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Total mercury concentrations in Tasman Sea mesopelagic fish: Exploring biotic and abiotic drivers

Bowen Zhang [a,b,*], Heidi Pethybridge [b], Caroline Sutton [b], Patti Virtue [a,b], Yunkai Li [c]

[a] Institute for Marine and Antarctic Studies, University of Tasmania, Battery Point, Tasmania 7004, Australia
[b] CSIRO Environment, Battery Point, Tasmania 7004, Australia
[c] College of Marine Sciences, Shanghai Ocean University, Shanghai, China

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ABSTRACT

Understanding mercury (Hg) concentrations in mesopelagic and mid-trophic fishes is important for assessing Hg accumulation in oceanic ecosystems and higher-order predators. This study measured total Hg (THg) concentrations in the whole body of 16 abundant mesopelagic fish species sampled in two distinct sites within the Tasman Sea. Across all species, total Hg concentrations ranged from 0.02 to 0.48 μg g^{-1} dry weight (0.01 to 0.15 μg g^{-1} wet weight). Total Hg concentrations varied with vertical migration patterns, with shallower migrators exhibiting higher THg. Females typically had statistically higher THg concentrations than males. Positive correlations between THg concentration and standard length were observed for some but not all species. At the community level, THg concentrations correlated positively with estimated trophic position and foraging habitat, as inferred by stable isotope values. These findings contribute to our understanding of Hg cycling in oceanic ecosystems and the potential for biomagnification in oceanic top-order predators.

1. Introduction

Mercury (Hg) is a highly toxic, persistent and mobile element with a global distribution (Selin, 2009; UNEP, 2013). It is derived from both anthropogenic sources such as industrial emissions, mining, and agriculture usages. Natural sources of Hg include atmospheric circulation and submarine volcanoes and geological deposits which encompass coal and other fossil fuels (Obrist et al., 2018). Atmospheric circulation further contributes to the widespread dispersion of Hg including its deposition into open ocean environments (Simpson et al., 1999; Wania and Mackay, 1996). When introduced into the oceanic environments, mercury undergoes various chemical and biochemical transformations (Bowman et al., 2020), and the adsorption and desorption processes of Hg play a significant role in determining the distribution of its different forms (Gworek et al., 2016). Ocean currents, temperature, and nutrient cycling (e.g. oligotrophy and upwelling) directly influence Hg deposition. The process of Hg bioaccumulation in marine ecosystems can also be influenced by various biological factors, where Hg concentrations are typically higher in older individuals and in higher-order consumers (Ackerman et al., 2014; Bloom, 1992; Coelho et al., 2013; Dehn et al., 2006; Goutte et al., 2014; Mason et al., 1995; Seco et al., 2021a; Tartu et al., 2014; Tavares et al., 2013).

Mercury is present in two distinct forms, including inorganic Hg: Hg^0 (metallic), Hg_2^{2+} (mercurous), and Hg^{2+} (mercuric) and organic Hg: methylmercury (MeHg; CH_3Hg^+) and dimethylmercury ($(CH_3)_2Hg$) (Clarkson et al., 2007). Methylmercury, the most hazardous form of Hg (Henriques et al., 2015), is the most common organic Hg form in the marine environment, and is recognized for the neurodevelopmental toxicity (Obi et al., 2015). Due to the potential risks posed by Hg, particularly MeHg, to both aquatic life and human health, substantial efforts have been made in recent years to reduce Hg emissions and monitor Hg concentrations in various organisms, particularly highly consumed seafood, at both regional Macleod and Coughanowr, 2019) and global scales (e.g. United Nations Minamata convention, (Mackey et al., 2014). Worldwide regulatory agencies (such as United States Environmental Protection Agency, USEPA; and Joint FAO/WHO Expert Committee on Food Additives, JECFA) have established regional intake limits and recommendations (Vieira et al., 2015). While guidelines and recommendations do vary by region and are subject to updates, typically seafood with Hg concentrations below 0.1 μg g^{-1} wet weight (WW) are categorized as being of low risk for human consumption, whereas those over 0.5 μg g^{-1} WW (0.1–0.2 μg g^{-1} dry weight: DW) considering moisture ranging from 60 % – 80 % (Ahmed et al., 2022) are deemed high and advised to be avoided (Balshaw et al., 2007). Among

* Corresponding author at: Institute for Marine and Antarctic Studies, University of Tasmania, Battery Point, Tasmania 7004, Australia.
E-mail address: b.zhang@utas.edu.au (B. Zhang).

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commercial species listed to be avoided are oceanic dwelling sharks and tunas (Goyanna et al., 2023), however, there's limited understanding of Hg concentrations in the prey of these sharks and tunas, such as mesopelagic mid-trophic fish. The bioaccumulation pathways from prey to predator and the cycling of Hg in open ocean and deep-sea ecosystems requires further investigation. Recent research has highlighted the deepest regions of the oceans as an overlooked sink for Hg (Liu et al., 2021) and that the mesopelagic habitat may serve as a major entry point for Hg into marine food webs (Choy et al., 2009). Predators originating from the deep ocean have been shown to exhibit notable enrichment in Hg presumably due to heightened methylation rates occurring in the mesopelagic zone (Chouvelon et al., 2012; Monteiro et al., 1996).

While mesopelagic fish, such as myctophids, represent the most abundant fish group in open ocean ecosystems, there is limited studies that have reported Hg concentrations in these species (Blum et al., 2013; Bustamante et al., 2003; Chouvelon et al., 2012; Gibbs Jr. et al., 1974; Lahaye et al., 2006; Martins et al., 2006; Monteiro et al., 1996; Seco et al., 2021a; Seco et al., 2020b). Concentrations of total Hg (THg) in myctophids exhibit consistently low concentrations, with mean values <0.5 μg g^{-1} dry weight (DW) across the global ocean bodies (reviewed by Zhang et al., 2023). Studies have shown that mesopelagic fish accumulate Hg through ingestion of contaminated prey and through direct absorption via the gills (Seco et al., 2020b). Most of the THg (70–97 %) in myctophid fish has been reported to consist of the toxic MeHg (Buckman et al., 2018). To date, most Hg studies on mesopelagic fish have focused on investigating species differences, size correlations, and understanding the influence on vertical distribution. There are studies that have explored the overall dietary habits and trophic interactions of mesopelagic fish worldwide (Flynn and Kloser, 2012; Hudson et al., 2014; Olivar et al., 2019; Van Noord et al., 2016). However, for most species and regions, more data is needed to understand the distribution, sources and factors influencing Hg concentrations in mesopelagic fishes and their ecological implications, including potential impacts on prey-predator relationships and overall health of oceanic ecosystems.

This study seeks to contribute baseline data and understanding on THg concentrations in mid-trophic mesopelagic fish from the Tasman Sea in the southwestern Pacific Ocean, an area that supports diverse top predator species and is influenced by changing climate regimes. Specimens were selected from two sites to explore the influence of nutrient availability on Hg cycling. The east area of the Tasman Sea is highly oligotrophic while the west experiences higher nutrient concentrations due to seasonal upwelling events (Chiswell et al., 2015). To explore biological and environmental influences on Hg accumulation in mesopelagic fish communities, our analysis included species from a range of taxonomic groups and sizes, and with different vertical migration patterns and trophic ecologies. We focus on abundant species as they are more likely to contribute to the trophic transfer and cycling of Hg to higher order predators. Lastly, as there is growing interest in the commercial harvest of mesopelagic fish to support aquafeeds and other protein industries (Alvheim et al., 2020), we considered regulatory limit guidelines. We also compared Hg concentrations in mesopelagic fish with other regions and seafood taxa.

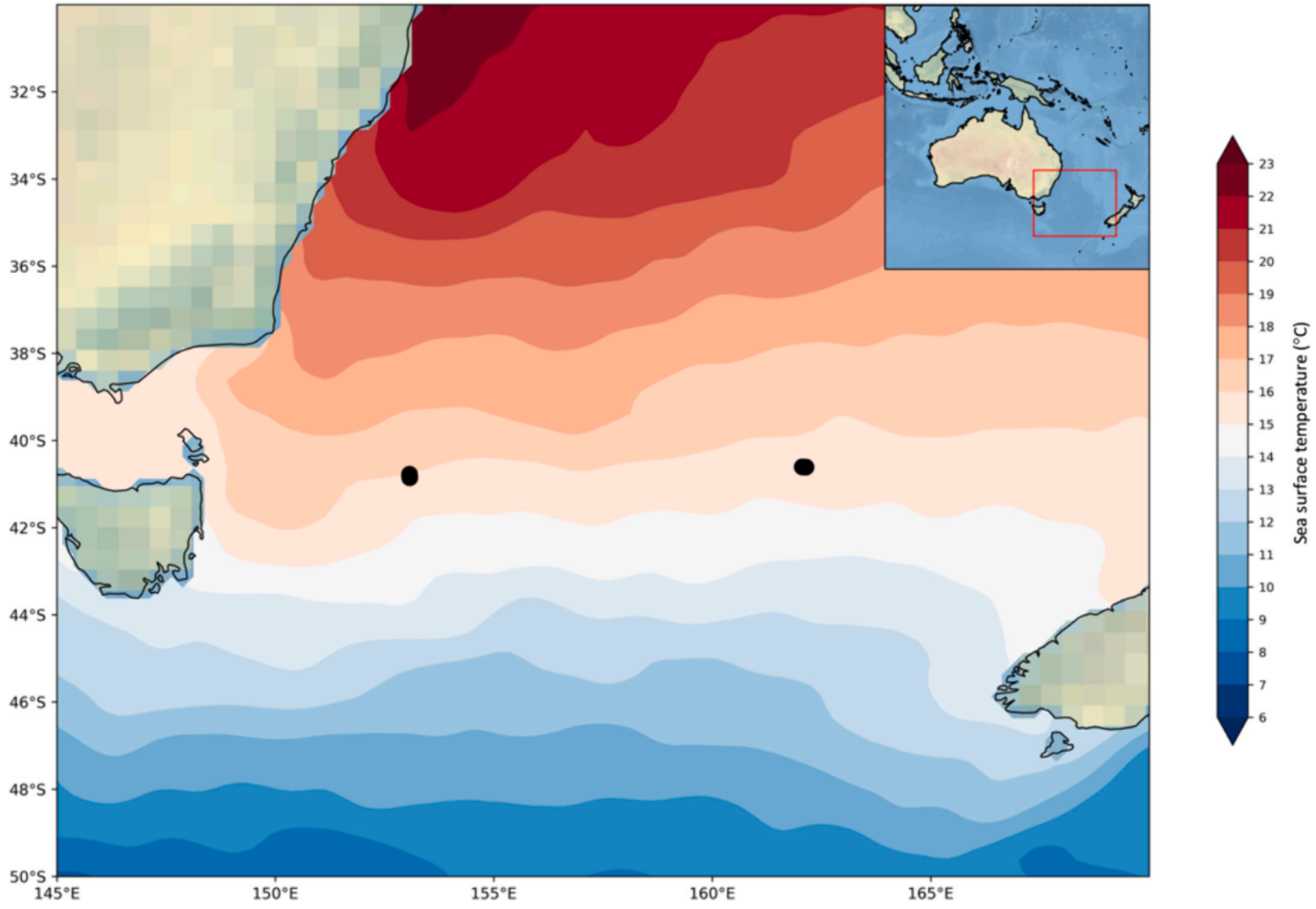

Fig. 1. Spatial distribution of sampling locations based with 2008 annual average sea surface temperature data from NOAA (Huang et al., 2021).

2. Material and methods

2.1. Sample collection and preparation

Fish samples were collected at two sites within the Tasman Sea (40°S-41°S, 153°E-163°E) (Fig. 1) from 14 to 16 June 2008 as part of an austral winter acoustic basin-scale monitoring program (Kloser et al., 2009). All samples were collected at night from 0 to 1000 m using a midwater open and closing (MIDOC) net system attached to the rear of a demersal trawl deployed from the fishing vessel *FV Rehua*. The net hauls were monitored in real-time via the Scanmars acoustic net monitoring system, which provided information on the progress and timing of the hauls. The mid-water net consisted of a series of mesh sections that gradually decreased in size, ranging from a single bar length of 16 m at the opening to 130 mm at the end of the net. Upon collection, samples were identified to the species level onboard and promptly frozen at −18 °C (Flynn et al., 2012). Each fish species was segregated and preserved in plastic bags. Subsequently, individuals were transferred to laboratory facilities and stored at −20 °C for further analyses. Standard length (SL) measurements were taken with precision to the nearest 0.01 mm, and weights were recorded to the nearest 0.0001 g wet weight (WW). Sex was determined through direct observation of the gonads.

To investigate the influence of vertical migration and depth distribution on THg concentrations, we used a simplified classification based on Flynn et al. (2012). Specifically, four vertical migration codes were assigned based on migration depth: 1 - small range nyctoepipelagic migration (from <500 m to 0–100 m); 2 - moderate range nyctoepipelagic migration (from 500 to 1000 m to 0–100 m); 3 - large range nyctoepipelagic migration (≥ 1000 m to 0–100 m); and 4 - small range lower mesopelagic to upper mesopelagic migration (from 500 to 1000 m to 100–400 m).

Mean stable carbon (C) and nitrogen (N) isotope data from Flynn and Kloser (2012) were used to investigate biomagnification and the trophic relationships between THg concentrations and both estimated trophic position (inferred by nitrogen isotope values) and foraging habitat (carbon isotope values). Specifically, isotope data were available for seven species (*Diaphus hudsoni*, *Electrona risso*, *Hygophum hanseni*, *Lampanyctus australis*, *Lampichthys procerus*, *Metelectrona ventralis* and *Bolinichthys supralateralis*). To assist in understanding likely routes of THg transfer to top predators in the study region, we utilized standardized abundance data (n 1000 m^{-3}) calculated from the same monitoring program as described in Sutton et al. (2018) and summarised in Table 1.

2.2. Mercury analysis

Prior to the analytical process, whole fish specimens were freeze-dried at −80 °C for 48 h and subsequently homogenized into a fine powder using the Mixer Mill MM 200 (Retsch). Approximately 0.05 g of each sample was measured for THg concentration by a sequence of thermal decomposition, amalgamation, and atomic absorption spectrometry, using a pre-calibrated DMA-80 Direct Mercury Analyzer (Milestone, Italy). The sequential steps were constituted by 100 s of desiccation, 150 s of decomposition, and 10 s waiting period. For quality control procedures, the precision and reproducibility of the method were evaluated through: i) blank (empty quartz boats, three before each sample); ii) replicated fish sample analyses for all individuals, and iii) certified reference material: DORM-4 (0.412 ± 0.036 μg g^{-1}). The THg concentrations in the blank samples varied from 0.002 to 0.015 μg g^{-1} and the relative difference of replicated samples exhibited a range of 1 to 3 %. The THg concentrations in the certified reference material ranged from 0.401 to 0.421 μg g^{-1} and the percentage recovery for DORM-4 ranged from 97 % to 102 %. Total mercury concentration was quantified by expressing it as the total amount of mercury per gram (μg g^{-1}) of dry weight (DW) and WW.

Table 1
Taxonomic classification, diel vertical migration patterns (MP), and standardized abundance (n 1000 m^{-3}) of 16 mesopelagic fish species. Diel vertical migration patterns: Group: 1 – small range nyctoepipelagic migration from <500 m to 0–100 m; 2 – moderate range nyctoepipelagic migration from 500 to 1000 m to 0–100 m; 3 – large range nyctoepipelagic migration from at least 1000 m to 0–100 m; and 4 – small range lower mesopelagic to upper mesopelagic migration from 500 to 1000 m to 100–400 m.

Family	Common Name	Species	Code	MP	Abundance
Myctophidae	Stubby lanternfish	*Bolinichthys supralateralis*	BS	3	0.2
	Hudson's lanternfish	*Diaphus hudsoni*	DH	3	1.99
	Ostenfeld's lanternfish	*Diaphus ostenfeldi*	DO	2	0.1
	Electric lantern lanternfish	*Electrona risso*	ER	3	0.45
	Hansen's lanternfish	*Hygophum hanseni*	HH	3	1.08
	Southern lanternfish	*Lampanyctus australis*	LA	2	0.85
	Doflein's lanternfish	*Lobianchia dofleini*	LD	2	0.33
	Blackhead lanternfish	*Lampichthys procerus*	LP	3	1.72
	Flaccid lanternfish	*Metelectrona ventralis*	MV	3	0.48
	Cripplefin lanternfish	*Nannobrachium achirus*	NA	3	0.07
	Norman's lanternfish	*Protomyctophum normani*	PN	4	0.05
	Barnard's lanternfish	*Symbolophorus barnardi*	SB	2	0.2
	Multispotted lanternfish	*Scopelopsis multipunctatus*	SM	2	0.13
Nomeidae	Blue Cubehead	*Cubiceps caeruleus*	CC	1	0.14
Stomiidae	Sloane's viperfish	*Chauliodus sloani*	CS	3	0.13
Platytroctidae	Spangled tubeshoulder	*Persparsia kopua*	PK	1	0.29

2.3. Statistical analysis and literature review

The results were expressed as range and mean ± standard deviation. The normality and homogeneity of the data were verified using the Shapiro-Wilk test and Bartlett's test, respectively. To investigate the effects of species and migration pattern on Hg concentrations, analysis of variance (ANOVA) was conducted. A parametric Student *t*-test was employed to examine the effects of site and sex. Statistical significance was determined using a significance level of $p < 0.05$. The relationship between Hg concentration and standard length of mesopelagic fishes was explored using correlation analysis with log10-transformed data. All statistical analyses were conducted under R version 4.2.1 (Team, 2022).

To assist with broader scale comparisons across species and regions, we undertook a comprehensive literature review of studies that reported THg concentrations of mesopelagic fish around the globe. Total mercury data was extracted from 15 published research papers which had reported THg concentrations for 80 species from 31 families sampled from 12 locations or regions (Table S1).

3. Results

3.1. Inter-specific drivers of THg concentrations

3.1.1. Species differences

Across the 16 species of mesoplelagic fish analyzed in this study, THg concentrations varied from 0.02 to 0.48 μg g^{-1} DW (0.01 to 0.15 μg g^{-1}

WW) (Table 2). There were significant differences in THg concentration found at the family level (ANOVA, F-value = 17.406, $p < 0.001$) and at the species level (ANOVA, F-value = 16.651, $p < 0.001$). Highest THg concentrations (means >0.23 μg g^{-1} DW) were found in the spangled tubeshoulder (*P. kopua*), doflein's lanternfish (*L. dofleini*), and sloane's viperfish (*C. sloani*). In contrast, the blue cubehead (*C. caeruleus*) had the lowest mean concentration (0.03 μg g^{-1} DW) with myctophid fishes *M. ventralis* and *D. ostenfeldi* also displaying low concentrations (0.06 and 0.07 μg g^{-1} DW, respectively). Most species had low variations of THg (standard deviations <0.1), except *C. sloani*.

Across all individuals, moisture content varied between 56.2 % and 87.2 %, and standard length ranged from 26.47 to 276.51 mm (Table 2). Cripplefin lanternfish (*N. achirus*) had the highest mean moisture content at 83.5 %, while L. *dofleini* recorded the lowest mean moisture content at 71.46 %. The dry: wet conversion factor ranged from 0.56 to 0.87. *C. sloani* had the greatest mean standard length (SL,197.13 mm, range 153.27–276.51 mm) and moisture content, with a high WW variability (mean 25.27 g, range 7.11–58.83 g). In contrast, *D. ostenfeldi* had the smallest mean SL (33.54 mm, range 26.47–38.96 mm) and the lowest moisture content, with a much lower mean WW (0.67 g, range 0.49–0.88 g).

When converting THg concentrations from DW to WW, based on moisture content, mean concentrations for all species were categorized as being of low risk (<0.1 μg g^{-1} WW). Only five individual specimens for three species were found to have moderate THg concentrations (between 0.1 and 0.5 μg g^{-1} WW) including L. *dofleini* (0.03–0.15 μg g^{-1} WW), *L. procerus* (0.01–0.13 μg g^{-1} WW), and *L. australis* (0.01–0.11 μg g^{-1} WW). No specimens were found to have high Hg concentrations of >0.5 μg g^{-1} WW.

3.1.2. Effects of vertical migration and depth of occurrence on THg concentrations

This study found a significant influence of vertical migratory patterns on the THg concentration in mesopelagic fish (ANOVA, F = 7.53, p < 0.001). Total mercury concentrations showed a decreasing

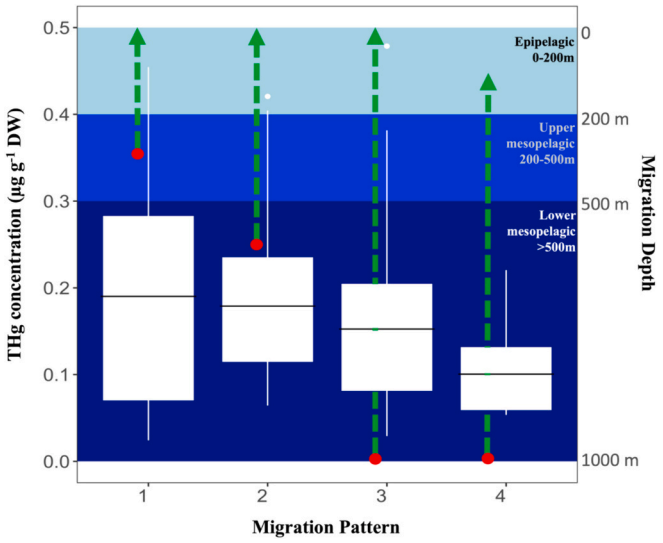

Fig. 2. Box plot of total mercury concentrations (THg; μg g^{-1} DW) in mesopelagic fish from the Tasman Sea classified by four vertical migratory patterns: 1. shallow migrator: small range nyctoepipelagic migration from <500 m to 0–100 m; 2. moderate migrator: moderate range nyctoepipelagic migration from 500 to 1000 m to 0–100 m; 3. deep migrator: large range nyctoepipelagic migration from at least 1000 m to 0–100 m; 4: deep to moderate migrator: small range lower mesopelagic to upper mesopelagic migration from 500 to 1000 m to 100–400 m. Red dots indicate the maximum depth range and migration pattern in green arrows. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Table 2
Sample size (n), standard length (SL), total wet weight (WW), moisture content (%), and total mercury concentrations (THg μg g^{-1} dry weight: DW; WW) of whole mesopelagic fish sampled from the Tasman Sea (mean ± standard deviations with ranges).

Species name	n	SL (mm)	WW (g)	moisture %	THg DW	THg WW
Bolinichthys supralateralis	7	86.82 ± 7.91	12.73 ± 5.3	77.49 ± 1.78	0.19 ± 0.03	0.04 ± 0.01
		79.09–100.9	7.06–21.3	74.53–78.98	0.14–0.24	0.03–0.06
Diaphus hudsoni	31	63 ± 9.43	4.13 ± 1.88	78.4 ± 4.75	0.2 ± 0.09	0.04 ± 0.02
		37.38–86.11	0.77–10.6	56.2–84.19	0.08–0.38	0.02–0.09
Diaphus ostenfeldi	5	33.54 ± 4.80	0.67 ± 0.14	77.92 ± 1.19	0.07 ± 0	0.02 ± 0
		26.47–38.96	0.49–0.88	75.94–78.95	0.06–0.07	0.01–0.02
Electrona risso	10	52.79 ± 13.96	4.73 ± 2.28	77.9 ± 1.53	0.1 ± 0.03	0.02 ± 0.01
		28.9–69.48	1.79–8.43	75.47–80.54	0.06–0.18	0.01–0.04
Hygophum hanseni	5	52.43 ± 2.20	1.87 ± 0.23	75 ± 1.12	0.09 ± 0.01	0.02 ± 0
		49.9–55.01	1.65–2.12	73.02–75.69	0.07–0.11	0.02–0.03
Lampanyctus australis	50	94.18 ± 6.96	9.15 ± 1.87	76.99 ± 2.26	0.19 ± 0.09	0.04 ± 0.02
		71.87–103.88	4.19–13.29	69.46–82.39	0.06–0.42	0.01–0.11
Lobianchia dofleini	10	38.1 ± 5.53	1.76 ± 0.66	71.46 ± 3.33	0.24 ± 0.09	0.08 ± 0.04
		32.58–45.44	0.83–2.61	65.54–74.75	0.12–0.4	0.03–0.15
Lampichthys procerus	21	73.18 ± 11.98	4.76 ± 2.14	77.41 ± 2.26	0.16 ± 0.09	0.04 ± 0.03
		55.86–90.1	1.56–7.63	73.32–81.76	0.06–0.34	0.01–0.13
Metelectrona ventralis	20	78.58 ± 5.42	8.99 ± 1.75	74.67 ± 3.17	0.06 ± 0.03	0.01 ± 0.01
		70.84–89	6.63–12.94	68.26–80.5	0.03–0.15	0.01–0.03
Nannobrachium achirus	12	101.65 ± 22.39	8.41 ± 5.81	83.5 ± 1.62	0.16 ± 0.06	0.03 ± 0.02
		63–143.83	2.06–21.54	71.61–87.14	0.09–0.24	0.02–0.06
Protomyctophum normani	10	48.48 ± 14.21	2.37 ± 1.67	77.36 ± 3.32	0.1 ± 0.06	0.02 ± 0.01
		31.45–63.87	0.59–4.43	74.24–84.95	0.05–0.22	0.01–0.05
Symbolophorus barnardi	5	106.91 ± 13.54	16.76 ± 5.94	72.66 ± 3.99	0.16 ± 0.08	0.04 ± 0.01
		90.62–122.35	1.69–2.20	72.87–79.59	0.12–0.15	0.03–0.06
Scopelopsis multipunctatus	5	54.46 ± 2.45	1.87 ± 0.2	76.64 ± 2.89	0.13 ± 0.01	0.03 ± 0
		51.97–57.65	10.44–24.48	68.29–76.26	0.09–0.24	0.03–0.04
Cubiceps caeruleus	5	38.97 ± 6.26	0.79 ± 0.29	76.99 ± 0.7	0.03 ± 0.01	0.01 ± 0
		32.72–46.94	0.48–1.19	75.98–77.81	0.02–0.05	0.01–0.01
Chauliodus sloani	8	197.13 ± 38.02	25.27 ± 21	81 ± 3.82	0.23 ± 0.14	0.04 ± 0.02
		153.27–276.51	7.11–58.83	74.27–87.2	0.11–0.48	0.02–0.09
Persparsia kopua	13	125.03 ± 16.64	27.27 ± 5.15	80.43 ± 3.72	0.25 ± 0.09	0.05 ± 0.02
		97.53–151.41	18.15–35.04	71.91–85.46	0.14–0.45	0.03–0.08

trend with fish that migrated to deeper waters (Fig. 2). Among the migration groups, group 1, characterized as shallow migrators and including 2 non-myctophid species (*P. kopua* and *C. caeruleus*), displayed the highest mean THg concentrations and greatest variability (0.19 μg g^{-1} DW; 0.04 μg g^{-1} WW). Group 2, consisting of five species of moderate migrators, showed the second-highest mean THg concentration (0.18 μg g^{-1} DW; 0.04 μg g^{-1} WW). Group 3, consisting of eight species undertaking large range migration, exhibited mean THg concentration of 0.15 μg g^{-1} DW (0.03 μg g^{-1} WW). Group 4 included only one species of deep to moderate migrators (Myctophidae: *P. normani*), which showed the lowest mean THg concentrations (0.10 μg g^{-1} DW; 0.02 μg g^{-1} WW) and low variability relative to other groups.

3.1.3. Influence of trophic ecology on THg concentrations

There were clear relationships observed between species-specific mean $\delta^{15}N$ and $\delta^{13}C$ values and log transformed THg concentrations (Fig. 3). There was a strong, significant positive correlation (Pearson's: $R = 0.703$, $p < 0.05$) between mean $\delta^{15}N$ values and THg concentrations (Fig. 3a). Those exhibiting elevated mean $\delta^{15}N$ values, indicative of higher trophic species, tended to have correspondingly higher mean THg concentrations. For instance, *M. ventralis*, had the lowest mean $\delta^{15}N$ value and THg concentrations. In contrast, species with higher $\delta^{15}N$ value including *D. hudsoni* and L. *procerus* had relatively higher THg concentrations. Two outliner species were *E. risso* and *H. hanseni* which both had higher mean $\delta^{15}N$ values relative to their lower THg concentrations. Stable isotope $\delta^{13}C$ values, indicative of the consumers foraging habitat, also yielded a positive Pearson's correlation coefficient with log-transferred THg although not significant ($R = 0.510$, $p = 0.090$, Fig. 3b). Similar to species patterns in $\delta^{15}N$ values, low THg concentrations in *M. ventralis* corresponded with the most negative $\delta^{13}C$ values, though other species patterns were not so clear, particularly in the west Tasman Sea with *E. risso* and *H. hanseni* again being obvious outliers along with *D. hudsoni, L. procerus* and *B. supralateralis*.

3.2. Intra-specific drivers of THg variability: Sex, size and site

Among the six species that had adequate samples sizes to test the effect of sex, a significant difference in the interaction between sexes and species was found (two-way ANOVA, F = 13.49, *p*-value <2e-16). For most examined species, females exhibited higher THg concentrations than males. For example, *D. hudsoni* females displayed a slightly elevated THg concentration of 0.25 ± 0.12 μg g^{-1} DW (0.07 ± 0.03 μg g^{-1} WW), in comparison to males with 0.19 ± 0.09 μg g^{-1} DW (0.04 ± 0.02 μg g^{-1} WW). A similar trend was observed in *E. risso*, *L. australis* and *L. procerus*, where females exhibited a THg concentration of 0.13 ± 0.04 μg g^{-1} DW (0.03 ± 0.01 μg g^{-1} WW), 0.21 ± 0.1 μg g^{-1} DW (0.05 ± 0.02 μg g^{-1} WW) and 0.24 ± 0.08 μg g^{-1} DW (0.06 ± 0.02 μg g^{-1} WW), THg compared to males with 0.09 ± 0.03 μg g^{-1}DW (0.02 ± 0.01 μg g^{-1} WW), 0.17 ± 0.09 μg g^{-1} DW (0.04 ± 0.02 μg g^{-1} WW) and 0.13 ± 0.07 μg g^{-1} DW (0.03 ± 0.02 μg g^{-1} WW) respectively. A contrasting trend was observed in *P. kopua* with females displaying a THg concentration of 0.22 ± 0.07 μg g^{-1} DW (0.05 ± 0.02 μg g^{-1} WW), while their male counterparts had a higher concentration of 0.27 ± 0.1 μg g^{-1} DW (0.06 ± 0.02 μg g^{-1} WW). In *M. ventralis*, there was no significant difference between females and males.

Size-related patterns in THg concentrations were assessed for 11 species that had adequate sample size ($n > 5$) across the expected size ranges. Pearson's correlation coefficient (r) values ranged from 0.009 to 0.76 with only six species found to have significant positive correlations between THg concentration and size ($r > 0.6$, $p < 0.05$, Fig. 4). There were no significant SL-THg correlations ($p > 0.05$) observed for *B. supralateralis*, *E. risso*, *M. ventralis*, *N. achirus*, and *P. kopua*.

At the community level, there was a significant positive correlation between SL and THg concentrations ($r = 0.4$, $p < 0.05$) (Fig. S1). Among smaller-sized species, such as *D. ostenfeldi* (mean size 33.54 mm) and *C. caeruleus* (mean size 38.97 mm), THg concentrations in DW were relatively low, measuring below 0.1 μg g^{-1}, and in WW below 0.05 μg g^{-1}. Conversely, *L. dofleni* (mean size 38.1 mm) exhibited higher THg concentrations, with a mean of 0.24 μg g^{-1} DW and 0.08 μg g^{-1} WW. However, among the larger-sized species (mean standard length > 100 mm) including *S. multipunctatus*, *C. sloani* and *P. kopua*, THg concentrations were notably elevated (>0.1 μg g^{-1} DW).

There were no significant differences in mean THg concentrations between the community of mesopelagic fish sampled from west and east of Tasman Sea (*t*-test, $t = 0.263$, $p = 0.793$). A two-way ANOVA showed that there was a significant interaction between species and site with distinct spatial differences in five of nine species examined (with n > 5) for both east and west sites (Fig. 5). Comparably lower mean THg concentrations were evident in specimens sampled in the west than east Tasman Sea for *D. hudsoni*, *L. procerus*, *L. dofleini*, *M. ventralis*, and *N. achirus*. These spatial differences were significant however, only for both *D. hudsoni* and *M. ventralis* ($p = 0.005$ and 0.028 respectively). Another three species (*E. risso*, *C. sloani* and *P. kopua*) showed relatively higher mean THg concentrations in the west compared to the east, although these differences were non-significant. Size – THg correlations were separately tested for *M. ventralis* and *P. kopua* in the west and east sites with Pearson r values ranging from 0.40 to 0.67. A significant positive correlation between SL and THg concentrations was only observed in the western Tasman Sea for *P. kopua*.

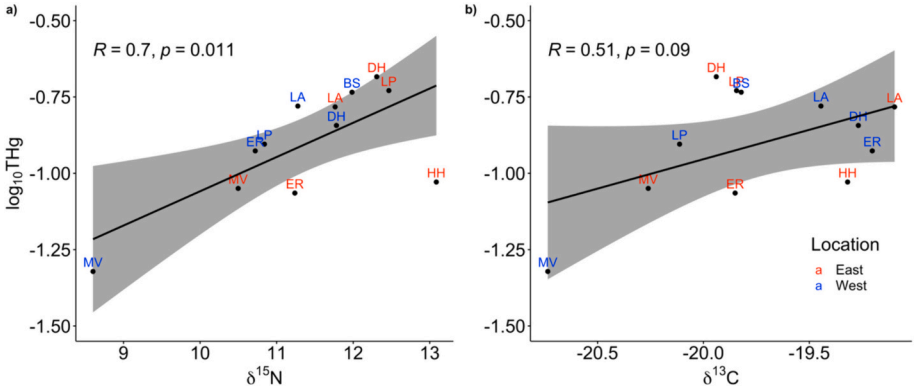

Fig. 3. Regression relationships between mean total mercury concentration (log_{10}THg, μg g^{-1} DW) and a) mean $\delta^{15}N$ values in ‰ as an estimate of trophic position, and b) mean $\delta^{13}C$ values in ‰ indicative of foraging habitat for 12 species of mesopelagic fish analyzed in this study. Mean isotope data taken from Flynn and Kloser (2012). BS: *Bolinichthys supralateralis*; DH: *Diaphus hudsoni*; ER: *Electrona risso*; HH: *Hygophum hanseni*; LA: *Lampanyctus australis*; LP: *Lampichthys procerus*; MV: *Metelectrona ventralis*.

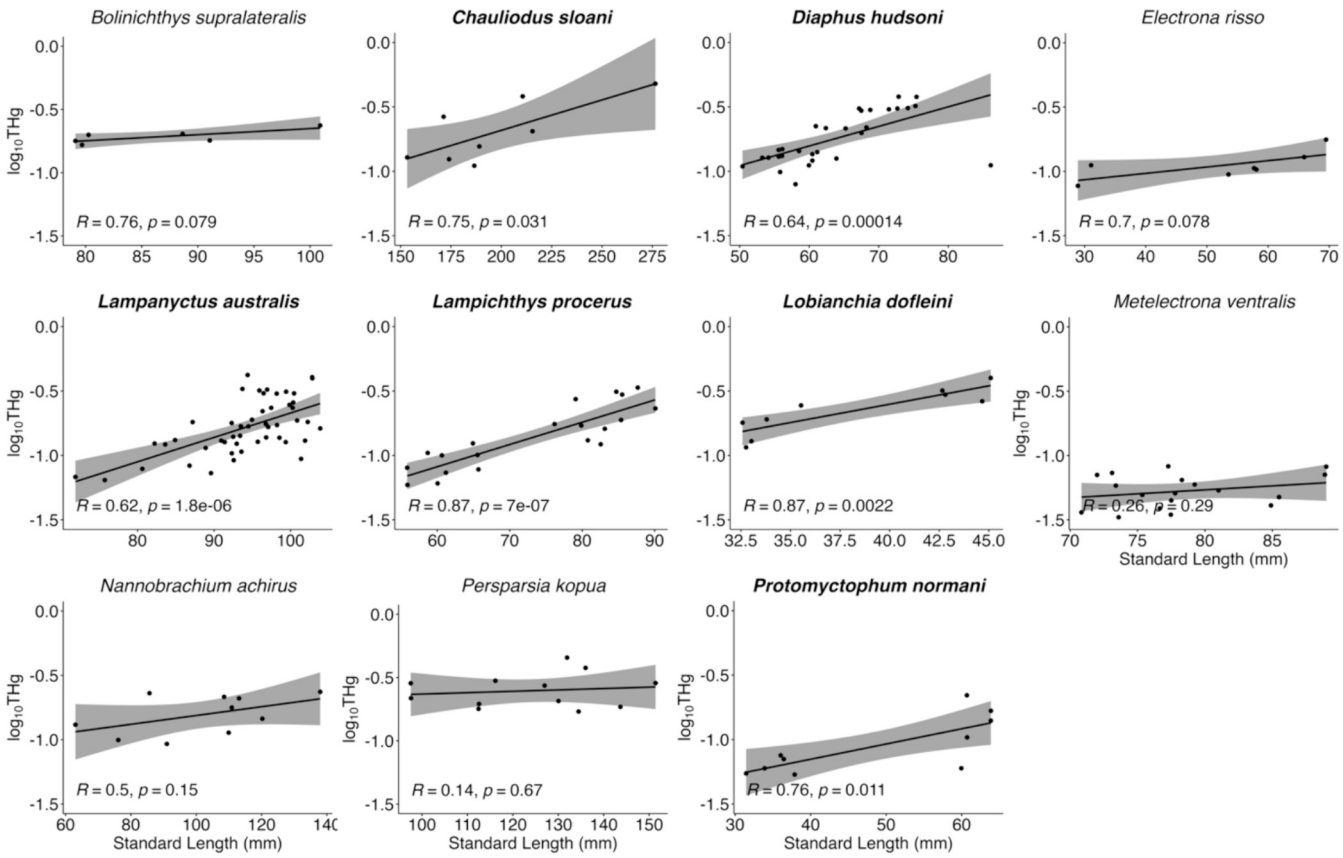

Fig. 4. Relationship between standard length (mm) and logarithmic mercury ($log_{10}Hg$) concentration in 11 species of mesopelagic fish. The Pearson correlation coefficient (R) with significance was determined by values of $p < 0.05$. Species that showed significant correlation are highlighted in bold.

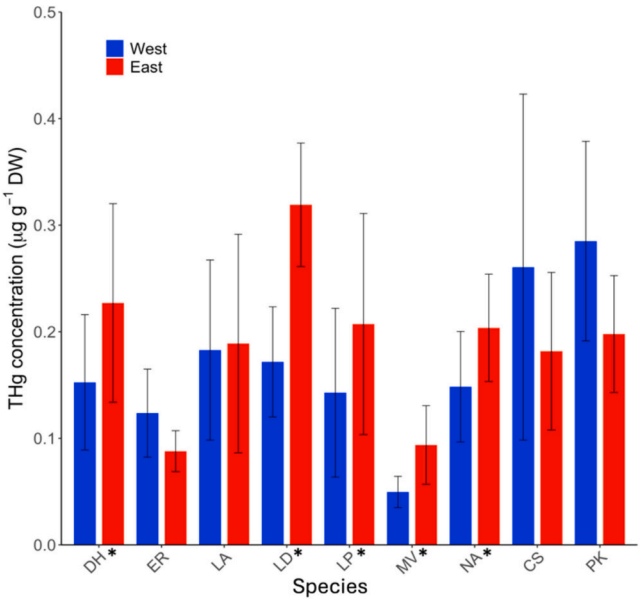

Fig. 5. Total mercury (THg) concentrations (expressed as mean values ± standard deviation; μg g^{-1} dry weight, DW) in whole mesopelagic fish collected from the east and west Tasman Sea, southwestern Pacific Ocean (DH: *Diaphus hudsoni*; ER: *Electrona risso*; LA: *Lampanyctus australis*; LD: *Lobianchia dofleini*; LP: *Lampichthys procerus*; MV: *Metelectrona ventralis*; NA: *Nannobrachium achirus*; CS: *Chauliodus sloani*; PK: *Persparsia kopua*).* species had significantly different spatial differences.

3.3. Broader scale comparisons

Literature revealed that THg concentrations vary greatly across 85 different species of mesopelagic fish, encompassing 30 families (Table S1). Of the 15 papers assessed, eleven report THg concentrations for 49 species in DW which were found to vary between 0.02 and 11.74 μg g^{-1}. Studies reporting in wet weight concentrations in 41 species showed variations ranging 0.02 to 0.46 μg g^{-1}. The lowest concentrations were often found in species from the family Myctophidae (which included 38 species). Only two species, both sampled in the Azores, northeast Atlantic Ocean, were reported to have concentrations >5 μg g^{-1} DW, with the highest concentrations reported in large Gadiformes (*Mora moro*; Magalhaes et al., 2007). Another eight species, mostly sampled from the northeast Atlantic Ocean, were found to have concentrations between 1 and 5 μg g^{-1} DW, including the myctophid *Notoscopelus kroeyeri*. Mesopelagic fish sampled in the Atlantic Ocean reported the largest range and highest values of THg concentrations across 27 species, with values ranging from 0.05 to 11.74 μg g^{-1} DW. Higher concentrations were more evident in the northeastern than northwestern Atlantic Ocean. The 14 species reported in the Indian Ocean showed a range of 0.16 to 1.51 μg g^{-1} DW with lower concentrations evident in the southwest than southeastern sections. The nine mesopelagic fish species studied in the Southern Ocean, had concentrations ranging from 0.02 to 0.47 μg g^{-1} DW. The region with the some of the lowest concentration range was in the north and south Pacific Ocean, with concentrations for 40 difference species ranging from 0.02 to 0.22 μg g^{-1} DW and 0.02 to 0.46 μg g^{-1} WW.

4. Discussion

This study represents the first to investigate THg concentrations in a

mesopelagic fish community within the oceanic ecosystem of the central Tasman Sea. Four species within this community have not been previously assessed for Hg concentrations. All the species examined here are known to be highly abundant in the Tasman Sea (Sutton et al., 2018) and are important prey to higher order predators, including tunas (Young et al., 2010), demersal fish (Bulman et al., 2002), sharks (Pethybridge et al., 2010a), seabirds (Raymond et al., 2010), and marine mammals (Goldsworthy et al., 2003; Hume et al., 2004). The study explored potential drivers of intra and inter-specific variability in THg concentrations. As expected, variability could be explained by taxonomy, individual length, and species-specific trophic ecologies including trophic position and foraging habitat. Smaller individuals and species occupying lower trophic positions generally exhibited lower Hg concentrations compared to larger species with higher trophic positions. For some species we also detected sex and spatial differences though these weren't always consistent or straightforward.

4.1. THg in Tasman Sea mesopelagic fish species

The range of mean THg concentrations observed in our study (0.02–0.48 μg g^{-1} DW; 0.01–0.15 μg g^{-1} WW) fall within the lower boundaries of those reported around the world for mesopelagic fish species (0.005 to 11.74 μg g^{-1} DW; 0.005–0.46 μg g^{-1} WW; Table S1). Our range of THg concentrations are most similar to those reported for the mesopelagic fish from other sites in the Pacific Ocean, including the western Tasman Sea (0.01–0.46 μg g^{-1} WW, Pethybridge et al., 2010b), the northern Pacific Ocean (0.02–0.22 μg g^{-1} DW, Blum et al. ., 2013), and in the central and north-western Atlantic Ocean (0.1–0.45 μg g^{-1} DW, Windom et al., 1973; Gibbs Jr. et al., 1974; Martins et al., 2006), and the Southern Ocean (0.02–0.47 μg g^{-1} DW, Seco et al., 2021a, 2021b).

Our study confirms that species from the Myctophidae family, typically display lower THg concentrations (typically <0.5 μg g^{-1} DW) compared to other mesopelagic fish species, such as those from the families Anguilliformes and Scombriformes. Within the family Myctophidae, of which included 13 of the total 16 species examined, there was a high degree of interspecific variability which has been observed in other community studies (e.g. Bustamante et al., 2003; Chouvelon et al., 2022; Seco et al., 2021a, 2021b; also see: Table S1). The variations can be attributed to the range of species examined, their lengths, trophic position and perhaps also to the horizontal and vertical spatial spread of sampling. These differences in Hg concentrations have potential implications for the health of top predators and ecosystems. The two highly abundant species in the Tasman Sea from the Myctophidae family including *D. hudsoni* and L. *procerus* (Sutton et al., 2018), both have low THg concentrations (mean of 0.2 and 0.16 μg g^{-1} DW respectively).

Within our study area, significant spatial differences were only observed for two Myctophidae fish species *D. hudsoni* and *M. ventralis* with higher THg concentrations found in the western than eastern sites of the central Tasman Sea. This pattern, although not significant, was also found in three other Myctophidae fish species. Further comparison with a THg study of mesopelagic fishes sampled from seamounts in the western Tasman Sea (Pethybridge et al., 2010b) also suggests that THg concentrations are higher in the western than eastern areas of the Tasman Sea. Interestingly, the western areas of the Tasman Sea are less oligotrophic than the eastern areas and have been shown to be higher in nutrients with regular seasonal upwelling events (Chiswell et al., 2015). Previous research has shown a correlation between elevated THg concentrations and regions with increased nutrients and upwelling, driven by augmented primary productivity and subsequent biomagnification in marine consumers (Conaway et al., 2009).

4.2. The influence of depth and migration pattern on THg concentrations

Vertical depth distribution and migration patterns of oceanic fish species has been shown to influence the Hg accumulation (Desta et al., 2008; Le Bourg et al., 2019). Prior research has reported a correlation between vertical habitat stratification and Hg concentrations, with slighter higher concentrations observed in bathypelagic species compared with mesopelagic species. Choy et al. (2009) found that THg concentration in predatory pelagic fish increased with water depth in the northeastern region of the Pacific Ocean. Monteiro et al. (1996) also found a significant pattern of increasing THg concentration with depth in small epi- and mesopelagic fish in the North Atlantic. These previously reported depth-related pattern appears to be associated with elevated water THg concentrations below the thermocline and at depths below 200 m (Cossa et al., 2009; Mason and Fitzgerald, 1990). Surprisingly, this study found a different pattern showing that fish species with shallower migration patterns tend to have higher THg concentrations compared to those that migrated deeper (Fig. 2). This finding is likely attributed to species composition and size range. Migration pattern group 1 (Table 1) consisted of the largest (*P. kopua*) and smallest (*C. caeruleus*) sized non-myctophid fish species. However, regional seawater Hg concentrations might explain this depth pattern as it has been reported that higher THg concentrations were found at mid-depth (0-500 m) rather than in deep water (1000 m) Cossa et al. (2011). In this present study, species residing at shallower depths may indeed be subject to lower Hg exposure compared to those found at greater depths in the central Tasman Sea. These findings shed light on the complex interplay of migration patterns and Hg accumulation in mesopelagic fish, underscoring the need for further research in this area.

4.3. The influence of size and trophic position on THg concentrations

It is widely recognized that THg concentrations in marine fish typically increase with size, both at the species level and on an ecosystem scale (Bastos et al., 2016; Dang and Wang, 2012; Gewurtz et al., 2011; Seco et al., 2021a; Seco et al., 2020b). This trend has been reported in species of mesopelagic fish (Acosta-Lizarraga et al., 2020; Choy et al., 2009; Le Bourg et al., 2019). Our results followed a similar trend with many of the mesopelagic species showing a strong positive correlation between THg concentrations and body size (Fig. 4). This observed correlation underscores the significance of size in evaluating the bioaccumulation and potential health implications associated with mercury exposure in these organisms. However, there was an absence of a size-THg relationship in five species (*D. ostenfeldi*, *H. hanseni*, *S. barnardi*, *S. multipunctatus* and *C. caeruleus*) that may be related to the restricted size range analyzed or the small sample sizes for some species.

Several ecological studies have shown a strong link between trophic position of fish and THg concentrations, particularly in the marine environment (Blum et al.2013; Bustamante et al., 2003; Chouvelon et al., 2012; Gibbs Jr. et al., 1974; Lahaye et al., 2006; Martins et al., 2006; Monteiro et al., 1996; Pethybridge et al., 2010b; Seco et al., 2021a; Seco et al., 2020b). This study found a positive correlation between THg concentration and trophic position, as indicated by stable nitrogen values, which was also found in other mesopelagic fish studies (Anderson et al., 2009; Seco et al., 2020a; Seco et al., 2020b). The food source and foraging habitat, inferred by $\delta^{13}C$ values, is not significant ($p = 0.09$) for THg accumulation in our study. Studies found that THg ingestion from prey with shorter life cycles, such as copepods, amphipods, and euphausiid larvae, may show varying degrees of THg accumulation in mesopelagic fish at broad spatial and temporal scales (Hopkins and Baird, 1981; Pethybridge et al., 2010b; Seco et al., 2021a). In this study, mesopelagic fish species shown similar $\delta^{13}C$ values suggesting slight differences in foraging behaviors such as feeding depth. A study from Seco et al. (2020b) also found minor fluctuations in $\delta^{13}C$ values and that they do not have a significant impact on THg concentrations within the mesopelagic fish community.

5. Conclusions

This study advances our understanding of THg concentrations in the

mesopelagic fish community of the central Tasman Sea and provides new insights into the mercury dynamics of oceanic ecosystem around the world. Our findings highlight the substantial variability in THg concentrations across different species, influenced by factors such as taxonomy, individual size, trophic position, and foraging habitat. Notably, species from the Myctophidae family generally exhibited lower THg concentrations compared to other mesopelagic fish, with considerable interspecific variability. The study further corroborates the positive correlation between fish size and THg concentration, underscoring the importance of considering body size in mercury exposure assessments. Additionally, a strong link between trophic position and THg levels was established, aligning with prior ecological research. Spatial differences were evident, with higher THg concentrations in the eastern Tasman Sea, potentially linked to regional nutrient levels and upwelling events. Interestingly, contrary to some previous studies, we observed that fish with shallower migration patterns had higher THg concentrations than those migrating to greater depths. Overall, these findings enhance our comprehension of mercury bioaccumulation in mesopelagic fish and its implications for the broader marine ecosystems. Ongoing monitoring efforts are necessary to track and understand Hg dynamics, including major transport pathways to higher predators. This includes a need to investigate the proportion of THg that is MeHg and measure selenium concentrations as it has been shown to reduce the toxicity of MeHg. By gaining a deeper understanding of Hg dynamics, we can work towards developing strategies for mitigating mercury pollution in marine ecosystems.

CRediT authorship contribution statement

Bowen Zhang: Writing – original draft, Validation, Methodology, Investigation, Data curation, Conceptualization. **Heidi Pethybridge:** Writing – review & editing, Validation, Supervision, Investigation. **Caroline Sutton:** Writing – review & editing, Validation, Investigation. **Patti Virtue:** Writing – review & editing, Validation, Supervision. **Yunkai Li:** Writing – review & editing, Methodology, Data curation.

Declaration of competing interest

The authors declare that there are no disclosed financial interests or personal relationships that could have potentially influenced the impartiality and objectivity of the findings reported in this manuscript.

Data availability

Data will be made available on request.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.marpolbul.2024.116676.

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