



Mercury trophic transfer and biomagnification in food webs within a tropical embayment as evidenced by nitrogen and carbon stable isotope analysis

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ABSTRACT

Mercury (Hg) contamination in marine ecosystems poses a significant environmental threat due to its high toxicity, persistence in the environment, and tendency to bioaccumulate in organisms and biomagnify in food webs. Understanding how Hg moves through these food webs is essential for assessing its ecological and health impacts. To investigate the trophic dynamics of Hg in Rayong Bay, Gulf of Thailand, we collected marine organisms from the pelagic and benthic food webs during 2022–2023 and analyzed the total mercury content (THg) in plankton (phytoplankton, zooplankton, and fish larvae) and in 81 marine animal species. Furthermore, the stable nitrogen and carbon isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) were measured to establish their trophic levels (TLs) and potential food sources in the food web. Based on these analyses, we calculated the biomagnification factor using TL-adjusted ratios (BMF_{norm}) and trophic magnification factor (TMF) for the different TLs. BMF_{norm} values exceeded 1.0 in over 40 % of cases for both the pelagic and benthic food webs, indicating THg biomagnification from prey to predator. Notably, the pelagic food web exhibited a markedly higher TMF value ($\text{TMF} = 6.68$) compared to that of the benthic food web ($\text{TMF} = 2.06$), suggesting stronger Hg biomagnification within the pelagic food web. Our findings also highlight the consumption risk of Hg in some fish species in the Rayong Bay food webs, emphasizing the need for continued monitoring and mitigation strategies to safeguard both human and ecological health.

1. Introduction

In recent years, aquatic environments have been affected by climate change, overfishing, aquaculture, eutrophication, and pollution, leading to substantial food web changes (du Pontavice et al., 2020; Yan et al., 2019). In particular, mercury (Hg) pollution poses a major environmental threat due to its toxicity, persistence, and accumulation in aquatic organisms (Qu et al., 2022). It is also a global concern, reaching even the most remote oceanic regions (Eagles-Smith et al., 2018), which

has led to growing awareness of Hg bioaccumulation in aquatic systems (Dang and Wang, 2010).

Several studies (e.g., Córdoba-Tovar et al., 2022; Hilgendag et al., 2022; Lavoie et al., 2013) have shown an increasing trend of Hg along the food webs. This trend is primarily driven by the biomagnification of methylmercury (MeHg), which accounts for over 90 % of total mercury (THg) in most marine fish tissues (e.g., Bloom, 1992; Kehrig et al., 2009; Windom and Cranmer, 1998). However, exceptions to this paradigm exist, such as in microplankton (Seixas et al., 2014), bivalves (Briant

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et al., 2017), and benthic macroinvertebrates (Bradford et al., 2023). These deviations are due to metabolism, absorption, and excretion pertaining to specific animal species (Bradley et al., 2017). As a bioavailable form of Hg, MeHg is much more extensively and rapidly absorbed than inorganic mercuric ion (Hg(II)) in the gastrointestinal tract (Clarkson and Magos, 2006). MeHg can easily be absorbed into the body and accumulates over time in soft tissues, making it the dominant form of Hg in marine food webs. MeHg poses risks to the nervous system, genetic material, reproductive systems, and various physiological processes in both marine organisms and humans, and can even cause death (Ackerman et al., 2016; Byczkowski, 2005; de Almeida Rodrigues et al., 2019; Scheuhammer et al., 2007, 2015). In a comprehensive review of 20 studies on human dietary exposure to seafood, Bradley et al. (2017) estimated that the bioaccessibility of MeHg is higher than that of Hg(II). As a result, MeHg is considered the most toxic form of Hg (Manceau et al., 2021).

Hg bioavailability, bioaccumulation, and biomagnification are influenced by various factors, including the chemical form of Hg, environmental and physical conditions, ecological factors (e.g., food web structure and size, population density), and biological factors (e.g., trophic level, food structure, and body size) (Dang and Wang, 2012; Gentès et al., 2021; Hosseini et al., 2013, 2014). Over 90 % of Hg ingested by most fish comes from their diet, which mostly consists of Hg in its organic forms (Murillo-Cisneros et al., 2019). Therefore, structural variations in food webs can affect the pathways of bioavailable Hg in aquatic systems. Understanding trophic ecology and food web dynamics allows for the approximation of the Hg found in members of varying trophic levels (TLs) and enables direct estimation of biomagnification (Cai et al., 2007; Ferriss and Essington, 2014; Murillo-Cisneros et al., 2019).

To elucidate Hg biomagnification, it is necessary to determine the TLs of the organisms, which are commonly estimated using bulk stable isotope analysis. This approach can reveal food sources, foraging environments, and the effectiveness of pollutant transport throughout food webs (Hobson et al., 2002; Hobson and Welch, 1992; Jardine et al., 2006). Since nitrogen isotopes ($\delta^{15}\text{N}$) increase predictably with each trophic step, typically enriched by 3 ‰ – 4 ‰ relative to the diet, they are frequently used to assess the trophic position (Deniro and Epstein, 1981; Minagawa and Wada, 1984; Peterson and Fry, 1987). As such, $\delta^{15}\text{N}$ can be used to calculate biomagnification metrics, linking trophic position to Hg concentrations. In contrast, carbon isotopes ($\delta^{13}\text{C}$) hardly change as carbon moves through food webs (DeNiro and Epstein, 1978; France and Peters, 1997; Rounick and Winterbourn, 1986). Therefore, $\delta^{13}\text{C}$ is typically used to evaluate the diet sources for an organism when the isotopic signatures of these sources are sufficiently different (Post, 2002).

Over the past few decades, rapid economic development and population growth in Southeast and South Asia (Oanh and Huy, 2024; Tsui et al., 2025) have increased human activities, contributing to elevated environmental contamination by heavy metals in these regions (Safur Rahman et al., 2019), including Hg in the Gulf of Thailand (GOT) (Ubonyaem et al., 2023). Hg in the GOT originates from various anthropogenic activities (Ritonga et al., 2022), including coastal erosion, deforestation, untreated domestic waste (Cheevaporn and Menasveta, 2003; Worakhunpiset, 2018), gold mining activities in different areas along Mekong River (Udomchoke et al., 2010), irrigation runoff from agricultural practices utilizing Hg-bearing pesticides, notably along the lower Mekong River Basin (Guédron et al., 2014), coal-fired power plants (Mahavong et al., 2017; Pham et al., 2015; Thepanondh and Tunlathorntham, 2020), untreated wastewater from industrial estates and petrochemical complexes (Cheevaporn and Menasveta, 2003), oil and gas exploration in the GOT (Le et al., 2023; Pojtanabuntoeng et al., 2011; Sompongchaiyakul et al., 2018; Yod-In-Lom & Doyle, 2002).

Several studies have assessed the levels of Hg in marine organisms in Rayong Bay (e.g., Agusa et al., 2007; Thongra-ar & Parkpian, 2002) and

in the GOT region (e.g., Prabakaran et al., 2024; Ritonga et al., 2022; Windom and Cranmer, 1998). However, research on Hg biomagnification in Thai water food webs using stable isotopic techniques is still lacking. Moreover, Hg biomagnification studies in tropical areas are significantly less documented than in temperate or polar regions (Lavoie et al., 2013). Thus, there is a pressing need for more research such as this current study to fill in the gaps in this subject.

In this study, marine organisms were collected from the pelagic and benthic food webs of Rayong Bay, Thailand. We analyzed THg along with $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values to elucidate food web structure and quantify THg biomagnification. This study aimed to: (1) investigate THg accumulation across various marine organisms and (2) assess THg biomagnification in the marine food web by calculating trophic magnification slopes (TMSs) and trophic magnification factors (TMFs) for the study area. By addressing this knowledge gap, we hope to contribute to the global understanding of THg bioaccumulation and to inform strategies for mitigating its detrimental effects on marine ecosystems and human health.

2. Materials and methods

2.1. Sampling location

Rayong is situated in Thailand's Eastern Economic Corridor (EEC) and contains numerous industrial estates. Notably, Map Ta Phut is the largest industrial zone, encompassing five industrial estates, one deep-sea port, and 151 major factories (Burnett et al., 2019). Industrial activities in this area have sparked significant environmental concerns, including air and water pollution, industrial accidents, and potentially illegal hazardous waste releases (Saengsupavanich et al., 2009; Sillapapiromsuk et al., 2022; Soyotong and Perera, 2017).

Rayong Bay, situated south of Rayong, serves multiple purposes, including fisheries, tourism, and natural conservation, and is also the coastal area near urban centers, fertile agricultural land, and export-oriented manufacturing and industry (Janmaimool, 2016; Kawichai et al., 2024; Kumar et al., 2023). Despite this, Rayong Bay remains a vital center for fisheries (both wild-capture fisheries and aquaculture) and tourism. Our sampling area was located on the eastern side of the deep-sea port (Fig. 1).

2.2. Sample collection and preparation

Plankton (phytoplankton, zooplankton, and fish larvae) were sampled from 18 stations during three campaigns: May 2022, August 2022, and February 2023. Fish and shellfish were collected from three trawling stations during four sampling campaigns: March 2022, May 2022, August 2022, and February 2023. Additionally, fish and shellfish were taken from the fishing gears of four nearby small-scale fishing communities, namely Kao Yod (KY), Laem Rung Rueang (LRR), Khlong Kacher (KKC), and Suan Son Beach (SS), during February 2022, July 2022, September 2022, November 2022, January 2023, and March 2023 (Fig. 1).

2.2.1. Plankton

Plankton samples were collected using pumping or trawling methods, depending on the target size. Phytoplankton were sampled from surface waters (1-m depth) using a submersible pump (DEXZON®, HP-550S) equipped with an 8-cm diameter tube and a nominal pumping rate of 60 L/min (e.g., Chauvelon et al., 2019). The pump was connected to a combined filtration system consisting of a 100- μm mesh net (T. Science®) to screen out any plankton larger than 100 μm (including most zooplankton). In turn, the targeted phytoplankton samples ($n = 13$) were collected in a 20- μm mesh plankton net (T. Science®). Microscopy examination identified the dominant species during sampling as *Chaetoceros* spp., *Bacteriastrium* spp., and *Rhizosolenia* spp.

To account for the patchy distribution and vertical movement of

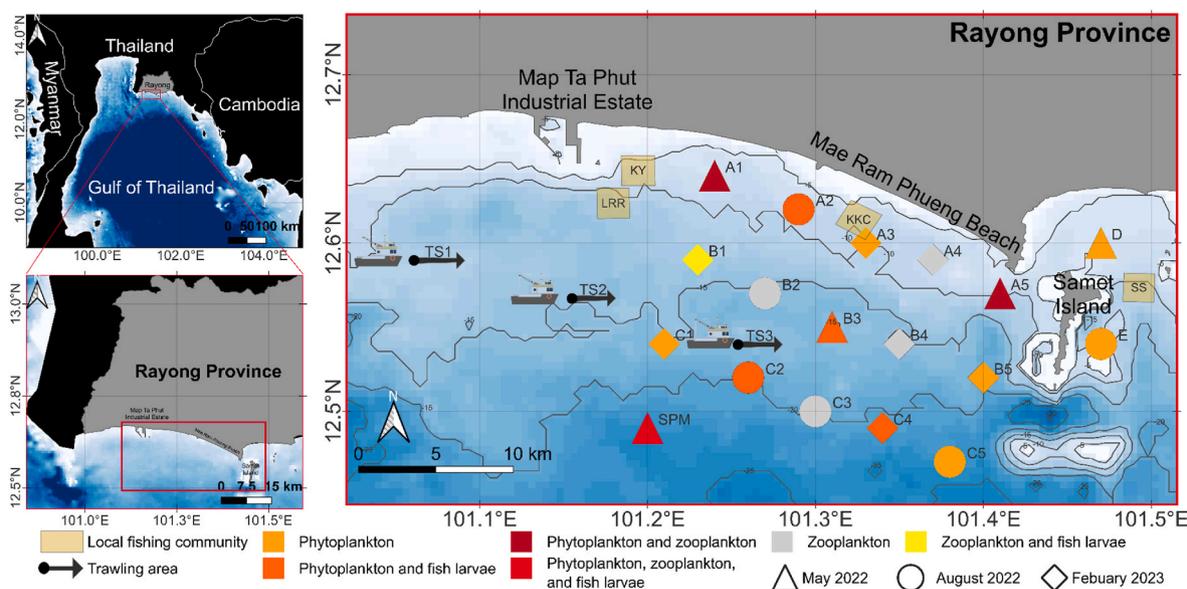


Fig. 1. Location of the Gulf of Thailand and Rayong Province (left) and Rayong Bay sampling stations (right). Bathymetric data were obtained from the General Bathymetric Chart of the Oceans (GEBCO) 2023 dataset, with depth contour intervals displayed at 5-m increments.

zooplankton, we conducted integrated vertical hauls from near-bottom depth to the surface using a 100- μm plankton net (T. Science®), following the method described by De Bernardi (1984). This approach specifically targeted zooplankton ($n = 8$). The dominant groups identified were copepod nauplii, calanoid copepods, and cyclopoid copepods.

Fish larvae or larger plankton ($n = 6$) were collected through 15-min surficial horizontal hauls using a 300- μm mesh plankton net (T. Science®) at a speed of 2.3-2.5 knots (e.g., Tesán-Onrubia et al., 2023). Apart from fish larvae, this so-called ichthyoplankton fraction contained harpacticoid copepods, *Lucifer* sp., and siphonophores.

All plankton samples were collected using bottles pre-cleaned with 10 % HNO_3 (v/v). To prevent contamination, powder-free latex gloves were worn during sampling. The collected samples were stored in ultraclean, acid-washed containers and promptly transported to the laboratory for processing. They were frozen, freeze-dried, and stored in a desiccator until chemical analyses, all of which were performed in triplicate.

2.2.2. Fish and shellfish

Fish and shellfish were collected using an otter trawl with double cod ends (4.0 and 2.5 cm mesh sizes) arranged in a stacked configuration to sort the catch by size. The otter trawl was towed parallel to the shoreline at a speed of 2.3-2.5 knots for 1 h (e.g., Phaksopa et al., 2021). Additionally, we collected samples from various small-scale fishing gears varied by target species, seasons, and community preferences. These gears included crab sinking nets and shrimp floating nets.

A total of 315 specimens were sampled for chemical analysis (Table S1), including two species of bivalves ($n = 23$), two species of gastropods ($n = 6$), three species of crabs ($n = 5$), two species of shrimps ($n = 4$), six species of squids ($n = 34$), 24 species of pelagic fishes ($n = 46$), and 41 species of demersal fishes ($n = 197$). All fish and shellfish samples were placed in clean zip-lock bags and frozen. In the laboratory, they were thawed, measured, weighed, and dissected under contamination-free conditions. The edible muscle tissue was then cut into smaller pieces and homogenized. These samples were divided into two portions: one frozen at -20°C for Hg analysis and another freeze-dried and stored in a desiccator for stable isotope analysis.

Samples were classified into pelagic and benthic food webs based on ecological characteristics and taxonomic identification using the FAO Species Identification Guides (Carpenter and Niem, 1998a, 1998b, 1999a, 1999b, 2001a, 2001b) while isotopic data were solely used to

establish the trophic relationships within the pre-determined food webs.

2.3. Analytical methods

2.3.1. Hg contents in marine organisms

THg content in marine organisms was analyzed via thermal decomposition, amalgamation, and cold-vapor atomic absorption spectrophotometry (DTD-AAS) following US-EPA method 7473 (US EPA, 2007). Briefly, dry plankton and wet marine animal samples (weighed by Sartorius® AX-224 balance) were introduced into a NIC® MA-3000 Mercury Analyzer. The samples were first heated to 150°C to remove moisture, and then to 850°C to convert all Hg to volatilized Hg^0 . Oxygen gas (>99 %) at a flow rate of 0.2 L/min carried the Hg^0 to a gold-coated sand amalgamator, while other gases were directed to a waste filter. The amalgamator was then heated to 200°C , releasing Hg^0 , which was transported to the measurement cell where its vapor attenuated monochromatic light at 253.7 nm, following the Beer-Lambert Law.

Performance metrics, such as the limit of detection (LOD), the limit of quantification (LOQ), recovery, and precision, were used to validate the analytical procedures. The LOD and LOQ, computed by multiplying the standard deviation by 3 and 10, were 0.0016 $\mu\text{g}/\text{kg}$ and 0.0050 $\mu\text{g}/\text{kg}$ respectively. Dry and homogenized certified reference material, DORM-4 (marine fish protein), from the National Research Council of Canada was used for quality assurance/quality control (QA/QC) standard for each batch. The recovery for DORM-4 was $99.81 \pm 4.37\%$ based on 25 repeated measurements.

All THg values were reported on a $\mu\text{g}/\text{kg}$ wet-weight basis. Wet-weight basis THg concentrations for dry samples (e.g., plankton) were calculated by assuming 95 % water content for microseston (0.2-200 μm size class), as suggested by Hammerschmidt et al. (2013) and 90 % in zooplankton larger than 200 μm based on Knauer and Martin (1972).

2.3.2. Carbon and nitrogen stable isotopes

Stable isotope analysis was conducted at the Asian School of the Environment/Earth Observatory of Singapore, Nanyang Technological University and Thailand Institute of Nuclear Technology, using a Thermo Scientific® Flash Elemental Analyzer (EA) coupled with a Delta V Advantage Isotope Ratio Mass Spectrometer (IRMS). Approximately 400 μg of freeze-dried and homogenized samples were weighed using a Mettler Toledo® XP6 microbalance and packed into pre-weighed Elemental Microanalysis® tin capsules (pressed 9×5 mm). The

capsules were introduced into the EA via the autosampler and combusted at 1000 °C in the presence of oxygen, producing carbon dioxide (CO₂) and nitrogen oxide (N₂) gases, which were carried by helium (He) gas into the IRMS for isotopic analysis. Results were reported in δ notation (Eq. (1)), relative to the international reference standards: V-Pee Dee Belemnite (VPDB) for carbon isotopes and atmospheric N₂ for nitrogen isotopes.

$$\delta (\text{‰}) = \left[\left(\frac{R_{\text{sample}}}{R_{\text{standard}}} \right) - 1 \right] \times 1000 \quad \text{Eq. 1}$$

where δ is the δ value for the isotope (in this case ¹⁵N or ¹³C), R_{sample} is the ratio of heavy to light isotopes in the sample, and R_{standard} is the ratio of heavy to light isotopes in the international standard.

In each run, two USGS reference standards (USGS-40 and USGS-41) were analyzed along with the samples to calibrate the raw data for the delta values of isotopes. Additionally, an in-house standard (L-glutamic acid) was included as a QA/QC measure to assess the quality of the analysis and to apply drift and size effect corrections. Based on the long-term analysis of this QA/QC standard, the analytical precision is 0.3 ‰ for ¹⁵N and 0.2 ‰ for ¹³C.

2.4. Data treatment

2.4.1. Biomagnification factors

Biomagnification factor (BMF) represents the ratio of the chemical concentration in the predator (numerator) to that of the prey (denominator) as shown in Eq. (2) (Conder et al., 2012; Gobas et al., 2009). However, BMFs are highly sensitive to errors in TL assignment, particularly when complex feeding groups, such as omnivores, are classified into binary categories (Sinclair et al., 2024). In this study, we applied a normalized BMF (BMF_{norm}) using TL-adjusted ratios (Eq. (3)), as done in numerous previous studies (e.g., Murillo-Cisneros et al., 2019; Pethybridge et al., 2012; Vainio et al., 2022). By using this TL-adjusted method, we can more accurately assess the true extent of BMF_{norm} by accounting for the expected increase in THg with increasing TLs (Franklin, 2016; Vainio et al., 2022). The BMF_{norm} was normalized by TL to standardize it to an exact TL difference of 1.0 between predator and prey. This adjustment is necessary when the actual TLs, as determined by ¹⁵N analysis, deviate from 1.0, either exceeding or falling short of this value (Franklin, 2016). If BMF_{norm} exceeds 1.0, THg is considered a potential bio-accumulator (Gobas et al., 2009).

$$BMF = \left[\frac{THg_{\text{predator}}}{THg_{\text{prey}}} \right] \quad \text{Eq. 2}$$

$$BMF_{\text{norm}} = \left[\frac{THg_{\text{predator}}}{THg_{\text{prey}}} \right] / \left[\frac{TL_{\text{predator}} - TL_{\text{prey}}}{1} \right] \quad \text{Eq. 3}$$

where THg_{predator} is predator's THg, THg_{prey} is prey's THg, TL_{predator} is predator's TLs from Eq. (4) (below), and TL_{prey} is prey's TLs from Eq. (4) (below).

2.4.2. Trophic magnification factor

Biomagnification of THg can lead to potentially toxic levels of Hg in aquatic animals (Burgess and Meyer, 2008). THg biomagnification was assessed using a linear relationship between TLs and logarithm-transformed THg (log₁₀[THg]) (Matias et al., 2022; Vainio et al., 2022). The trophic magnification slope (TMS) and trophic magnification factor (TMF) were calculated for the food webs using the following formulas:

$$TL = \left[\left(\delta^{15}N_{\text{consumer}} - \delta^{15}N_{\text{producer}} \right) / \Delta^{15}N \right] + \lambda \quad \text{Eq. 4}$$

$$\log_{10}[THg] = a + b TL \quad \text{Eq. 5}$$

$$TMF = 10^b \quad \text{Eq. 6}$$

where TL represents the trophic level for each consumer species,

$\delta^{15}N_{\text{consumer}}$ is the $\delta^{15}N$ value for each consumer species, and $\delta^{15}N_{\text{producer}}$ is the $\delta^{15}N$ value for the baseline organism. For the pelagic food web, phytoplankton was used as the baseline ($\lambda = 1$; primary producers), while filter-feeding Asian moon scallops (*Amusium pleuronectes*, $\delta^{15}N = 3.59 \text{‰}$) were treated as primary consumers ($\lambda = 2$) for the benthic food web. The trophic enrichment factor ($\Delta^{15}N$) of 3.4 ‰, commonly used in marine studies (e.g., Borgå et al., 2012; Deniro and Epstein, 1981; Minagawa and Wada, 1984) was used in this study. In Eq. (5), the parameter "a" represents the intercept indicating the baseline concentration in a specific ecosystem and "b" is the slope of the linear relationship between the log₁₀[THg] and TL values, also known as the TMS.

A positive slope for TMS (TMS>0) indicates the potential for biomagnification, where Hg concentration increases with each TLs (Gao et al., 2021; Monferrán et al., 2016; Saidon et al., 2024). Meanwhile, TMF for Hg represents the average increase in Hg concentration per TLs and is calculated for each food web as the antilog of the regression slope (Eq. (6)) (Borgå et al., 2012; Hilgendag et al., 2022; Lavoie et al., 2013). A TMF of 1 indicate that the chemical of interest does not biomagnify through the food web. When TMF>1, the biomagnification occurs, with an average factor of TMF per TLs. Conversely, a TMF<1 suggests that the decrease in chemical of interest with an average factor of TMF per each TLs in the food web (Valladolid-Garnica et al., 2023). TMF values are commonly compared across different ecosystems or chemicals of interest to understand variation in biomagnification (Borgå et al., 2012). The intercept, a in Eq. (5), at the baseline variability among ecosystems caused by different inputs of contaminants to the base of food webs, such as between different pelagic or benthic food webs. This allows the "rate of increase" per TL in the food web to be studied independently of the original exposure level.

2.5. Statistical analysis

Statistical analyses were conducted using Microsoft® Excel 2021 and IBM® SPSS®. The data's normality was tested to choose between parametric and non-parametric tests. Non-parametric results were compared using the Kruskal-Wallis test, whereas parametric results were compared using ANOVA to assess differences in THg among different marine organisms.

Generalized linear mixed models (GLMMs) are an extension of generalized linear models that allow for the inclusion of both fixed effects and random effects, and can handle non-normally distributed dependent variables (Dean and Nielsen, 2007). Fixed effects represent influences that are constant across all observations in a study. They are typically categorical variables, but can also be continuous. On the other hand, Random effects capture variability that is not explained by the fixed effects. They are often associated with grouping factors or individual differences. More details on GLMMs can be found in McCullagh and Nelder (2019).

In this study, GLMMs with a gamma distribution and a log link function were defined as follows: $g(\mu) = a + X_i B + Z_i b_i + a_i + e_i$ (Linder et al., 2017) where g is the link function relating the linear predictor to the expected value (μ) of the exponential family distribution function and $X_i B$ represents fixed-effects independent variables in the model. X_i is the design matrix for the predictor variables, and B is the matrix of predictor variables. $Z_i b_i$ represents the random effects component of a GLMM. In this specific case, the random effects component in the equation represents the different species. Z_i is the design matrix for the random effects, and b_i is the subject i . The term a_i is the random intercept and e_i is the error term.

Log₁₀[THg] data were applied when necessary to meet normality assumptions. The absolute values of normalized regression coefficients (β) were used to evaluate the relative importance of different variables.

revealed that $\delta^{13}\text{C}$ of phytoplankton communities fluctuates throughout the year, reflecting the dominant phytoplankton species during different seasons. Additionally, temperature (Fontugne and Duplessy, 1981; Sackett et al., 1965) and the $\delta^{13}\text{C}$ of the inorganic carbon source used for photosynthesis (Deuser, 1970; Parker, 1964; Smith and Kroopnick, 1981), which often change seasonally, have also been demonstrated to influence the $\delta^{13}\text{C}$ signature of phytoplankton (Goering et al., 1990).

In the ocean surface layer, the $\delta^{15}\text{N}$ of small organic particles is significantly influenced by how phytoplankton assimilate nitrogen from the seawater (Goering et al., 1990). This initial $\delta^{15}\text{N}$ signature is then passed on through the food web. In this study, the $\delta^{15}\text{N}$ value in phytoplankton (4.81 ± 1.25 ‰) is the lowest in the pelagic food web, followed by zooplankton (5.34 ± 1.24 ‰), fish larvae (6.10 ± 0.90 ‰), cephalopods (9.68 ± 0.86 ‰), and fishes (9.85 ± 1.54 ‰), respectively. This pattern indicates that $\delta^{15}\text{N}$ becomes progressively higher as it moves up the pelagic food web (Fig. 2a).

Organic matter in our pelagic food web is passed from plankton all the way up to the apex species such as barracuda (*Sphyræna putnamae*, SP and *Sphyræna obtusata*, SOC), whose $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values were enriched relative to cephalopods and other fishes (Fig. 2a). It is important to note that the bluetail mullet (*Crenimugil buchanani*, CB) is isotopically distinct from the rest of the food web in terms of carbon isotopes. CB is a species commonly found in estuaries and rivers (Roshith et al., 2022) and frequents these habitats, ascending rivers and coastal creeks as juveniles (Blaber and Whitfield, 1977). They feed primarily on detritus (Whitfield and Durand, 2023). As a result, they exhibit distinct $\delta^{13}\text{C}$ values (-12.2 ± 2.57 ‰).

Based on $\delta^{15}\text{N}$, the TLs in the pelagic food web ranged from 1.61 \pm 0.37 in phytoplankton to 4.07 in obtuse barracuda (*Sphyræna obtusata*, SOC). In principle, phytoplankton should have a TL of 1 as primary producer. However, in this study, phytoplankton were collected by filtering seawater through 20- μm nets, with a 100- μm screen used to exclude larger particles and plankton. Consequently, this fraction may contain various particles ranging from 20 μm to 100 μm in size, including phytoplankton, particulate organic matter (POM), and detritus. As a result, the sample may have included POM containing detritus and microheterotrophs (Kopprio et al., 2023; Minor and Nalathambay, 2004; Wang et al., 2024), which could influence the $\delta^{15}\text{N}$ value and potentially lead to an overestimation of the TL of this fraction (e.g., Kopprio et al., 2015). As expected, the obtuse barracuda (*Sphyræna* spp.) occupy high TLs, consistent with their classification as apex predators in marine ecosystems (D'Alessandro et al., 2011; O'Toole et al., 2010). This aligns with the established principle that top predators tend to have high $\delta^{15}\text{N}$ values (Moteki et al., 2001; Richert et al., 2015).

3.1.2. Benthic food web

In the benthic food web, the $\delta^{13}\text{C}$ values for all species ranged from -20.0 ‰ in the razorfish (*Aeolisus strigatus*, AS) to -13.9 ± 0.81 ‰ in the pink ear emperor (*Lethrinus lentjan*, LL). In addition, the $\delta^{15}\text{N}$ values in the benthic food web for all species ranged from 3.59 ± 1.23 ‰ in the Asian moon scallop (*Amusium pleuronectes*, APL) to 12.6 ‰ in the tigertooth croaker (*Otolithes ruber*, OR). As expected, finfish showed higher $\delta^{15}\text{N}$ values than invertebrates similar to other previous studies (e.g., Murillo-Cisneros et al., 2019).

The shifts in $\delta^{13}\text{C}$ (0 – 1 ‰) and $\delta^{15}\text{N}$ (3 – 4 ‰) per TL, following widely-accepted values in previous literature (Deniro and Epstein, 1981; Minagawa and Wada, 1984; Peterson and Fry, 1987) allow us to track matter moves through the food web as evidenced in isotopic enrichments. Udom (2015) reported sediment organic matter (SOM) collected from Rayong Bay in October 2014 to have $\delta^{13}\text{C}$ values of -19.5 ± 1.09 ‰ and $\delta^{15}\text{N}$ values of 1.75 ± 0.77 ‰. Following this shift in trophic enrichment, APL ($\delta^{13}\text{C} = -19.6 \pm 0.98$ ‰ and $\delta^{15}\text{N} = 3.59 \pm 1.23$ ‰) showed enrichment of approximately 0.07 ‰ ($\delta^{13}\text{C}$) and 1.84 ‰ ($\delta^{15}\text{N}$) relative to SOM. He et al. (2019) studied the feeding habit of APL from South China Sea and found their main diet (as determined by gut content) to be mostly diatoms. Hence, we used APL as a primary consumer

(TL = 2) for this benthic food web.

The TLs of APL acts as the basis species in the benthic food web, was 2.72 ± 0.36 , while move up to invertebrate (e.g., *Penaeus merguensis* and *Portunus pelagicus*) and fishes (e.g., *Chiloscyllium hasseltii*, *Terapon jarbua*, and *Terapon theraps*) and at the same time food source for top consumers (Fig. 2b). However, exceptions to this pattern exist for $\delta^{13}\text{C}$. The Indian volute (*Melo melo*, MME) is recognized as a specialized predator of other predatory gastropods (Morton, 1986). The shift in $\delta^{13}\text{C}$ to less negative values (-15.2 ± 0.64 ‰) suggests that MME derives its energy from different carbon sources. MME's diet of other predatory gastropods could be enriched with $\delta^{13}\text{C}$ derived from different sources, such as detritus or estuarine organic matter.

While not explicitly discussed or explored in this study, decomposers are essential contributors to the benthic food web (Bongiorni, 2012). Bacteria and fungi break down detritus and release nutrients back into the system, making them available for primary producers like micro-phytobenthos (Christianen et al., 2017). The different components and interactions within the benthic food web help us gain a deeper appreciation for the complex ways organisms obtain energy and nutrients in this environment.

A high degree of niche overlap is evident within the benthic food web. Compared to the pelagic food web (Fig. 2a), the benthic food web exhibits a broader range of carbon sources, greater trophic redundancy, and larger niche sizes (Fig. 2b). These results align with the relatively high complexity of coastal marine benthic food webs observed in previous studies (e.g., McMeans et al., 2013; Rooney et al., 2006; Sokolowski et al., 2012). In terms of trophic redundancy, multiple species in the benthic food web occupy similar trophic positions, potentially enhancing ecosystem stability by providing functional redundancy in energy transfer pathways (Schlenker et al., 2024). This redundancy is thought to buffer the system against environmental fluctuations such as climate and land-use changes (Cardinale et al., 2002; Price et al., 2019; Sanders et al., 2018), as the loss of one species could be compensated by others fulfilling a similar ecological role. In fact, Hilgendag et al. (2022) found that the greater trophic diversity and trophic redundancy in the benthic food web appeared to reduce the efficiency by which Hg was transferred between TLs, resulting in lower trophic magnification of Hg compared to the pelagic food web. These findings highlight the importance of understanding the complexities and redundancy within the benthic food web in maintaining ecosystem function and resilience.

3.1.3. Coupling between the two food webs

The overlap in the isotopic values between the benthic and pelagic food webs (Fig. 2a and b) suggests that some species may utilize carbon sources from both food webs. This reflects potential dietary plasticity or movement between habitats, highlighting the coupling between pelagic and benthic food webs, particularly in shallow coastal ecosystems and well-mixed waters (e.g., Briand et al., 2016; Giraldo et al., 2024; Giraldo et al., 2017; Nagata et al., 2015; Timmerman et al., 2021). In fact, most of our samples were collected at depths of less than 20 m (Fig. 1), further supporting this connection.

In coastal ecosystems, pelagic food webs primarily rely on phytoplankton (Reynolds, 2008), whereas benthic food webs are supported by a diverse range of carbon sources (Hilgendag et al., 2022), including phytodetritus (Tamelander et al., 2006), benthic macrophytes (Bode et al., 2006), and terrestrial organic matter (Marcelina et al., 2018; Vinagre et al., 2019). The overlap between pelagic and benthic food webs is likely due to the diverse carbon sources utilized by benthic organisms, including those derived from pelagic inputs (e.g., Hilgendag et al., 2022; Iken et al., 2010).

The classification of species into pelagic or benthic groups in this study followed FAO guidelines (Carpenter and Niem, 1998a, 1998b, 1999a, 1999b, 2001a, 2001b), which provide a meaningful framework for initial ecological classification. However, as some species exhibit mixed feeding strategies, future research integrating complementary approaches—such as compound-specific isotope analysis of amino acids

or bulk sulfur isotope analysis—could offer deeper insights into trophic interactions and resource use (e.g., Góngora et al., 2018; Kim et al., 2023; Lacombe et al., 2024; Trifari et al., 2024) beyond what was revealed using bulk nitrogen and carbon isotope analysis in this study. By employing these additional approaches, researchers could better delineate the actual food web to which each sample belongs or assess the degree of overlap between the two food webs.

3.2. THg levels in marine organisms

We analyzed plankton, shellfish, crustaceans, cephalopods, and pelagic and demersal fishes for THg ($n = 342$). The THg in these organisms ranged from 0.45 ± 0.16 $\mu\text{g}/\text{kg}$ in fish larvae to 708 ± 318 $\mu\text{g}/\text{kg}$ in Hasselt's bambooshark (*Chiloscyllium hasseltii*, CH) (Table S2). Apart from plankton, considering all invertebrate and fish species

together, the median, mean, and geometric mean of THg in the pelagic food web ($n = 69$) are 25.5, 49.4, and 25.9 $\mu\text{g}/\text{kg}$, respectively. Similarly, in the benthic food web ($n = 246$), THg concentrations are 52.0, 113, and 55.5 $\mu\text{g}/\text{kg}$ for both invertebrates and fish. In both invertebrate and fish species, THg values in the pelagic food web are approximately half of those in the benthic food web.

Animal size is one of the most significant factors affecting Hg in muscle tissues (Wren, 1986). In the GLMMs analysis, THg was modeled as a function of two predictors: total length and weight. This model, the fixed effect coefficient for total length was 0.065, indicating a significant positive relationship between THg and total length ($p < 0.001$), with increasing Hg concentration with greater total length. In contrast, weight has a non-significant effect on THg ($p > 0.05$). This size-dependent Hg accumulation is likely influenced by various bio-kinetic parameters, such as dietary assimilation efficiency, growth rate,

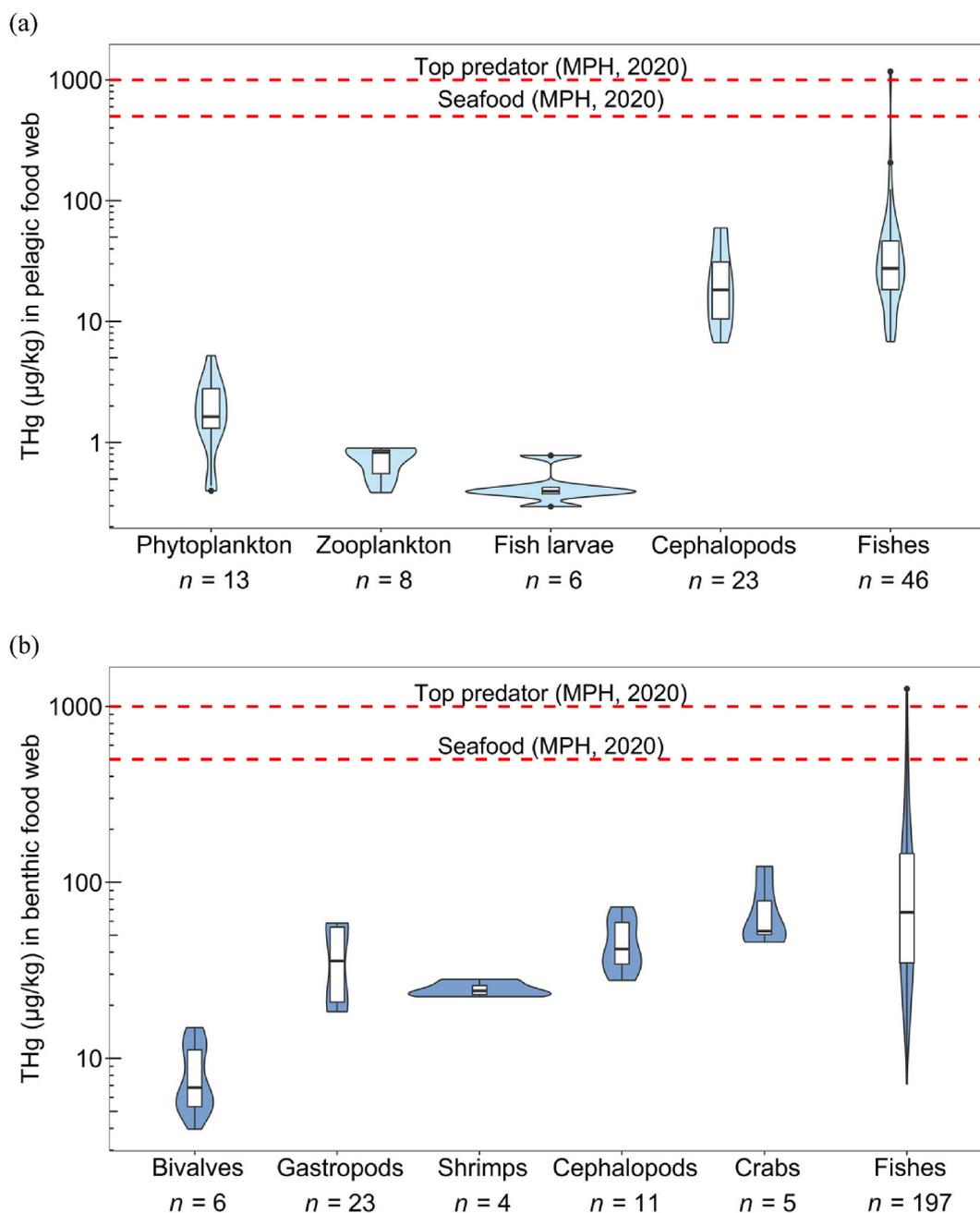


Fig. 3. Distributions of Hg levels (THg, $\mu\text{g}/\text{kg}$ wet weight) in marine organisms from (a) the pelagic food web and (b) the benthic food web of Rayong Bay. Levels of 500 and 1000 $\mu\text{g}/\text{kg}$ indicate the upper permissible level for Hg in seafood and top predators, respectively (MPH, 2020).

and efflux rate (Dang and Wang, 2012). Furthermore, the model shares the random effect revealed significant difference among species ($p < 0.05$), suggesting that species-specific factors are important determinants of Hg accumulation in marine animals, in addition to total length and weight.

In the pelagic food web (Fig. 3a), THg increased progressively from fish larvae ($0.45 \pm 0.16 \mu\text{g/kg}$) to zooplankton ($0.72 \pm 0.19 \mu\text{g/kg}$), phytoplankton ($2.00 \pm 1.25 \mu\text{g/kg}$), and then to cephalopods ($24.2 \pm 17.3 \mu\text{g/kg}$) and to fishes ($61.9 \pm 168 \mu\text{g/kg}$). The Kruskal-Wallis test revealed that fish larvae, zooplankton, and phytoplankton have significantly lower THg than cephalopods and fishes ($p < 0.001$), while squids and fishes did not show any significant difference in THg ($p = 0.153$). Furthermore, there were no significant differences between fish larvae, zooplankton, and phytoplankton ($p > 0.05$). Similarly, the benthic food web (Fig. 3b) shows increasing THg levels from bivalves ($8.17 \pm 3.39 \mu\text{g/kg}$) to shrimp ($24.7 \pm 2.21 \mu\text{g/kg}$), gastropods ($38.4 \pm 17.8 \mu\text{g/kg}$), cephalopods ($45.5 \pm 14.7 \mu\text{g/kg}$), crabs ($70.1 \pm 28.9 \mu\text{g/kg}$), and finally fishes ($134 \pm 200 \mu\text{g/kg}$). ANOVA revealed that bivalves have significantly lower THg than cephalopods, crabs, and fishes ($p < 0.001$), while cephalopods, crabs, and fishes did not show any significant difference in THg ($p > 0.05$). Furthermore, there were no significant differences between bivalves, gastropods, and shrimps ($p > 0.05$). These results indicate a potential for Hg biomagnification within certain marine food webs, particularly within fish populations. Considering the significant role of fish in the Thai diet, this finding emphasizes the critical need for continued monitoring of Hg levels in seafood to ensure consumer safety (Prabakaran et al., 2024, 2025; Ritonga et al., 2022; Windom and Cranmer, 1998).

3.2.1. Hg accumulation at the base of the food web

Hg in aquatic ecosystems are influenced by various factors, including trophic status and plankton density. The extent of biomagnification can vary depending on specific ecosystem characteristics. Indeed, phytoplankton generally accumulates lower Hg than other groups marine organisms (Wu and Wang, 2014). As zooplankton consume phytoplankton, it concentrates the Hg in their bodies (Watras and Bloom, 1992). This biomagnification continues at higher TLs, such as fish consuming zooplankton, leading to higher Hg in each successive TL (Morel et al., 1998). In some cases, higher plankton densities (i.e., during bloom events) are associated with lower Hg in phytoplankton, zooplankton, and fish (Chen and Folt, 2005). This phenomenon is called biodilution (Sun et al., 2020).

It is surprising that THg in fish larvae, zooplankton, and phytoplankton from this study are not significantly different (Fig. 3a) possibly through several plausible mechanisms. Firstly, small phytoplankton have high surface area-to-volume ratios, and subsequently high Hg uptake efficiencies, contributing to the relatively high concentrations (Fisher, 1985; Lee and Fisher, 2016; Wu et al., 2020), consistent with Koski (2024) who reported the lowest THg was observed in the $>200 \mu\text{m}$ size fraction ($18 \pm 3.51 \mu\text{g/kg}$) and the highest concentration in the size fraction of $50 - 200 \mu\text{m}$ ($25.5 \pm 3.7 \mu\text{g/kg}$). Furthermore, Tesán-Onrubia et al. (2023) also found higher THg in phytoplankton ($0.7 - 20 \mu\text{m}$ in size) than in the zooplankton of size classes from 60 to 200 to $>2000 \mu\text{m}$ in size. Secondly, in quickly expanding populations, growth rates may outpace rates of metal uptake leading to lower mass-specific Hg concentrations at high biomass, known as growth dilution (Sunda and Huntsman, 1998).

In eutrophic and hypereutrophic systems, Hg uptake by phytoplankton tends to be lower, and trophic magnification factors are reduced compared to less productive lakes (Poste et al., 2015) as a result of biodilution as discussed above. On the other hand, oligotrophy likely drives the higher Hg bioaccumulation in the food web (Chouvelon et al., 2018). Other factors such as dissolved organic carbon (DOC) and plankton community composition can affect Hg bioaccumulation (Long et al., 2018). Coastal and offshore waters differ in their DOC and composition. Taki and Suzuki (2001) posited that offshore waters of the

subtropical and equatorial Pacific typically have lower DOC concentrations and this DOC pool is more biologically derived and less degraded DOC compared to coastal and shelf environments. This difference likely leads to weaker binding of Hg and MeHg in these waters compared to terrestrial-derived and humic-rich organic matter, thereby increasing Hg bioavailability to plankton (Gosnell and Mason, 2015). Understanding these complex interactions is crucial for predicting Hg concentrations in aquatic food webs and assessing potential risks to higher TL organisms, including humans.

THg in primary producers (i.e., phytoplankton) provides crucial insights into how much Hg enters the food web. Here we compiled THg concentration in plankton from this study and those from other regions (Table 1). Although regional variations in Hg levels exist, we need to recognize that different size classes and analytical techniques for Hg may indeed prevent a direct comparison. We attempted to convert all different reported units to $\mu\text{g/kg}$ and found samples in our study had lower THg than most other studies.

3.2.2. Hg in fish and shellfish

Both invertebrate and fish species in the pelagic food web from this study have average THg concentrations ($49.3 \pm 139 \mu\text{g/kg}$) that were

Table 1
Compiled THg concentrations ($\mu\text{g/kg}$ wet weight) in plankton by size fractions.

Location	Size (μm)	THg	Reference
East Coast of Thailand	N/A	0.1	Cheevaporn et al. (2000)
Guanabara Bay	70–290	0.80–2.01	Kehrig et al. (2009)
	≥ 290	4.01–18.05	
Northwest Atlantic Ocean	0.2–200	1.41–15.24	Hammerschmidt et al. (2013)
	200–500	0.90–10.83	
	500–1000	1.36–13.84	
	1000–2000	1.22–12.44	
	>2000	1.32–6.82	
Ilha Grande Bay	25	$0.15^a \pm 0.02^a$	Seixas et al. (2014)
Ilha Grande Bay	1.2–70	$1.25^a \pm 0.60^a$	Seixas et al. (2015)
	70–290	$0.15^a \pm 0.06^a$	
	290–500	$0.66^b \pm 0.41^b$	
	≥ 500	$0.88^b \pm 0.57^b$	
Central Pacific Ocean	<5	0.26–6.30	Gosnell and Mason (2015)
	5–20	4.07–166.49	
	>20	11.63–288.25	
	200–500,	1.00–27.08	
	500–1000,		
	1000–2000, and		
	>2000		
Long Island Sound	0.2–5, 5–20, and 20–200	<0.30	Gosnell et al. (2017)
Southern Baltic Sea	>50	$3.3^{a,c} - 3.9^{a,c}$	Beldowska and Mudrak-Cegiołka (2017)
Mediterranean Sea	0.7–2.7	$4.30^a \pm 1.55^a$	Tesán-Onrubia et al. (2023)
	2.7–20	$2.10^a \pm 1.35^a$	
	60–200	$1.10^a \pm 0.50^a$	
	200–500	$2.4^b \pm 0.7^b$	
	500–1000	$2.6^b \pm 0.1^b$	
	1000–2000	$4.5^b \pm 4.4^b$	
	>2000	$2.1^b \pm 1.8^b$	
Danshuei Estuary, northern Taiwan.	35–75	$10.0^a - 207.5^a$	Fang and Chang (2024)
	75–125	$5.5^a - 381.0^a$	
	125–212	$7.5^a - 535.0^a$	
	>212	$9.0^b - 1040.0^b$	
Rayong Bay, Thailand	20–100	2.00 ± 1.25	This study
	>100	0.72 ± 0.19	
	>300	0.45 ± 0.16	

Note.

^a Calculated from 95 % water content for microseston (size class of $0.2-200 \mu\text{m}$: bacteria, phytoplankton, microzooplankton, and suspended particulate organic matter) as suggested by Hammerschmidt et al. (2013).

^b Calculated from 90 % water content in zooplankton larger than $200 \mu\text{m}$ based on Knauer and Martin (1972).

^c Median values.

approximately half of those found in the benthic food web (113 ± 84.0 $\mu\text{g}/\text{kg}$), similar to the findings reported by Le Croizier et al. (2019) conducted in fish residing in tropical water along the Senegalese coast of West Africa and Hilgendag et al. (2022) conducted in Arctic marine food webs of Frobisher Bay in Canada. Additionally, pelagic fish collected were lower in THg than benthic, bottom-feeding fish, which exhibited the highest THg of all fish species collected. This is consistent with other previous work in the nearby areas such as the Lower GOT (Windom and Cranmer, 1998) and GOT (Prabakaran et al., 2024). Furthermore, pelagic fish collected in the Upper GOT were reported to have approximately half of those found in the THg concentrations than demersal fish (Chongprasith and Wilairatanadilok, 1999).

Several factors such as feeding habits and methylation may contribute to the lower THg levels in the pelagic food web compared to the benthic food web. Benthic organisms, such as bivalves and crustaceans, often exhibit more diverse diets and feeding strategies than pelagic organisms (Hilgendag et al., 2022; McMeans et al., 2013; Renaud et al., 2011). This diversity in diets and feeding strategies affects how much Hg organisms can accumulate. Many bottom-dwelling invertebrates, such as bivalves and crustaceans, can absorb Hg in two ways: via food ingestion and via seawater through their gills (Gagnon and Fisher, 1997; Gray, 2002; Pan and Wang, 2011). In the case of fish, the former pathway accounts for most Hg intake (Murillo-Cisneros et al., 2019).

Another factor is methylation that is more prevalent in benthic environments especially in anoxic sediments compared to the water column (Compeau and Bartha, 1985; Merritt and Amirbahman, 2009), suggesting that the base of the benthic food web may be more enriched in MeHg relative to the pelagic food web. In addition, differences in seawater conditions between pelagic and benthic environments may lead to varying Hg exposure for different marine organisms. Indeed, the different chemical and physical conditions between pelagic and benthic environments lead to variations in Hg exposure, particularly in its most readily absorbed form, MeHg (Hilgendag et al., 2022). In oxygen-depleted zones of pelagic environments, MeHg formation is believed to be driven by the heterotrophic organic matter remineralization (Bowman et al., 2016; Kim et al., 2017) stemming from the growth of phytoplankton (primary production) associated with subsurface chlorophyll maxima (Bowman et al., 2015; Bratkić et al., 2016; Wang et al., 2022).

Both oxidized and reduced sediments have the capacity to retain Hg. However, changes in redox conditions within the bottom water and upper sediment layers can trigger the release of Hg species into the water column. Conditions such as eutrophication or limited vertical mixing promote reducing environments, which enhance the formation of MeHg in sediments, with periodic releases into the water column (Pakhomova et al., 2018). Conversely, the oxygenation of previously anoxic waters can also result in the mobilization of Hg species into the water, increasing their bioavailability and potential uptake by organisms, thereby introducing Hg into the food web (Pakhomova et al., 2018). Throughout the study period, the area under investigation experienced no hypoxia in the water column. Therefore, any MeHg entering the base of the pelagic food web might originate from the underlying sediments or perhaps in the settling particles (e.g., Monperrus et al., 2007; Sunderland et al., 2009).

In benthic environments, bottom-dwelling organisms (i.e., benthic biota) experience variable MeHg exposure. The types of microbes present in the sediments can influence MeHg production while the amount of organic matter can act as a chelating agent of MeHg, thus reducing its bioavailability for organisms (Lawrence and Mason, 2001; Tomczyk et al., 2018). The wider range of THg observed in benthic food webs compared to pelagic one's stems from three key factors. Firstly, bottom-dwelling organisms have more diverse food sources, potentially leading to a broader range of Hg exposure. Secondly, they likely have unique mechanisms for accumulating and eliminating Hg compared to open water organisms. Finally, the varied seawater chemistry conditions

experienced by bottom-dwellers throughout their habitat can contribute to more variable Hg exposure.

Most THg in the studied invertebrates and fish species ($n = 315$, Table S2) fell below the guideline levels established by international organizations (e.g., EC, 2023; UNEP, 2002) and national regulations (e.g., Bugang and Woolsey, 2010; Canada, 2007; FSANZ, 2024; Jinadasa et al., 2021; MPH, 2020) (500 $\mu\text{g}/\text{kg}$ wet weight). However, some exceptions were found in some fish species. In the pelagic food web ($n = 96$), one pickhandle barracuda (*Sphyaena jello*, SJE; $n = 1$) exceeded the limit. Similarly, the benthic food web ($n = 246$) contained 10 samples (five species) that surpassed the guideline levels: lattice monocle bream (*Scolopsis taenioptera*, STA; $n = 1$), large scaled terapon (*Terapon theraps*, TT; $n = 5$), jarbua terapon (*Terapon jarbua*, TJ, $n = 1$), butterfly whiptail (*Pentapodus setosus*, PS; $n = 1$), and Hasselt's bambooshark (*Chiloscyllium hasseltii*, CH; $n = 2$). These species exceeding the guideline levels are thought to occupy higher or intermediate TLs compared to most organisms in this study based on the $\delta^{15}\text{N}$ values (Table S2).

The highest THg in the pelagic food web was found in pickhandle barracuda (*Sphyaena jello*, SJE), a fast-swimming and long-lived carnivorous fish, with high energy demands due to its active lifestyle (Dananjanie et al., 2009; Hajisamae et al., 2003). Its high consumption rate makes it more susceptible to accumulating pollutants like Hg in its organs and tissues (e.g., Ritonga et al., 2023). In this study, the average THg in SJE is 595 ± 576 $\mu\text{g}/\text{kg}$, higher than those reported in Port Moresby (61 $\mu\text{g}/\text{kg}$) (Sorentino, 1979) and the artisanal fisheries of Seychelles (360 ± 31 $\mu\text{g}/\text{kg}$) (Robinson and Shroff, 2020). Several previous studies showed a strong correlation between SJE length and Hg concentration (e.g., Saei-Dehkordi et al., 2010; Shalini et al., 2021). These studies highlight regional variations in Hg concentrations and the potential for bioaccumulation in larger predatory fish species. Also, it is important to note that the two SJE in this study had drastically different lengths (i.e., 12.8 vs 59.0 cm) resulting in varying THg therein (i.e., 18.3 vs 1171 $\mu\text{g}/\text{kg}$). The regional variations in Hg concentrations observed in SJE emphasize the need for targeted monitoring and management strategies to protect human health and marine ecosystems from Hg contamination. By understanding the factors driving Hg accumulation in SJE, we can develop effective measures to reduce Hg exposure and mitigate its negative impacts.

In contrast, the benthic food web shows the highest THg in Hasselt's bambooshark (*Chiloscyllium hasseltii*, CH) at 708 ± 318 $\mu\text{g}/\text{kg}$, followed by jarbua terapon (*Terapon jarbua*, TJ, 663 ± 523 $\mu\text{g}/\text{kg}$) and large scaled terapon (*Terapon theraps*, TT, 470 ± 370 $\mu\text{g}/\text{kg}$). *Terapon* spp., typically found in Indo-West Pacific coastal waters, brackish areas, and even freshwater, have higher THg and exhibit interesting life stages. Adults prefer the near-shore environment, while juveniles hitch rides on floating weeds, venturing far out to sea (Lim, 2015; Russell and Houston, 1989). Their omnivorous diet includes invertebrates, algae, decomposing matter, and also small fish (Nagarani and Kumaraguru, 2012). They are not only nutritious for human consumption but also serve as valuable indicators of environmental contamination of Hg (e.g., Nagarani et al., 2011). In this study, the average concentration of THg in TT and TJ is lower than the *Terapon* spp. In the GOT (1050 ± 721 $\mu\text{g}/\text{kg}$) (Prabakaran et al., 2024). The THg in TT was lower than that reported for Buru Island (970 $\mu\text{g}/\text{kg}$) (Reichert-Brushett et al., 2017). Conversely, the concentration in TJ was higher than those reported for Dapeng Bay (48.4 ± 18.3 $\mu\text{g}/\text{kg}$) (Pan et al., 2014), the South China Sea (417 $\mu\text{g}/\text{kg}$) (Liu et al., 2014), and the Talawaan watershed, Indonesia (175 $\mu\text{g}/\text{kg}$) (Kaunang et al., 2018).

This study highlights that some predatory fish (i.e., *Sphyaena jello* sp. and *Chiloscyllium hasseltii*) and some demersal fish (*Terapon* spp.) tend to accumulate higher levels of Hg due to their higher position in the food web. As a result, it is recommended to limit the consumption of fish occupying high TLs. To effectively mitigate the potential health impacts of Hg on humans, further research on its uptake and depuration mechanisms is essential. This knowledge could be used to create targeted guidance, such as recommendations on which fish species, age groups,

or body parts to avoid consuming, and even contribute to the development of safer food practices.

3.3. Prey-predator dynamics impact on THg biomagnification

Over 46 % of BMF_{norm} values in the pelagic food web (Fig. S1) and over 40 % in the benthic food web exceeded 1.0 (Fig. S2), indicating Hg biomagnification (Borgå et al., 2012; Vainio et al., 2022). The pelagic food web exhibited a BMF_{norm} range of 1.015 to 1285 (28.2 ± 19.6), while the benthic food web ranged from 1.001 to 476 (13.9 ± 32.9). Equation (3) considers a TLs to account for differences in how THg accumulates at different TLs. In some cases, however, BMF_{norm} values can be lower than one or even negative (shown as white boxes in Figs. S1 and S2). This is due to the predator's TL values being lower than those of its supposed prey (e.g., Vainio et al., 2022).

In the pelagic food web (Fig. S1), the three barracuda species, including the *Sphyrna jello* (SJE) exhibits the highest BMF_{norm} values, indicating the greatest Hg accumulation from prey ($BMF_{norm} = 188 \pm 30.4$, range: 12.7 to 1285), followed by the *Sphyrna putnamae* (SP) ($BMF_{norm} = 27.3 \pm 48.9$, range: 1.0 to 243) and the *Sphyrna obtusata* (SOC) ($BMF_{norm} = 14.2 \pm 27.1$, range: 1.8 to 135). Given this, SJE is likely a top predator within this pelagic food web, while SP and SOC may occupy upper TLs. Similarly, in the benthic food web (Fig. S2), the *Chiloscyllium hasseltii* (CH) demonstrates the highest BMF_{norm} values, implying the most substantial Hg uptake from prey ($BMF_{norm} = 68.8 \pm 82$, range: 7.6 to 364), with the *Terapon jarbua* (TJ) ($BMF_{norm} = 40.4 \pm 73.7$, range: 2.9 to 476) and the *Terapon theraps* (TT) ($BMF_{norm} = 26.8 \pm 22.2$, range: 4.2 to 87.7) following. The range of BMF_{norm} values in marine organisms in this study is higher than those reported by Vainio et al. (2022) for homeotherms ($BMFs = 4.40$ to 508) and poikilotherms ($BMFs = 0.44$ to 33.5), as well as for pelagic predators ($BMFs = 1.61$ to 9.35) and benthic predators ($BMFs = 0.44$ to 30.9) in the Archipelago Sea a Baltic Sea basin at the southwestern coast of Finland. This discrepancy could be attributed to variations in ecosystem characteristics. GOT might represent a different marine environment with distinct food web structures and prey composition compared to the Baltic Sea. Additionally, environmental factors like salinity, seawater temperature, organic matter content, and sediment characteristics can all influence Hg bioavailability and bioaccumulation in organisms (Bradford et al., 2024; Lawrence and Mason, 2001). Together, these factors likely contribute to the observed differences in BMF and BMF_{norm} values.

While the BMF and BMF_{norm} values provide insights into how contaminant concentrations increase up the food web, they have limitations particularly because they do not account for the variations observed in real-world ecosystems. Different species have unique food source and body temperature regulation strategy. Both of which can significantly influence the contaminant accumulation, making BMF and BMF_{norm} values less precise for some organisms (Vainio et al., 2022; Van den Brink et al., 2013). To improve our understanding of contaminant movement in food webs, models that incorporate these ecological and physiological differences are needed.

3.4. THg biomagnification in pelagic vs benthic food webs

Trophic indicators (BMF_{norm} , TMS, and TMF) can be used to explore the dynamics of THg in the Rayong Bay tropical food web. The BMF_{norm} values characterize the increase in contaminant concentration between adjacent TLs, while the TMF values represent the average BMF_{norm} across multiple TLs, potentially encompassing the entire food web (Franklin, 2016).

Varying degrees of THg biomagnification were observed in different habitats. Our GLMM analysis revealed a significant positive relationship between TLs and THg concentrations with a fixed effect coefficient of 0.352 ($p < 0.05$). This result indicates that organisms at higher TLs tend to accumulate greater Hg. The TMF values of 6.68 for the pelagic food web and 2.06 for the benthic food web further support this trend,

demonstrating that THg biomagnifies more effectively in the pelagic food web (TMS = 0.83, Fig. 4a) compared to the benthic food web (TMS = 0.31, Fig. 4b). This highlights the significance of investigating THg pathways in various environmental environments. Consistent with previous findings that pelagic food webs generally exhibiting higher biomagnification rates than benthic food webs (e.g., Hilgendag et al., 2022; Vainio et al., 2022), our study confirms that THg biomagnification occurs in both Rayong Bay food webs, with greater TMF and TMS values indicating higher levels of Hg biomagnification. Consequently, consumers at higher TLs are more likely to accumulate significant amounts of Hg, posing a risk to human health (Scheuhammer et al., 2007).

Both pelagic and benthic food webs with TMF values exceeding 1.0 indicate that THg entered organisms at the base of the food web and biomagnified through trophic transfers. Our TMF values align with previous studies, which reported higher TMFs in the pelagic food web compared to the benthic one in the Gulf of St. Lawrence, Canada (Lavoie et al., 2010), the Archipelago Sea (Vainio et al., 2022) and Frobisher Bay (Hilgendag et al., 2022) (Table 2). The biomagnification of the same contaminant differs among food webs, influenced by the unique characteristics of each web (Wang et al., 2021). The distinct TMF values observed in both food webs could be linked to differences in THg bioavailability (Bisi et al., 2012). In fact, simpler food webs in our study, such as the pelagic system, appeared to rely on fewer carbon sources and exhibited higher rates of Hg biomagnification consistent with other previous studies (e.g., Hilgendag et al., 2022; Muto et al., 2014). Notably, the factors driving Hg biomagnification in marine food webs appear consistent across diverse environments, from polar to temperate to tropical regions (Campbell et al., 2005; Lavoie et al., 2013).

A comprehensive overview of TMF values, calculated by taking the antilogarithm of the slope ($\log_{10}THg$ vs $\delta^{15}N/\log_{10}THg$ vs TL) from the estimated regression with base 10, for Hg across various marine food webs globally is presented (Table 2). TMF values exhibit even greater variability, ranging from 1.10 to 13.39, highlighting significant differences in TMF values across marine food webs. This variability is further evidenced by discrepancies between our findings and those of previous studies, some of which involved seabirds (e.g., Jæger et al., 2009; Lavoie et al., 2010; Ruus et al., 2015). These discrepancies may primarily arise from variations in the quantity of Hg entering the base of the food web (Thera and Rumbold, 2014), as well as differences in the structure and complexity of the food web. Geographical differences can also influence the quantity of bioavailable Hg generated (Murillo-Cisneros et al., 2019). However, trophic contaminant dynamics within food webs are specific to each system due to variations in the physiochemical characteristics of the environment and instance and the intrinsic variety in the contamination pathways that arise (Vainio et al., 2022). Our findings highlight the critical importance of examining variations in the trophic transmission of Hg along distinct food web pathways to gain a deeper comprehension of contaminants dynamics.

4. Conclusion

This study integrated food web structure analysis with biomagnification estimations to explore dietary Hg pathways in the marine environment of Rayong Bay, a relatively unexplored area within the GOT. To our knowledge, this is the first investigation into THg biomagnification in Thai waters. Our results revealed a significant positive relationship between THg and total length and TLs in marine animals. This relationship indicates that THg levels increase as organisms ascend the food web. Larger predators, including fish such as *Sphyrna* sp., *Chiloscyllium* sp., and certain demersal fish (*Terapon* spp.), exhibit significantly higher concentrations than smaller organisms. Although most THg levels were well below established safety guidelines, the presence of biomagnification warrants further exploration.

This research utilized three trophic indicators (BMF_{norm} , TMS, and TMF) to assess THg movements within the food webs in Rayong Bay. Over 40 % of the BMF_{norm} values in the pelagic and benthic food webs

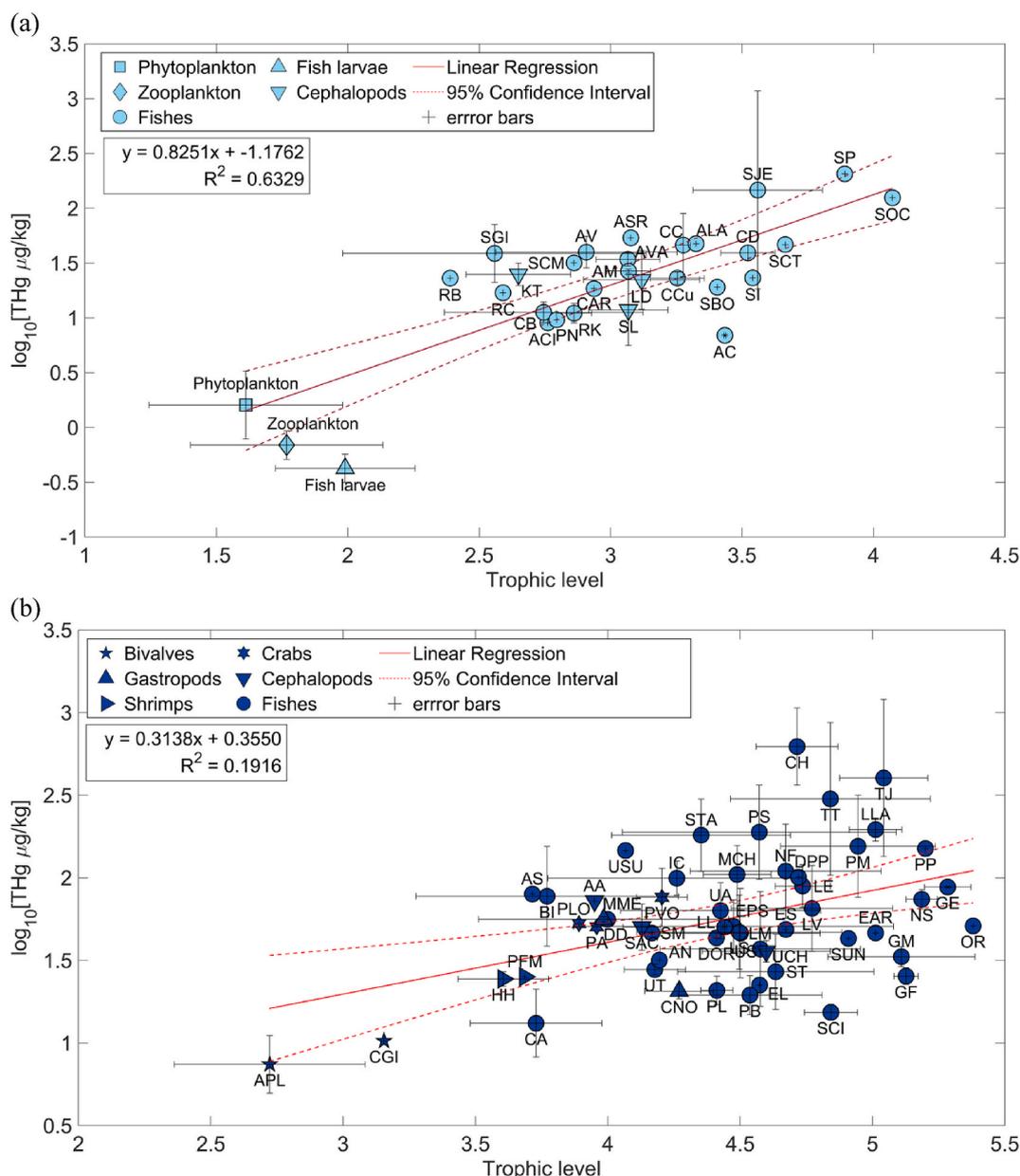


Fig. 4. Linear regressions between $\log_{10}[\text{THg}, \mu\text{g}/\text{kg}$ wet weight] and trophic levels for (a) the pelagic food web and (b) the benthic food web in Rayong Bay. Refer to [Table S1](#) for detailed information on the corresponding code.

exceed one, indicating that THg increase as organisms moves up the food web in these ecosystems. Additionally, the TMF values show that THg biomagnifies more effectively in the pelagic food web than in the benthic food web in Rayong Bay. This finding aligns with the comparison of food web structure and computed biomagnification values (TMFs and TMSs) between the two food webs.

Overall, the findings emphasize the occurrence of Hg biomagnification in Rayong Bay. While plankton exhibits minimal enrichment, predators at higher TLs accumulate substantial amounts of Hg. The higher biomagnification in the pelagic system also necessitates further investigation into the specific factors driving this pattern.

CRedit authorship contribution statement

Suriyapong Kumsopar: Writing – review & editing, Writing – original draft, Visualization, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Chawalit Charoenpong:** Writing – review & editing, Writing – original

draft, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Formal analysis, Conceptualization. **Shaoneng He:** Writing – review & editing, Methodology, Investigation. **Paco Bustamante:** Writing – review & editing. **Bernie Wee:** Writing – review & editing, Methodology, Investigation. **Xianfeng Wang:** Writing – review & editing, Methodology, Investigation. **Narainrit Chinfak:** Writing – review & editing, Investigation. **Kiattipong Kamdee:** Writing – review & editing, Investigation. **Penjai Sompongchaiyakul:** Writing – review & editing, Supervision, Resources, Project administration, Funding acquisition, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Suriyapong Kumsopar reports financial support was provided by Chulalongkorn University. Suriyapong Kumsopar reports financial support was provided by Thailand Institute of Nuclear Technology. Chawalit

Table 2
Compiled previously published trophic magnification slopes (TMSs) and trophic magnification factors (TMFs) of Hg.

Location	Food web	Samples	Data analysis	TEF	TMSs	TMFs	Reference
Mekong Delta, South Vietnam	Not specified	Phytoplankton – Fishes	Log ₁₀ THg vs δ ¹⁵ N	–	0.114	1.30	Ikemoto et al. (2008)
Kongsfjorden, Svalbard	Pelagic	Seabirds	Log ₁₀ THg vs Tls	3.4	0.14	3.02	Jæger et al. (2009)
	Pelagic	Fishes — seabirds			NA	4.87	
Baltic Sea	Pelagic	Phytoplankton — fishes	Log ₁₀ THg vs δ ¹⁵ N	3.5	0.175	1.50	Nfon et al. (2009)
Gulf of St. Lawrence	Pelagic	Zooplankton — seabirds	Log ₁₀ THg vs Tls	3.4	0.697	4.98	Lavoie et al. (2010)
	Benthopelagic	Invertebrates — seabirds			0.649	4.46	
	Benthic	Invertebrates — fishes			0.416	2.60	
Sepetiba Bay, Norway	Not specified	Invertebrates — fishes	Log ₁₀ THg vs δ ¹⁵ N	–	NA	1.71–1.91	Bisi et al. (2012)
Guanabara Bay, Norway					NA	1.51–1.55	
Ilha Grande Bay, Norway					NA	1.63–1.67	
Hudson Bay, Canada	Not specified	Zooplankton	Log ₁₀ THg vs δ ¹⁵ N	3.8	NA	1.1–1.9	Foster et al. (2012)
Northern Rio de Janeiro State, southeastern Brazil	Not specified	Phytoplankton — fishes	Log ₁₀ THg vs Tls	3.4	0.835	6.84	Di Benedetto et al. (2012)
Southeastern Australia	Whole community	Zooplankton — fishes	Log ₁₀ THg vs Tls	3.4	1.13	13.39	Pethybridge et al. (2012)
	Benthic	Fishes			0.89	7.70	
Nain Bay, Canada	Not specified	Algae (<i>Fucus</i> sp.) — fishes	Log ₁₀ THg vs Tls	3.4	0.37 ± 0.06	2.35	van der Velden et al. (2013)
Okak Bay, Canada		Algae (<i>Fucus</i> sp.) — fishes			0.37 ± 0.06	2.33	
Saglek Bay, Canada		Algae (<i>Fucus</i> sp.) — fishes			0.20 ± 0.05	1.59	
Dry Bay, Canada		Algae (<i>Fucus</i> sp.) — fishes			0.22 ± 0.04	1.65	
Iqaluit, Canada		Plankton — fishes			0.44 ± 0.03	2.77	
Pond Inlet, Canada		Algae (<i>Fucus</i> sp.) — fishes			0.45 ± 0.03	2.82	
Southwest Florida, USA	Not specified	Invertebrates — fishes	Log ₁₀ THg vs Tls	3.4		5.05	Thera and Rumbold (2014)
Santo shelf, São Paulo, Brazil	Pelagic	Zooplankton – Fishes	Log ₁₀ THg vs δ ¹⁵ N	–	0.26	1.82	Muto et al. (2014)
	Benthic	Bivalves – Fishes			0.13	1.35	
Nasaruvaalik Island, Nunavut, Canada	Not specified	<i>C. hyperboreus</i> — fishes	Log ₁₀ THg vs Tls	3.8	0.036	1.37	Clayden et al. (2015)
		<i>C. hyperboreus</i> — seabirds			0.095	2.13	
Kongsfjorden, Svalbard, Norwegian Arctic	Pelagic	Zooplankton — seabirds	Log ₁₀ THg vs Tls	3.8	NA	8.8	Ruus et al. (2015)
		Zooplankton — seabirds (without krill)			NA	8.7	
East coast of Peninsula, Malaysia	Not specified	Sediment — fishes	Log ₁₀ THg vs δ ¹⁵ N	2.2*	0.163	1.5	Le et al. (2017)
					3.4**		
Chukchi Sea	Not specified	Phytoplankton — whelk	Log ₁₀ THg vs Tls	3.4	0.05	1.5	Fox et al. (2017)
			Log ₁₀ MMHg vs Tls	3.4	0.15	3.2	
Bahia Tortugas, Mexico	Benthic	Zooplankton — fishes	Log ₁₀ THg vs Tls	3.4	0.8051	6.38	Murillo-Cisneros et al. (2019)
Laizhou Bay, China	Not specified	Phytoplankton — fishes	Log ₁₀ THg vs Tls	3.4	0.23	1.69	Cao et al. (2020)
Frobisher Bay	Pelagic	Zooplankton — fishes	Log ₁₀ MeHg vs δ ¹⁵ N	–	0.183	1.52	Hilgendag et al. (2022)
	Benthopelagic	Invertebrates — fishes			0.201	1.59	
	Benthic	Invertebrates — fishes			0.079	1.20	
Archipelago Sea	Pelagic	Zooplankton — fishes	Log ₁₀ THg vs Tls	3.4	0.55–0.60	3.58–4.02	Vainio et al. (2022)
	Benthic	Bivalves — fishes			0.32–0.37	2.11–2.34	
Gulf of Ulloa, Mexico	Not specified	Zooplankton — fishes	Log ₁₀ THg vs Tls	3.4	NA	3.4	Pantoja-Echevarria et al. (2023)
Yanpu Bay, China	Not specified	POM — fishes	Log ₁₀ THg vs δ ¹⁵ N	–	NA	1.42	Hu et al. (2024)
Lower Cape Fear River and the Pamlico Sound	Not specified	Sediment — seabirds	Log ₁₀ THg vs δ ¹⁵ N	3.4	NA	2.96–3.92	Hardy et al. (2024)
Haizhou Bay, China	Not specified	Gastropods — fishes	Log ₁₀ THg vs Tls	3.4	NA	1.64	Chen et al. (2024)
Rayong Bay, Thailand	Pelagic	Phytoplankton — fishes	Log ₁₀ THg vs Tls	3.4	0.83	6.68	This study
	Benthic	Bivalves — fishes			0.31	2.06	

Note: TEF stands for trophic enrichment factor. Le et al. (2017)'s TEF values *for invertebrates and ** for fishes. Meanwhile, POM stands for particulate organic matter, and NA is not available.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.envres.2025.121599>.

Data availability

Data will be made available on request.

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