Answer to R1

Author Response

Dear Reviewer,
Thank you very much for reviewing the manuscript and for your invaluable input. Below, we have posted your comments and suggestions in grey boxes, with our responses highlighted in blue boxes and proposed manuscript changes shown in red boxes.
We hope you find our proposed revisions appropriate and agree with the suggested changes to the manuscript. We acknowledge that the availability of observational data is limited and that model uncertainty is therefore higher than would be ideal. Nevertheless, we believe that the manuscript clearly presents the proposed mechanisms and that the suggested revisions substantially improves the clarity, transparency, and robustness of the study.

Reviewer Comment

This study constructed a model to trace the bioaccumulation of MeHg within the Mediterranean Sea food web in the Bay of Villefranche. The model initially enabled assessing the levels of iHg and MeHg accumulating in LMA sponges. The model was also used to assess the differences in MeHg bioaccumulation in fish in a setup with and without sponges to see if sponges influence the MeHg bioaccumulation in fish. Although an advanced model was developed and the design of scenarios was ingenious in this study, the article reads rather obscure. Many paragraphs are suggested to be refined, and the logicality should be simultaneously increased. Major revision is needed and some comments are shown as follows.

Reviewer Comment

(1) Line 85: The sentence “This is proposed in (Amptmeijer et al., 2025b), which is a. . . . . .” is confused. Please rewrite the sentence.

Author Response

We updated this as below:

Suggested edit

Line 7839
An alternative proposal for the low MeHg concentration in HMA sponges is that it is low due to the consumption of DOM. This is suggested in Amptmeijer et al. (2025b), which presents a modeling study examining how the feeding strategy influences iHg and MeHg dynamics. In that model, the feeding strategy is considered in isolation, and other biological factors that could affect bioaccumulation are not included, such as in vivo demethylation, the long lifespan of sponges, and their low metabolic rate.

Reviewer Comment

(2) Section 2.1: A map is needed for the model domain in the main text.

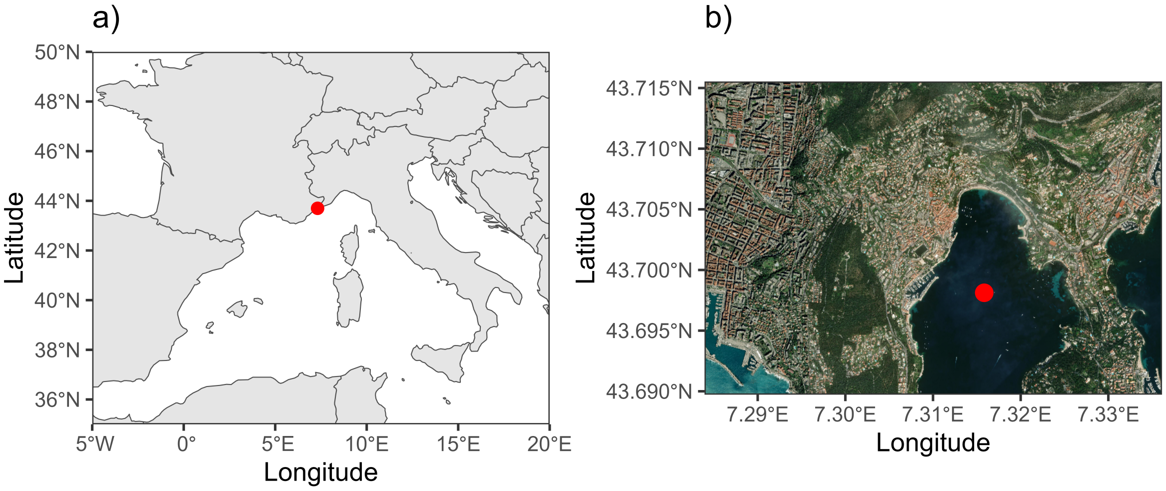

Figure 1: The modelled station is indicated by the red dot. (a) Overview map of the western Mediterranean Sea showing the location of the Bay of Villefranche. (b) Detailed map of the bay showing the exact sampling location.

Author Response

We added the map as shown in Fig. 1 and the statement below to the manuscript to make it clear where the model is simulated. Additionally this is mentioned in the text at line 124.

Suggested edit

Line 129
In Figure 1, we show the model domain, we show the model domain; where Fig. 1 a) depicts the Western Mediterranean Sea, while Fig. b) shows the exact modeled location in the Bay of Villefranche. The maps were created in R using Esri WorldImagery.

Reviewer Comment

(3) For the subtitles of sections 2.1, 2.2, 2.3, and 2.3.2, dashes are better than semicolons. And capitalize the first letter of "semi-labile" in Section 2.6.

Author Response

The subtitles are updated as below:

Suggested edit

2.1 The model domain - The Bay of Villefranche
2.2 The hydrodynamic model - GOTM
2.3.1 Hg cycling and speciation - the MERCY v2.0 model
2.3.2. Carbon cycling and ecosystem dynamics - the ECOSMO E2E model
2.6 Semi-labile DOM

Reviewer Comment

(4) Section 3.4: In my opinion, the observations of Hg and MeHg in the study domain are too few to support the model evaluation. I suggest more observations particularly for various environments and functional groups.

Author Response

We agree with this point, but because the model is implemented in a one-dimensional framework, it is primarily designed to represent a single, well-defined environment; accordingly, the evaluation focuses on whether the simulations for the Bay of Villefranche are consistent with the available observations. We do agree that the table provided in the previous version was too limited in scope. We therefore propose replacing it with the revised text below, which provides a more detailed discussion of model behaviour and performance.

During this renewed assessment of the observational dataset, we noted that the fish observations used for comparison predominantly represent species at relatively low trophic levels, such as sardines, whereas the fish compartment in the model represents species at somewhat higher trophic levels. In a recently published manuscript (Amptmeijer et al., 2025), we describe an updated parameterisation that results in higher bioaccumulation at higher trophic levels. To improve consistency between the model and the available observations, we therefore updated the MeHg bioaccumulation parameterisation for fish, while keeping the sponge parameterisation unchanged. After rerunning the simulations, this update did not alter the conclusions regarding the role of sponges and the difference in bioaccumulation between simulations with and without sponges remained 53%, comparable to the previously reported 45%.

We therefore propose adopting this updated parameterisation in the revised manuscript. This preserves the main conclusions of the study while improving agreement between modelled benthic fish and the trophic level of the observed species used for evaluation. The updated parameterisation has already been published for the ECOSMO model; however, absolute bioaccumulated values for fish may deviate from those reported in the preprint.

In addition to the expanded evaluation text, we suggest moving Table 1 to the appendix as Table A1.

Suggested edit

Line 400
We first discuss the base case, the simulation without rDOM. Then we discuss the differences in the simulation with 2.5 gC m^{-2} and how this compares to observations. When data were reported in dry weight, we assumed a 1:3 dry-weight-to-carbon ratio for plankton and a 1:2 ratio for megabenthos and fish to compare our model output in mgC with the observed bioaccumulation in dry-weight measurements. When fish were reported in wet weight, an additional 1:5 dry-weight-to-wet-weight ratio was assumed (Menden-Deuer et al., 2000; Sicko-Goad et al., 1984). Overall, the model reproduces the observed ranges and trophic-level trends reported in the literature. MeHg bioaccumulation in phytoplankton is observed at 2.4 ± 0.8 ng Hg gC^{-1} by Tesán-Onrubia et al. (2023), compared to 1.8 ± 4.2 ng Hg gC^{-1} in the model. Zooplankton observations range from 9–21 ng Hg gC^{-1}, with copepods reaching up to 31 ng Hg gC^{-1} (Buckman et al., 2019) while the model predicts 11.8 ± 4.5 ng Hg gC^{-1} for microzooplankton and 12.6 ± 3.6 ng Hg gC^{-1} for mesozooplankton, so the model is within the observed range.
Filter feeders (oysters and mussels) show observed bioaccumulation of 18–290 ng Hg gC^{-1} along the French coast, and 48–148 ng Hg gC^{-1}, with a mean of 100 ng Hg gC^{-1}, in the Bay of Cannes, which are their closest observations to the Bay of Villefranche (Briant et al., 2017). The model predicts 35 ng Hg gC^{-1}, indicating that the model likely underestimates MeHg bioaccumulation in filter feeders, but the modeled mean still falls within the observed range. Benthic predators have roughly double the MeHg of filter feeders, consistent with biomagnification. Observed MeHg in benthic fish (437 ng Hg gC^{-1}) aligns with mid-trophic Mediterranean species such as common sole (400 ng Hg gC^{-1}) and white seabream (310 ng Hg gC^{-1}). In the 2.5 gC rDOM m^{-3} scenario, low-trophic biota show slightly higher bioaccumulation, likely due to reduced growth dilution. In this scenario filter feeders are largely outcompeted by sponges. The benthic predator shifts its diet toward HMA sponges, reducing its MeHg to 32 ng Hg gC^{-1} (still approximately three times higher than its diet), and benthic fish MeHg decreases to 205 ng Hg gC^{-1}, consistent with lower-end observations for common sole and closer to species with lower MeHg, such as blackspot seabream or common pandora. Due to the 1D model structure and limited observations, detailed quantitative validation is not possible, but both setups, with and without rDOM, simulate bioaccumulation consistent with observations.

Reviewer Comment

(5) All the figures should be improved due to their rough presentation.

Author Response

We thank the reviewer for the suggestion to improve the presentation of the figures. We agree that the model overview figure could benefit from clearer formatting and have improved the readability of the text boxes, as shown in Fig. 2. Additionally, due to the altered model parameterization, the MeHg levels in fish are no longer compatible with the original Fig. 7. Therefore, we split it into Fig. 7a and 7b, as can be shown in Fig. 3. We would, of course, be happy to update other figures if any are found to have problematic presentation, and would appreciate any specific guidance on which figures require further improvement.

Table 1: Table A1. Mean biomass and mercury bioaccumulation for all functional groups across the three main model setups investigated in this study. Benthic biomass is reported in mgC m^{-2}, while pelagic biomass (phytoplankton and zooplankton) is reported in mgC m^{-3}. Inorganic mercury (iHg) and methylmercury (MeHg) bioaccumulation are expressed in ng Hg mgC^{-1}. Bioaccumulation values are omitted when mean biomass was negligible (< 0).

	Biomass		MeHg		iHg	
	Mean	SD	Mean	SD	Mean	SD
Base Case						
Generalist feeder	256	177	37	8	69	8
Deposit feeder	1741	614	61	16	80	9
Filter feeder	158	118	35	11	59	10
HMA sponge	252	82	29	6	162	37
LMA sponge	1375	692	27	9	111	19
Predator	382	425	79	14	63	6
Benthic fish	226	231	422	524	57	10
Microzooplankton	16	26	12	4	32	21
Mesozooplankton	25	23	13	4	49	13
Phytoplankton	41	32	2	4	1	3
2.5 gC rDOM m^{-2}						
Generalist feeder	335	287	48	22	64	12
Deposit feeder	1186	797	97	44	82	18
Filter feeder	0	0	–	–	–	–
HMA sponge	6649	4388	13	6	82	15
LMA sponge	21	29	71	14	71	10
Predator	2578	4204	32	22	56	10
Benthic fish	963	1482	205	1614	56	16
Microzooplankton	18	22	17	9	32	23
Mesozooplankton	12	12	23	11	50	14
Phytoplankton	30	25	4	8	2	4
2.5 gC rDOM m^{-2} (No HMA)						
Generalist feeder	287	169	36	8	68	10
Deposit feeder	1568	659	53	15	79	11
Filter feeder	204	134	35	12	57	12
HMA sponge	0	0	–	–	–	–
LMA sponge	660	495	18	8	72	11
Predator	385	567	71	18	55	7
Benthic fish	179	209	437	536	51	11
Microzooplankton	19	28	13	6	32	22
Mesozooplankton	20	19	15	5	47	13
Phytoplankton	39	33	3	5	2	4

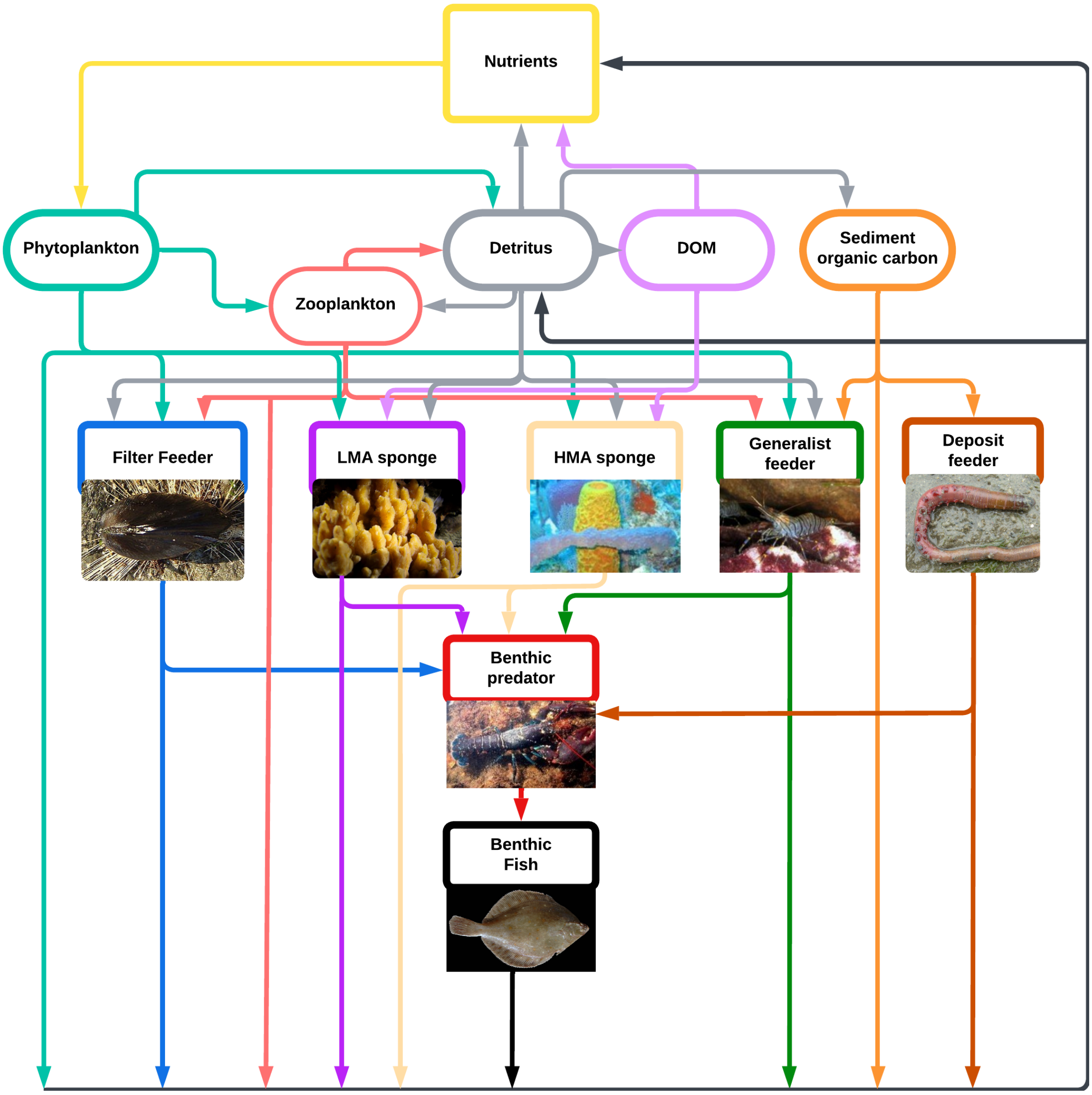

Figure 2: Updated model overview Figure.

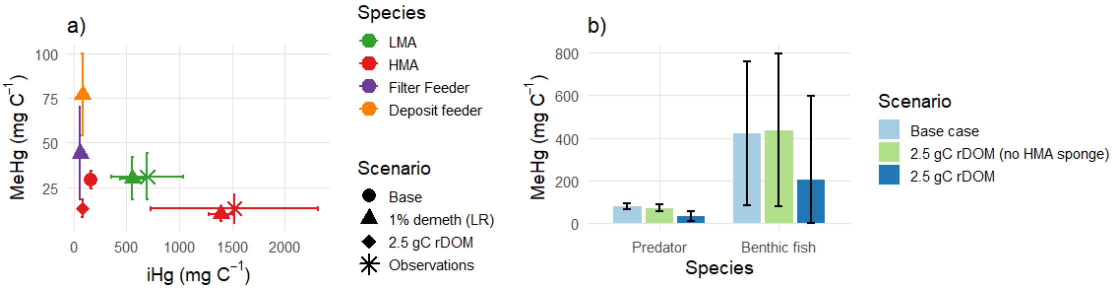

Figure 3: Summary of key results. Panel a shows the modeled bioaccumulation of iHg and MeHg in megabenthos compared with observed bioaccumulation in LMA and HMA sponges, where triangles indicate model values and circles indicate observations. The scenario with a demethylation rate of 1% d^{-1} and reduced Hg release shows strong agreement with the observed sponges. Panel b shows the modeled bioaccumulation of MeHg in predators and benthic fish, with concentrations in fish (blue) reduced by 53% in the scenario with 2.5 gC rDOM m^{-3} compared to the same simulation without sponges.

Reviewer Comment

(6) Section 4.2: What's the underlying mechanisms for low MeHg due to DOM consumption in HMA sponges? I only see the results of model scenarios. However, the mechanistic inference is more meaningful.

Author Response

We agree that this is underexplained. We added the new subsection to the discussion starting in line 505

Suggested edit

Line 511

Mechanistic explanation for the special role of DOM in iHg and MeHg bioaccumulation

The difference in bioaccumulation of iHg and MeHg highlights mercury as a unique pollutant. Certain biological pathways, such as the direct absorption of MeHg via membrane channels in phytoplankton, enable highly efficient MeHg bioaccumulation. As a result, MeHg concentrations in biota can exceed iHg concentrations, even in primary producers, despite dissolved iHg being more abundant than MeHg. In DOM, which primarily consists of dead organic particles, these preferential uptake pathways are absent, and DOM binds iHg and MeHg only through scavenging. DOM composition strongly influences its binding capacity: thiol-rich fractions of terrestrial DOM efficiently bind MeHg (Seelen et al., 2023), whereas marine DOM fractions show a higher affinity for iHg (Tesán Onrubia et al., 2020), which underpins the partitioning behavior used in the MERCY V2.0 model (Bieser et al., 2023).

The lack of efficient MeHg uptake mechanisms, combined with low dissolved MeHg concentrations, results in low MeHg bound to DOM in our model, while iHg is higher due to the efficient scavenging of iHg by DOM and the higher dissolved concentration of iHg than MeHg. Consequently, when HMA sponges feed on DOM, they accumulate very low MeHg concentrations, while, on the other hand, the efficient partitioning of iHg to DOM results in elevated iHg levels, even though iHg is not typically transferred via diet very efficiently.

Author Response

In addition to this, we added a mechanistic summary. Starting on line 668. Since the quantification of these model results is not really possible, adding a seperate section to highlight the proposed mechanism can really help to manuscript to translate the core message.

Suggested edit

Line 674

Mechanistic summary of the model results

There are two main conclusions that the model demonstrates, but it is important to clarify the proposed mechanisms. First, measurements show that sponges have elevated iHg and low MeHg levels, particularly HMA sponges. Both HMA and LMA sponges can consume DOM, although HMA sponges do so more efficiently. Additionally, measurements indicate that DOM contains relatively more iHg and less MeHg compared to phytoplankton. Consequently, our model suggests that an ecosystem with (HMA) sponges at its base can rely partially on DOM consumption rather than phytoplankton, resulting in elevated iHg and reduced MeHg at the base of the food web.

Second, we propose that because the biomagnification factor of iHg is very low, while it is extremely high for MeHg, a sponge dominated ecosystem with significantly lower MeHg concentrations at the base would show significant reduction in MeHg in higher trophic levels. While the 1D model used in this study is not suitable for reliable quantification of this effect, it is mechanistically intuitive that an ecosystem with filter feeders at its base with MeHg levels between 48–148 ng Hg gC^{-1} would lead to higher bioaccumulation in upper trophic levels than a system dominated by HMA sponges with low MeHg concentrations around 13 ng Hg gC^{-1}.

Naturally, these proposed mechanisms should be empirically validated. Therefore, the main contribution of this manuscript lies in proposing these mechanisms to explain why the model indicates that sponges could be significant for MeHg bioaccumulation, with the aim of stimulating further empirical studies to validate or refute the proposed processes.

Reviewer Comment

(7) For model studies, uncertainty analysis is necessary to explain the credibility of the model results. I recommend the supplement of uncertainty analysis.

Author Response

We thank the reviewer for this suggestion. The most uncertain factor in our model is the uptake efficiency of rDOM by HMA sponges. To address this, we performed a targeted sensitivity study varying rDOM uptake efficiency, and we propose including this analysis in the manuscript. This approach supports the robustness of our mechanistic conclusions while acknowledging the key source of uncertainty in the model.

Suggested edit

line 486
As discussed in the Methods section, the uptake of rDOM and its efficiency are poorly understood and we consequently used this parameter for model tuning. In the 2.5 gC rDOM m^{-2} scenario, we assumed an rDOM uptake efficiency of 0.1. To analyse how rDOM consumption and sponges influence MeHg bioaccumulation in benthic fish, we ran the model with rDOM uptake efficiencies of 1, 1/5, 1/10, 1/15, 1/30, 1/75, and 1/100. The results are shown in Fig. 4. Figure 4a shows that increasing rDOM uptake efficiency leads to an increase in the fraction of sponge biomass, while Fig. 4b shows that HMA sponges comprise a larger fraction of benthic biomass. At 10 gC m^{-2}, further sponge growth becomes limited in our model due to an assumed substrate limitation. As a result, the fraction of benthic biomass composed of HMA sponges increases rapidly until, at an uptake efficiency of approximately 0.25, sponges represent about 70–80% of the benthic biomass. Further increases in uptake efficiency up to 1 do not lead to additional increases in the HMA sponge fraction. Figure 4b also shows that as the fraction of benthic biomass composed of HMA sponges increases, MeHg bioaccumulation in benthic fish decreases. A visual clustering is observed once sponges exceed approximately 50% of the benthic biomass, suggesting a potential saturation effect whereby sponges dominate predator diets. However, this pattern is likely influenced by model structure and feeding parameterisations and may not reflect a general ecological mechanism, as natural systems typically include multiple specialised predators rather than a single generalist consumer.

Author Response

There are 2 final notable changes made to the paper that I wanted to highlight for clarity. We realised that in the 2.5gC rDOM scenario LMA sponges did not have a consistent biomass. Therefore we removed them Table 2 and the mention of the LMA sponges of that scenario in the results.

Finally we gave the introduction a light general restructuring.

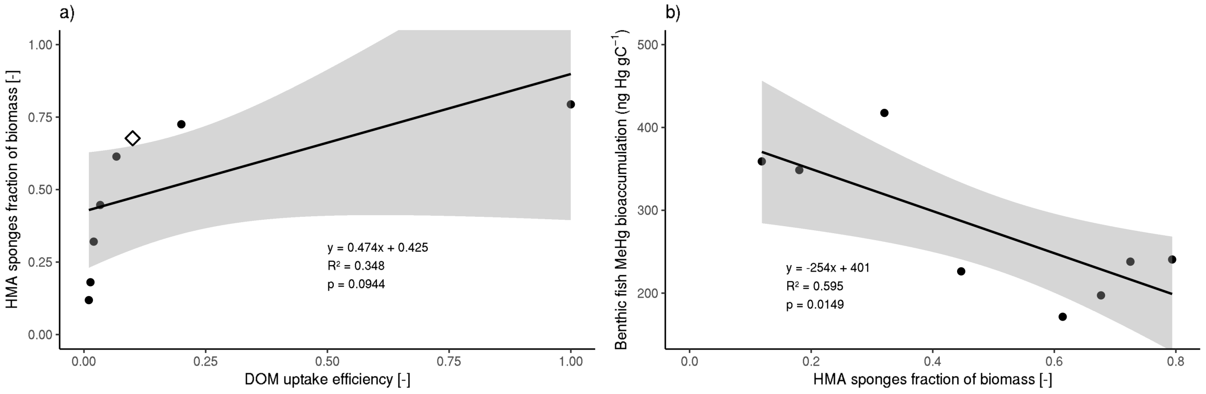

Figure 4: Sensitivity of the model results to the feeding efficiency of HMA sponges on rDOM. Figure a shows that as the feeding efficiency of rDOM increases, the fraction of HMA sponges among the primary benthic consumers (sponges, filter feeders, deposit feeders, and generalist feeders) also increases. The 0.10 rDOM uptake efficiency that we used in the model is marked as the larger point. Even with the relatively low efficiency of 0.10, as used in the model, HMA sponges remain a major component of the primary benthic consumer biomass. Figure b illustrates how this increase in the fraction of HMA sponges in the benthic community leads to a decrease in the bioaccumulation of MeHg in fish.

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Bioconcentration, bioaccumulation and biomagnification of mercury in plankton of the Mediterranean Sea. *Marine Pollution Bulletin*, *194*, 115439.

Answer to R2

Author Response

Dear Reviewer,
Thank you very much for reviewing the manuscript and for your invaluable input. Below, we have posted your comments and suggestions in grey boxes, with our responses highlighted in blue boxes and proposed manuscript changes shown in red boxes.
We hope you find our proposed revisions appropriate and agree with the suggested changes to the manuscript.

Reviewer Comment

The manuscript addresses a significant and persistent anomaly in marine ecotoxicology: the observation that marine sponges, particularly those with high microbial abundance, accumulate high concentrations of inorganic Hg while maintaining unexpectedly low levels of MeHg. The authors employ a coupled 1D hydrodynamic-biogeochemical model to test the hypothesis that trophic dilution via DOM consumption, rather than microbial mediated MeHg demethylation, drives these patterns. Furthermore, the study posits a potentially massive ecosystem service, suggesting that sponge grounds could reduce MeHg bioaccumulation in benthic fish by up to 45%. The overall manuscript is well organized, and a minor revision is needed. My specific comments are as below:

Reviewer Comment

Title: MeHg demethylation

Author Response

We updated the title as below:

Suggested edit

DOM consumption and demethylation of MeHg as potential drivers of low MeHg in Mediterranean Sea sponges and benthic fish: a modelling perspective

Reviewer Comment

Abstract: The second sentence is too long. The complex role of sponges and their significance should be more clearly emphasized.

Reviewer Comment

Line 6: demethylation of MeHg

Reviewer Comment

Line 11-12: This conclusion is overly speculative and requires additional supporting evidence.

Author Response

We updated the abstract as posted below to the take above 3 points into account. We suggest to rewrite the first 3 sentences to explain why we think sponges might play an important role in MeHg bioaccumulation. Additionally, we suggest we remove the statement about sulfated polysacherides from the abstract. It is an interesting point for the discussion indeed but lacks the supporting evidence to be placed in the abstract.

Suggested edit

abstract

Methylmercury (MeHg) is a bioaccumulative neurotoxin that poses a risk to human health through seafood consumption. Sponges have unique mercury (Hg) profiles. Measurements show an unusually high inorganic Hg (iHg) content in Low Microbial Abundance (LMA) sponges and an even higher iHg content in High Microbial Abundance (HMA) sponges, while MeHg concentrations remain low, particularly in HMA sponges. Combined with the recently improved understanding of the important ecological role of sponges as a food source for other biota, suggests their low MeHg content may influence MeHg transfer within benthic food webs. In this study, we used a 1D water-column model to investigate the bioaccumulation of MeHg in sponges. It has been hypothesized that the low MeHg content in HMA sponges may result from active MeHg demethylation. Our model results indicate that the consumption of dissolved organic matter (DOM) can already explain the low observed MeHg content in LMA sponges, and higher DOM consumption in HMA sponges can account for the even lower MeHg levels in HMA species. Alternatively, if MeHg demethylation occurs, a low rate of 1% per day could explain the differences between LMA and HMA sponges. Although DOM consumption increases iHg bioaccumulation in both sponge types, it does not explain the extremely high iHg concentrations observed. Finally, our model suggests that HMA sponges could potentially reduce MeHg concentrations in benthic fish by up to 45% when they dominate at the base of the food web. These findings highlight the potentially important role of sponges in Hg cycling and indicate that sponge-dominated systems could help reduce MeHg accumulation in benthic food webs.

Reviewer Comment

Lines 17-24: Links between sponges Hg and fish Hg are needed here.

Author Response

We added the following statement to the early introduction to clarify. We also give the introduction a mild restructuring to introduce sponges and their role in bioaccumulation earlier.

Suggested edit

Line 37 Since sponges are actively consumed by higher trophic levels and can dominate benthic biomass (Mortimer et al., 2021), unique MeHg accumulation patterns in sponges compared to other megabenthos could influence seafood contamination levels.

Reviewer Comment

Line 36: ?

Author Response

Apology that was a reference mistake which we overlooked. Corrected it to (Hao et al., 2022).

Reviewer Comment

Lines 33-43: This section is overly general and would benefit from greater conciseness.

Author Response

We would suggest to shorten and rewrite that section as below.

Suggested edit

Line 28
The primary pathway of MeHg bioaccumulation in aquatic ecosystems is direct uptake from the water column via respiration, diffusion, or ingestion. When this uptake results in organism concentrations exceeding those in the surrounding water, the process is termed bioconcentration. This occurs because MeHg binds strongly to organic matter, particularly thiol (-SH) groups in proteins Hao2022, increasing internal concentrations by 10^5–10^6-fold relative to water Lee2016. Bioconcentration is surface-area dependent and thus especially efficient in small organisms, making it critical at the base of the food web Mason1995. Efficient trophic transfer of bioconcentrated MeHg results in increasing concentrations with trophic position, a process known as biomagnification. This typically increases MeHg bioaccumulation 3–10-fold per trophic level Mason1996UptakeDiatom,Lavoie2013. This drives high MeHg levels in top predators, including human-consumed seafood. This means that the MeHg concentration at the base of the food web strongly controls bioaccumulation in higher trophic levels, making processes at the base of the food web critical for understanding ecosystem-wide MeHg dynamics. Since sponges are actively consumed by higher trophic levels and can dominate benthic biomass Mortimer2012, unique MeHg accumulation patterns in sponges, compared to other megabenthos, could influence seafood contamination levels.

Reviewer Comment

Lines 45-48: In the case of inorganic mercury (iHg), iHg-DOM binding determines the bioavailability of iHg for methylation.

Author Response

We rewritten the statement at line 56 to include that.

Suggested edit

Line 56

Like phytoplankton, DOM can also bind Hg, but how DOM interacts with Hg depends on several factors, including the source of DOM. Marine DOM enhances phytoplankton MeHg uptake by facilitating active transport through membrane channels Garcia2024,Schartrup2015, whereas terrestrial DOM inhibits the uptake of MeHg by biota due to stronger thiol binding Seelen2023. DOM also binds inorganic Hg (iHg), influencing its speciation and bioavailability for microbial methylation Graham2012. Since sponges can consume DOM, and DOM has different Hg binding patterns from phytoplankton, it raises the question of whether DOM consumption in sponges would consequently have different Hg bioaccumulation patterns compared to phytoplankton consuming benthos.

Reviewer Comment

Section2:In this section, the role of sponges in Hg cycling and MeHg accumulation in biota should be clearly highlighted. This is important and helps readers understand the significance of this study.

Author Response

We suggest to add the following addition to the current section 1.2 (starting at line 96). This helps highlight why we think the unique bioaccumulation patterns of sponges are significant and should be studied.

Suggested edit

Line 94
Most ecosystems rely on phytoplankton as the base of the food web, meaning that MeHg bioaccumulation can often be estimated from trophic level and phytoplankton MeHg concentrations. Sponge-dominated systems differ in that sponges can efficiently utilize DOM as a food source and exhibit extremely low MeHg concentrations compared to other megabenthos (Orani et al., 2020). This is important because the main predictor of MeHg concentrations in high trophic levels is the MeHg concentration at the base of the food web and the trophic level itself (Lavoie et al., 2013; Wu et al., 2019). Because sponges can form the majority of the benthic biomass in sponge reefs and are commonly predated upon, the MeHg content of sponges is likely directly linked to the MeHg content of higher trophic level animals, although this relationship remains understudied. We therefore hypothesize that the low MeHg concentrations in sponges lead to reduced MeHg bioaccumulation in high trophic level animals inhabiting sponge grounds compared to animals of similar trophic position in phytoplankton-based ecosystems.

Reviewer Comment

Section 1.3: Why DOM consumption can result in low MeHg concentrations?

Author Response

We agree that this is underexplained. We updated the sentence at line 79 to clarify that.

Suggested edit

Line 79

An alternative proposal for the low MeHg concentration in HMA sponges is that it is low due to the consumption of DOM. This is suggested in Amptmeijer et al., 2025, which presents a modeling study examining how the feeding strategy influences iHg and MeHg dynamics. In this model, the MeHg partitioning to DOM, which is based on the Mercy V2.0 model, results in lower MeHg concentration in DOM compared to phytoplankton. This results in DOM consuming suspension feeders, such as sponges, having less MeHg bioaccumulation than other megabenthos such as filter feeders.

Author Response

Additionally we suggest to add this to section to the discussion

Suggested edit

Line 511

Mechanistic explanation for the special role of DOM in iHg and MeHg bioaccumulation

The difference in bioaccumulation of iHg and MeHg highlights Hg as a unique pollutant. Certain biological pathways, such as the direct absorption of MeHg via membrane channels in phytoplankton, enable highly efficient MeHg bioaccumulation. As a result, MeHg concentrations in biota can exceed iHg concentrations, even in primary producers, despite the fact that dissolved iHg is generally more abundant than MeHg. In DOM, which consists primarily of dead organic particles, these preferential uptake pathways are absent, and DOM binds iHg and MeHg only through scavenging. The composition of DOM strongly influences its binding capacity: thiol-rich fractions of terrestrial DOM efficiently bind to MeHg (Seelen et al., 2023), while marine DOM fractions show a higher affinity for iHg (Tesán Onrubia et al., 2020), which underpins the partitioning behavior used in the MERCY V2.0 model (Bieser et al., 2023).

The lack of efficient MeHg uptake mechanisms, combined with low dissolved MeHg concentrations, results in low MeHg bound to DOM in our model, while iHg is higher due to the efficient scavenging of iHg by DOM and the higher dissolved concentration of iHg compared to MeHg. Consequently, when HMA sponges feed on DOM, they accumulate very low MeHg concentrations, whereas the efficient partitioning of iHg to DOM results in elevated iHg levels, even though iHg is not typically transferred via diet very efficiently.

Reviewer Comment

Lines 567-570: Yes, The validation of the model relies on a limited sample sizes (n=4 for HMA and n=6 for LMA sponges). The use of Kolmogorov-Smirnov (KS) tests on such sparse data provides a misleading sense of statistical robustness, as the test lacks the power to reject the null hypothesis, thereby creating a "false positive" agreement between model and observation. The author should strengthen the discussion by explicitly addressing how the limited sample size may influence the validity and generalizability of the findings, rather than simply noting the limitation.

Author Response

Thank you for this excellent suggestions. We suggest to rewrite the section at line 321 to the text as below to better explains how the limited sample size affects the results.

Suggested edit

Line 339
There is a large difference in sample sizes, with 3,652 model data points compared to only 4 (HMA) and 6 (LMA) observations. This imbalance reduces the power of the KS and Wilcoxon tests, making them especially susceptible to false-negative outcomes. This means that high p-values cannot confirm model fit, whereas low p-values (<0.05) are more reliable indicators of a mismatch between the model and observations.
This limitation is particularly relevant for the Kolmogorov–Smirnov test, as it evaluates the distribution. With only 4 and 6 data points, the observational distribution cannot be robustly defined, but significantly low (<0.05) p-values still strongly indicate a mismatch between the modeled distribution and the limited observations.
Therefore, these metrics are mainly used to compare which setup performs better relative to other setups and to flag poor-performing configurations. However, they cannot be used to fully determine whether the model simulations are in agreement with observations due to the limited number of observations.

Author Response

And we suggest to expand the statement at line 567 to further mention how more data can help improve the model.

Suggested edit

Line 623
Beyond the limitations of the rDOM implementation, several major limitations affect the model. The most important is the low data availability. Our conclusions rely on a single study of MeHg and iHg bioaccumulation in Mediterranean sponges, with small sample sizes ($n = 4$ for HMA and $n = 6$ for LMA sponges). While the model–data comparison allows identification of clear mismatches between the model and observations, the limited number of observations prevents reliable validation of simulated Hg bioaccumulation patterns. Therefore, the agreement between model simulations and observations should be interpreted with care.
In addition, key processes remain poorly mechanistically understood. The mechanisms and rates of (r)DOM consumption by sponges, the role of sponges in ecosystem-level Hg bioaccumulation, and the functional differences between LMA and HMA sponges are not fully understood. These knowledge gaps limit process-based parameterization and

increase structural uncertainty in the model.
Because of this, targeted empirical studies on Hg bioaccumulation in sponges, including controlled experiments focused on the bioaccumulation pathways that were flagged as potentially significant in this model, such as the role of the uptake of DOM by sponges on Hg bioaccumulation and the consumption and trophic transfer of Hg of sponges by predators, could substantially improve model development by enabling more robust validation.

Author Response

There are 3 final notable changes made to the paper that I wanted to highlight for clarity. I realised that in the 2.5gC rDOM scenario LMA sponges did not have a consistent biomass. Therefore I removed them Table 2 and the mention of the LMA sponges of that scenario in the results.

Additionally, there was an improvement in the parameterization of MeHg biaoccumulation in higher trophic levels which incorporated in the newer version of the model. It does not influence the carbon cycling at all but results in netto higher levels of MeHg bioaccumulation in higher trophic levels of fish. The core proposed mechanism of HMA sponges reducing fish bioaccumultion is consistent under this new parameterization (the result is new 53% rather than 45%. The new evaluation is described in detail in line 394.)

Finally we gave the introduction a light general restructuring.

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