stored in 70% absolute ethanol for further analysis.

Molecular Analysis

20 *Anisakis* larvae were randomly selected from each host and underwent DNA extraction using GF-1 Viral Nucleic Acid Extraction Kit (Vivantis) according to the manufacturer's instructions. The extracted DNA was stored at -20°C until further analysis. Internal transcribed spacer (ITS) from the genomic DNA was isolated and amplified by using the primer 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). The PCR was performed in 50 µl of reaction mix, containing approximately 0.025 µl⁻¹ Taq DNA polymerase, 0.2 mM dNTPs, 2.5 mM MgCl₂, 50 mM KCl, 10 mM Tris-HCl (pH 9.1 at 20°C), 0.01% Triton™ X-100, 1 µM of each primer and 2.5 µM of sample. The amplification conditions were as follows (Zhu et al., 2000): 94°C for 5 minutes, followed by 30 cycles at 94°C for 30 seconds, 55°C for 30 seconds and 72°C for 30 seconds and final extension at 72°C for 5 minutes.

After that, the PCR products were electrophoresed with 1,000 bp DNA ladder in 1% agarose gel with cybersafe under 90 V for 60 minutes. The targeted ITS genomic DNA sequences produced DNA fragments with 972 bp length. The UV transilluminator (OmegaLumG, Aplegen) was used to visualize the positive bands. Six PCR products with positive bands were sent for DNA sequencing. Bioedit Alignment Sequence Editor Ver. 7.0.5.3 was used to edit and assemble the forward and reverse sequence of ITS1-5.8S-ITS of rDNA. The ITS genomic DNA sequenced from the specimens were compared to the ITS genomic DNA sequence retrieved from GenBank for species identification. Retrieved ITS genomic DNA sequences are listed in Table 1. CLUSTAL X Version 2.1 Multiple Sequence Alignments was used to align obtained sequences with previous characterized sequences of *Anisakis* spp. registered in GenBank (<https://www.ncbi.nlm.nih.gov/genbank>). Maximum likelihood (ML) and neighbour-joining (NJ) phylogenetic trees with 1,000-replicates bootstrap were generated by using *MEGA* version 5.

Table 1: List of the sequences used in the phylogenetic analysis

Accession Number	<i>Anisakis</i> Species	Host	Region	Size	References
MZ895523	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	934	Present study
MZ895793	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	943	Present study
ON075544	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	923	Present study
ON075545	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	941	Present study
ON075546	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	939	Present study
ON075547	<i>Anisakis typica</i>	<i>Decapterus macrostoma</i>	Malaysia	940	Present study
JX648312	<i>Anisakis typica</i>	<i>Decapterus macarellus</i>	Papua New Guinea	907	Koinari <i>et al.</i> , 2013
MN420659	<i>Anisakis typica</i>	<i>Nemipterus japonicus</i>	Thailand	910	Tunya <i>et al.</i> , 2020
MT020146	<i>Anisakis typica</i>	<i>Nemipterus japonicus</i>	China	921	Guo <i>et al.</i> , 2020
JX523715	<i>Anisakis typica</i>	<i>Platycephalus indicus</i>	China	921	Zhang <i>et al.</i> , 2013
KC928262	<i>Anisakis typica</i>	<i>Katsuwonus pelamis</i>	Indonesia	952	Anshary <i>et al.</i> , 2014
AB479120	<i>Anisakis typica</i>	<i>Steno bredanensis</i>	Japan	933	Umehara <i>et al.</i> , 2010
JN005760	<i>Anisakis typica</i>	<i>Pagellus bogaraveo</i>	Portugal	954	Hermida <i>et al.</i> , 2012
EU718476	<i>Anisakis typica</i>	<i>Merluccius polli</i>	Africa	907	Kijewska <i>et al.</i> , 2009
JQ934866	<i>Anisakis typica</i>	<i>Thunnus thynnus</i>	Croatia	888	Vardic Smrzlic <i>et al.</i> , 2012
EU624345	<i>Anisakis paggiae</i>	<i>Theragra chalcogramma</i>	Japan	921	Quiazon <i>et al.</i> , 2009
KM658332	<i>Anisakis brevispiculata</i>	<i>Scomber australasicus</i>	Taiwan	854	Chan and Shih, 2015
MH211473	<i>Anisakis pegreffii</i>	<i>Lophius litulon</i>	China	908	Zhang <i>et al.</i> , 2018
MT448531	<i>Anisakis simplex</i>	<i>Gadus morhua</i>	Greenland	953	Severin <i>et al.</i> , 2020
JQ912692	<i>Anisakis nascettii</i>	Marine fish	Rome	884	Mattiucci <i>et al.</i> , 2014
JQ912691	<i>Anisakis ziphidarum</i>	Marine fish	Rome	888	Mattiucci <i>et al.</i> , 2015
MH211517	<i>Hysterothylacium aduncum</i>	<i>Lophius litulon</i>	China	998	Zhang <i>et al.</i> , 2018

Morphological Study

Scanning Electron Microscope (JEOL JSM6360 LA) (SEM) was used for more distinct morphological structure study of *Anisakis* nematode. The *Anisakis* nematodes were taken out from 70% absolute ethanol (HmbG) and underwent fixing and dehydration by using the procedure provided from INOS, UMT (Abdullah, M.N., 2021) and Kashi *et al.* (2014) with slight modifications: The nematode samples were fixed in 2.5% glutaraldehyde (Merck) in 0.1 M sodium cacodylate buffer (EMS), pH 7.2 for 2 hours. Then, the samples were taken out from the solution and washed with 0.1 M sodium cacodylate buffer (EMS) for 1 hour by changing the solution every 15 minutes. Next, the nematode samples were placed into 1% osmium tetroxide (Sigma-Aldrich) in 0.1 M sodium cacodylate buffer (EMS), pH 7.2 for 2 hours as the post-fixation process. After that, the nematode samples were washed with 0.1 M sodium cacodylate buffer (EMS) for 15 minutes by changing the solution every 5 minutes. The nematode underwent dehydration with different ethanol concentration (Sigma-Aldrich) from 35%, 50%, 60%, 70%, 80%, 90%, 95% until 100% for 10 minutes per solution. After dehydration, the nematode samples were placed in HMDS solution (AcroSeal®) for 3 minutes and air dried for 5 minutes. The prepared samples were mounted on stub by using a tissue double-sided tape (APOLLO). Next, the samples were coated with aurum using auto fine coater (Quorum). The distinct morphology structure of the sample was viewed and captured under scanning electron microscope (JEOL JSM6360 LA). Significant characterising organs such as lips bulge, external papillary structure, amphids and boring tooth, viewed from the SEM were labelled on the captured picture (Weerasooriya *et al.*, 1986; Molina-Fernández *et al.*, 2018).

Statistical Analysis

For the determination of the prevalence, mean intensity and mean abundance of the *Anisakis* larvae in *Decapterus macrosoma*, these formula from Bush (1997) were used:

$$\text{Prevalence (P)} = \frac{\text{Number of individual infected host}}{\text{Total host sample}} \times 100\%$$

$$\text{Mean intensity (M.I.)} = \frac{\text{Number of individual parasite}}{\text{Number of individual infected host}}$$

$$\text{Mean abundance (M.A.)} = \frac{\text{Number of individual parasite}}{\text{Total host sample}}$$

The data were presented as mean \pm standard deviation. Statistical analysis were done using SPSS version 25 statistical software. Correlation study was also done between the size of fish and prevalence and mean intensity of *Anisakis* by using Pearson's correlation method. Non-normally distributed data underwent log transformation. Kruskal-Wallis test was used to understand the differences among visceral organs infected and paired *t* test was used to determine the significant preference in the distribution of anisakid nematode on visceral organs. The significance level was set at $p \leq 0.05$.

Results and Discussion

Molecular Identification of L3 *Anisakis* Larvae

20 PCR products of *Anisakis* larvae showed positive band in gel electrophoresis. The electrophoresis of six selected PCR products for the DNA sequencing is shown in Figure 1.

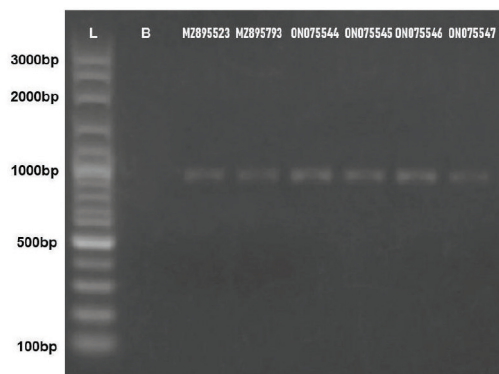


Figure 1: Gel electrophoresis of PCR product from ITS region of L3 *Anisakis typica* from shortfin scad, *Decapterus macrosoma*. L, 1,000 bp DNA ladder (Vivantis); B, blank

The amplification of entire ITS regions of *Anisakis* larvae from *Decapterus macrosoma* generated approximately 943 bp nucleotides. The ITS1-5.8S-ITS2 of rDNA gene sequences of the present *Anisakis* larvae were deposited into Genbank with accession numbers MZ895523, MZ895793, ON075544, ON075545, ON075546 and ON075547. The ITS region of the specimen was assigned to the species, *Anisakis typica* due to the high blast score (100% similarity) with *A. typica* accession numbers MN420659, MT020146, KC928262 and AB479120 when comparing the nucleotide sequences of rDNA in GenBank (Figure 2 and Figure 3).

From the maximum likelihood and neighbour-joining phylogenetic trees constructed from this study, *Anisakis typica* was a distinct lineage among *Anisakis* species (Chen & Shih, 2015). *Anisakis typica* was genetically related to *Anisakis ziphidarum* and *Anisakis nascettii* and heterogeneous with *Anisakis pegreffii* and *Anisakis simplex* (Anshary *et al.*,

2014). Moreover, *Anisakis* sp.1 was reported to be present in *Nemipterus japonicus* in Malaysian waters and it might be the sibling species of *A. typica* from the Central Pacific water based on the mtDNA COX2 region (Mattiucci & Nascetti, 2008; Mattiucci *et al.*, 2018). Our study was the first report of the presence of *A. typica* in *D. macrosoma* from Terengganu, Malaysia that had high similarity with other characterised *A. typica* in the GenBank (accession numbers MN420659, MT020146, KC928262 and AB479120). The polygenetic tree and genetic distance showed that *A. typica* from *D. macrosoma* was closely related to the *A. typica* found in the nearest countries located in the South China Sea (0.000) and Australian waters (0.000-0.0029) (Table 2).

Different *Anisakis* species are present in different geographical areas (Mattiucci *et al.*, 2007; Mattiucci *et al.*, 2018; Rahmati *et al.*, 2020). Thus, studying the geographic distribution of *Anisakis* spp. is important to ascertain the hot spot of Anisakiasis and

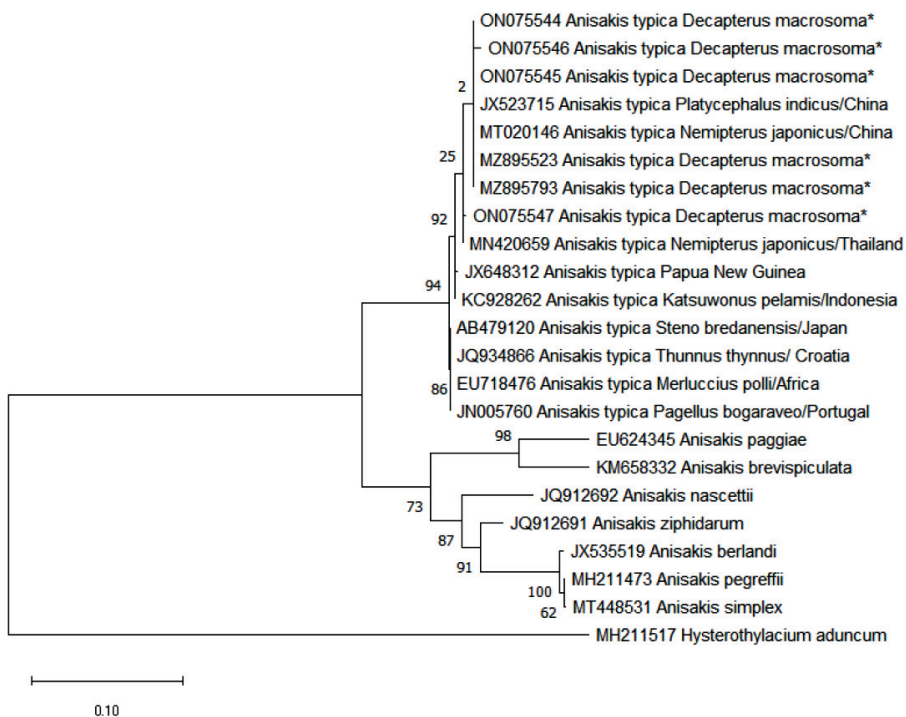


Figure 2: Maximum likelihood phylogenetic tree for *Anisakis* spp. based on ITS region of rDNA under the K2P (Kimura-2-parameter). Accession numbers are listed in the text and *Hysterothylacium aduncum* was used as out group. Number of nodes is 1,000 bootstrap replication. *state for *Anisakis* nematode in present study

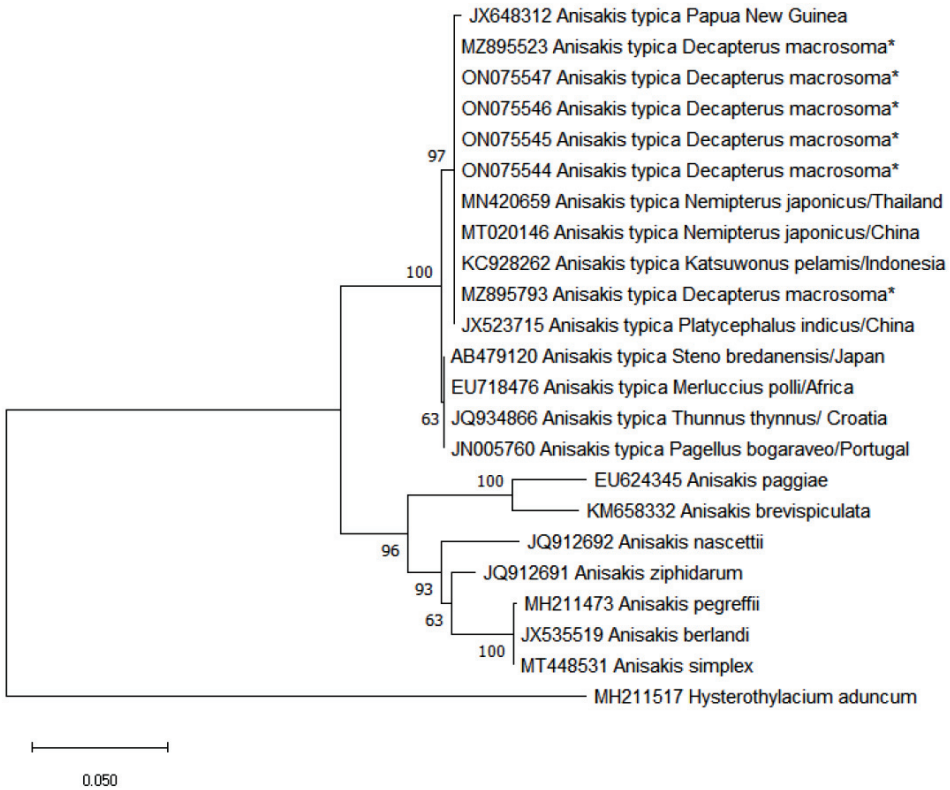


Figure 3: Neighbour-joining phylogenetic tree of *Anisakis* spp. based on ITS region of *rDNA* under the K2P (Kimura-2-parameter). Accession numbers are listed in the text and *Hysterothylacium aduncum* was used as out group. Number of nodes is 1,000 bootstrap replication. *state for *Anisakis* nematode in present study

Table 2: Genetic distance of *Anisakis typica* based on ITS1-5.8S-ITS2 of *rDNA*

Taxa	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
MZ895523_ <i>Anisakis typica</i> *		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
MZ895793_ <i>Anisakis typica</i> *	0.0000		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
ON075544_ <i>Anisakis typica</i> *	0.0000	0.0000		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
ON075545_ <i>Anisakis typica</i> *	0.0000	0.0000	0.0000		0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
ON075546_ <i>Anisakis typica</i> *	0.0000	0.0000	0.0000	0.0000		0.0000	0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
ON075547_ <i>Anisakis typica</i> *	0.0000	0.0000	0.0000	0.0000	0.0000		0.0000	0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
JX523715_ <i>Anisakis typica</i> /China	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		0.0000	0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
MT020146_ <i>Anisakis typica</i> /China	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		0.0000	0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
MN420659_ <i>Anisakis typica</i> /Thailand	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		0.0000	0.0020	0.0029	0.0029	0.0029	0.0029
KC928262_ <i>Anisakis typica</i> /Indonesia	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		0.0020	0.0029	0.0029	0.0029	0.0029
JX648312_ <i>Anisakis typica</i> /Papua New Guinea	0.0029	0.0029	0.0029	0.0029	0.0029	0.0029	0.0029	0.0029	0.0029	0.0029		0.0036	0.0036	0.0036	0.0036
AB479120_ <i>Anisakis typica</i> /Japan	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0087		0.0000	0.0000	0.0000
JQ934866_ <i>Anisakis typica</i> /Croatia	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0087	0.0000		0.0000	0.0000
EU718476_ <i>Anisakis typica</i> /Africa	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0087	0.0000	0.0000		0.0000
JN005760_ <i>Anisakis typica</i> /Portugal	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0058	0.0087	0.0000	0.0000	0.0000	

control the infection (Rahmati *et al.*, 2020). The dominant *Anisakis* species in *Merluccius merluccius* and *Xiphias gladius* from Northeast Atlantic is *A. simplex* (Mattiucci & D’Amelio, 2014). In the Mediterranean Sea, *A. pegreffii* (79%) was reported as the dominant species,

followed by *A. typica* (9.21%), *A. physeteris* (6.38%) and *A. simplex* (4.6%) (Farjallah *et al.*, 2008). The nearest countries to Malaysia such as Indonesia, Thailand and Vietnam have *A. typica* population in their water area (Anshary *et al.*, 2014; Eamsobhana *et al.*, 2018; Tunya *et al.*,

2020; Hein *et al.*, 2021). Moreover, Anshary *et al.* (2014) found a high prevalence (92.3%) of *A. typica* in *Katsuwonus pelamis*. In the present study, there was only a single *Anisakis* species (i.e., *A. typica*) found in the *D. macrosoma* populations from Terengganu waters. This phenomenon has also been observed in the Indian Ocean located from 30 °S to 35 °N in temperate and tropical waters possibly due to the presence of Oceanic dolphins, which are the definitive host for *A. typica* (Mattiucci *et al.*, 2002; Mattiucci & Nascetti, 2008; Iñiguez *et al.*, 2011; Cavallero *et al.*, 2012). Nonetheless, Irrawaddy dolphins (*Orcaella brevirostris*) present on the east coast of the Peninsular Malaysia, may become the reservoir of *A. typica* in Terengganu waters (Mahmud *et al.*, 2018; Jackson-Ricketts *et al.*, 2020; Ismail *et al.*, 2021).

Morphological Study

30 *Anisakis* samples were randomly selected from each fish samples and classified into *Anisakis* Type I larvae (Berland, 1961) which was characterized by long ventriculus, oblique connection between ventriculus and intestine and presence of mucron at the posterior end. It was mentioned in the previous study that there was difficulty to differentiate between *Anisakis* species because their morphology was highly similar (Koinari *et al.*, 2013). However,

microphotographs are able to describe the L3 larvae of *Anisakis pegreffii* and *Anisakis typica* based on morphological and molecular studies (Chen & Shih, 2015). Based on Tunya *et al.* (2020), the posterior mucron of L3 larvae of *A. typica* was cylindrical while *Anisakis simplex* was cone-shape with wider and shorter mucron than *A. typica*. Under the Scanning Electron Micrograph (SEM) (JEOL JSM6360 LA), the anterior end of *A. typica* had three lips (labial protuberances) with papillae. The dorsal lip had two cephalic papillae and each ventrolateral lip had one cephalic papilla at the site. Besides that, the amphid was also located on both of the ventrolateral lips. The mouth was an open and triradiate form of a triangular aperture. The boring tooth was located between two ventrolateral lips (Figure 4 (a)). At the ventral part, there was an excretory pore below the boring tooth. The excretory pore was pointing forward with the mouth in same area. Then, there was an irregularly distributed striation from the anterior until the posterior end of *A. typica*. The posterior end of *A. typica* was a conical-like structure with a mucron end, having a C-shaped anus pointing toward the posterior end (Figure 4 (b)). Consequently, the *Anisakis* specimens in this study were defined as *A. typica* based on the morphology described in the previous studies (Koinari *et al.*, 2013; Gregori *et al.*, 2015; Chen & Shih, 2015; Tunya *et al.*, 2020).

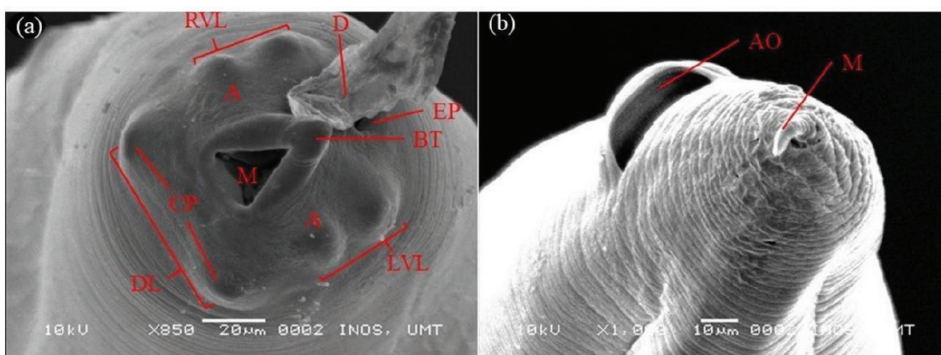


Figure 4: Scanning electron micrographs of mouth part (a) and tail part (b) of L3 *Anisakis typica* from shortfin scad, *Decapterus macrosoma*. (a) Using 850X magnification with 10 kV accelerating voltage. A, amphid; BT, boring tooth; CP, cephalic papillae; D, debris; DL, dorsal lip; EP, excretory pore; LVL, left ventrolateral lip; M, mouth; RVL, right ventrolateral lip. (b) Using 1,000 X magnification with 10 kV accelerating voltage. AO, anus opening; M, mucron. Pictures were taken using SEM (JEOL JSM6360 LA)

Anisakis Larvae Infection in Decapterus macrosoma

The mean body weight and mean total body length of fish samples (n = 30) were 132.51±12.96 g and 23.16±0.93 cm, respectively. The prevalence, mean intensity, abundance of *Anisakis* larvae found in *Decapterus macrosoma* are shown in Table 3.

Clade 1 *Anisakis* species such as *Anisakis simplex*, *Anisakis pegreffii* and *Anisakis berlandi* are commonly found in pelagic, benthopelagic and benthic demersal fish (Mattiucci et al., 2018) while *Anisakis typica* is mainly present in pelagic and reef-associated teleost fish species (Kuhn et al., 2013). Consequently, there was a high infection level of *A. typica* in *D. macrosoma* in our study (P = 100%, M.I. = 23.31±17.26) (Table 3). Besides that, the reservoir of *A. typica* (Delphinidae) was found in epipelagic zone (Gregori et al., 2015). The upwelling and downwelling conditions in mesozooplankton communities (Farjallah et al., 2008; Kuhn et al., 2013) were also the factors that caused high prevalence of *A. typica* in the pelagic fish such as *D. macrosoma* (Table 3) and *Scomber japonicus* (85.7%) from Taiwan waters (Hien et al., 2021).

In recent studies, the bioaccumulation of *Anisakis* larvae occurred in *Alosa alosa*, *Engaraulis encrasicolus* and *Gadus morhua* (Bao et al., 2015; Münster et al., 2015; Cipriani et al., 2018). The larger size of *D. macrosoma* had higher infection level of *A. typica*. The body weight ($r = 0.36, p = 0.05$) and total length ($r = 0.42, p = 0.02$) of *D. macrosoma* also showed a positive linear correlation with the number of *Anisakis* larvae collected from the infected fish (Figure 5). This could be caused by the transmission of *Anisakis* nematodes into another

host (predator) during the prey-predator system (Mattiucci et al., 2018). Moreover, a larger

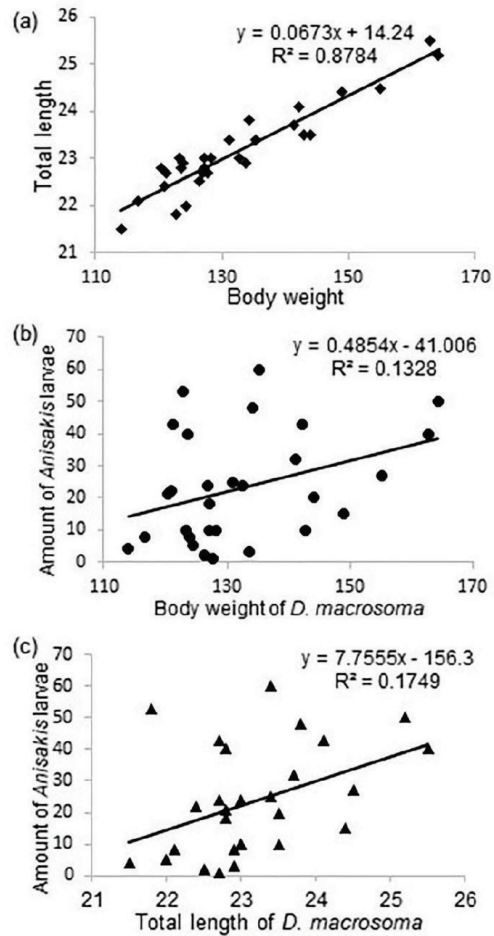


Figure 5: Correlation of size of *Decapterus macrosoma* and number of *Anisakis*. (a) is body weight and total length of shortfin scad, *D. macrosoma*, (b) is body weight and number of *Anisakis* larvae in shortfin scad, *D. macrosoma*, (c) is total length and number of *Anisakis* larvae in shortfin scad, *D. macrosoma*

Table 3: Prevalence, mean intensity, mean abundance and range of *Anisakis* larvae in shortfin scad, *Decapterus macrosoma*

Fish Species	Shortfin Scad (<i>Decapterus macrosoma</i>)
Prevalence of <i>Anisakis</i> larvae	100%
Mean intensity of <i>Anisakis</i> larvae	23.31±17.26
Mean abundance of <i>Anisakis</i> larvae	24.6
Range	1-60

or older fish that consumes a large number of small fish (intermediate host) may cause the bioaccumulation of *Anisakis* larvae, increasing the infected amount of *A. typica* larvae when size of *D. macrosoma* increases.

During infection, *Anisakis* larvae such as *A. simplex* and *A. pegreffii* migrate to the muscular part of the host (Strømnes, 2014) while *A. typica* is rarely found in fish flesh (Palm, 2017). A previous study has shown that the digestive method and incubation method could yield more accurate and higher nematode counts in the fish host. However, visual examination was used in the present study because the migration of *A. typica* into the muscle was blocked by the enzyme activity (unfavourable temperature and pH value), reducing the movement of *A. typica* during the incubation in specific infected organ (Šimat *et al.*, 2015). In our study, *A. typica* accumulated in the visceral organs of *D. macrosoma*. The highest distribution of *Anisakis* nematodes was in the gonad of *D. macrosoma* (49%), followed by the gut (22%), intestine (13%), pyloric caeca (12%) and lastly, the liver (4%) (Figure 6). The infected number of *Anisakis* nematodes showed significant differences among the visceral organs (Kruskal-Wallis: $X^2 = 34.47$, $p = 5.98 \times 10^{-7}$). The gonad of *D. macrosoma* was surrounded by fatty tissue (Figure 7) and *Anisakis* nematode infection on the gonad showed significant difference ($p <$

0.003) among other visceral organs such as gut, pyloric caeca, liver and intestine. Coincidentally, a report has stated that the growth and migration behaviour of *Anisakis* spp. were dependent on lipid concentration in the organ (Šimat *et al.*, 2015). There is a co-relationship between the migration of *Anisakis* spp. and fat tissue (Münster *et al.*, 2015; Šimat *et al.*, 2015), corroborating our observation of a high percentage of *A. typica* found on organ surrounded by fatty tissues.

Conclusion

In conclusion, shortfin scad, *Decapterus macrosoma* from Terengganu waters was exclusively infected with *A. typica* L3 larvae. All the extracted ITS1-5.8S-ITS2 of rDNA gene sequences from the present study were identified as *Anisakis typica*. The microphotograph of *A. typica* showed a triangular open mouth, boring tooth, excretory pore, one dorsal lip with two papillae, two ventrolateral lips with one papilla and one amphid at the anterior end and that the posterior end was a conical-like structure with a mucron end, with a C-shaped anus.

All of the fish samples ($n = 30$) with 132.51 ± 12.96 g body weight and 23.16 ± 0.93 cm body length was infected with this zoonotic nematode (100% prevalence) with an average of 23.31 ± 17.26 individual nematodes present in one infected fish. The intensity of *A. typica*

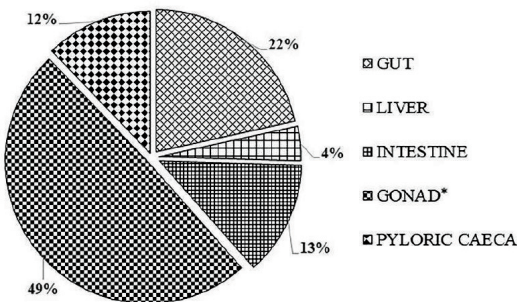


Figure 6: Percentage of amount of *Anisakis* larvae found on different organs in shortfin scad, *Decapterus macrosoma*. *represent significant difference

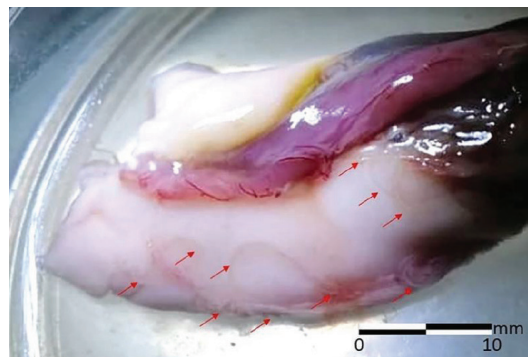


Figure 7: *Anisakis* larvae accumulated in fatty tissue on gonad of shortfin scad, *Decapterus macrosoma*. Arrow represent *Anisakis* larvae

in *D. macrosoma* was significantly correlated to the body weight ($r = 0.36$, $p = 0.05$) and total length ($r = 0.42$, $p = 0.02$) of host, showing that the infection of *A. typica* could happen in prey-predator relationship and cause bioaccumulation in larger host. Besides that, *A. typica* was found in the fatty tissues of the gonad of the infected fish, reflecting the *Anisakis* migration behaviour.

Further studies such as the migration behaviour of *A. typica* within the host environment condition can be conducted to understand the affecting factors that inhibit *A. typica* migration to the muscle tissue of fish host and prevent migration of other *Anisakis* species. The investigation on allergen profile of *A. typica* is also recommended to understand the excretory substance of *A. typica* that causes the immune sensitivity in humans.

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