Your response letter should list all review comments along with either an explicit description of what changes you have made in response (refer to line numbers in the tracked-changes document whenever possible) or convincing arguments why you disagree with a comment.  
  
Please make sure to not only answer questions in the response letter but also make appropriate changes in the manuscript text, since other readers would likely have the same questions.  
  
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Contributing Editor comments:  
  
I have received three reviews of your manuscript. As you will see from the comments made by the reviewers, there are some serious concerns about your manuscript, which may require major revisions. I agree with the reviewers' assessment, but because of the potential interest of your study, I am recommending major revision. Specifically, this paper was unclear in many places, which made it difficult to get through. There are some issues with the English language, and the ms lacks structure in the Intro and Discussion that develops the general need for this type of work beyond just monitoring mussels in the particular locations studied. In addition, there are methodological aspects that require further clarification. A decision on the acceptability of your manuscript will most likely be made after another round of review.

Dear Editor!

Thank you very much for the assessment of our work and for inviting the reviewers who provided valuable advice. We have substantially revised our manuscript. In order to address the reviewers’ comments, we had to add some new data and perform some new analyses. To compensate for these additions, we have shortened the other text, so that the new manuscript has approximately the same length as the first version.

Below we provide the responses to the reviewers. References in parentheses are to lines in the text with labeled changes.

Reviewer 1  
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Major concern.  
  
For the insights gained from the manuscript I feel the reader must do too much work to make sense of the outcomes. To make things worse, there are several incorrect references to figures etc (outlined below, in minor concerns below).

Thank you for pointing this out. We have corrected the references to figures. References in parentheses are to lines in the **pdf-file with labeled changes**.

Several of the parameters are not accurate measurements of environmental factors:  
- Salinity was measured at low tide, and may not represent the salinity experienced by intertidal mussels. (The authors acknowledge this, but do not have a solution.)

It is relevant that Ptros (taxonomic structure) varies with salinity at low tide (as well as with distance to the nearest river). These are our own results, and we are confident that they are valid. It would be indeed interesting to see how Ptros is affected by salinity at high tide, and we mentioned this in the text (L 590-592), but this is not crucial for the purposes of this study.

- Because 80% of MT have the dark, prismatic strip, up to 20% of MT may be misidentified.

This is a misunderstanding. You are right that it is impossible to accurately assign individuals to species, because the marker is semi-diagnostic. However, we do not perform individual assignments; we determine the proportion of the species in the samples using a robust procedure from Khaitov et al. 2021.

Several of the results may impact the interpretation of the study, but their relevance is lost because their context is left for the reader to interpret, e.g. Lines 287-306 : many suigniuficannt patterns are listed, but their relevance is left open.

We have rewritten the Discussion and hope that our interpretations of the patterns have become clearer.

Minor concerns  
Line 58 “In THE North Atlantic”

Corrected (L68)  
  
Although mussels were taken from the “fucoid belt to minimize differences in depth” the fucoid belt could vary from location to location depending on wave exposure, salinity etc.

Thanks for the comment. We have removed the reference to the choice of the fucoid belt as a way to standardize depth from Materials and Methods. However, we would like to note that mussels occur from the upper littoral down to a depth of 30 meters, and the variability of the depth of the fucoid belt is quite small as compared to this range.

Line 190 : The breakdown of the equation doesn’t make sense, the text states “where PT – proportion of T-morphotype.” Is the “-“ here supposed to be “=”.

Corrected (L224)

Line 270: Instead of “(Fig 1B)” it looks like it should be “(Fig 1C)”.

Corrected (L334)

Line 305: “Fig. 1 C, D” is mislabeled and should be “Fig. 1 D, E”.

Corrected (L381-382)

Also if PC2 explains only 20% of the variation in ME distribution, can it really be considered a “proxy”?

The transition from initial abundances to PC is a technical trick that allows us to avoid the problem of predictor collinearity. The principal components are just new coordinates that are characterized by the fraction of explained variance of the initial data. How much of the variance describes the PCs is not important for the aim of our analysis. What is important is that PCs are highly correlated with the abundance of T-morphotype (PC1) and E-morphotype (PC2), both on algae and on bottom. This means that we can accurately translate PC values into the abundance of mussels of a particular morphotype (as illustrated in Fig. 3 B, C).

The Introduction and Discussion are way too long.

We tried to keep the Introduction and Discussion as short as possible considering that we had to take into account the recommendations of the other reviewers.

Line 470: How do the authors know that hybrids are rare in the Kola zone? Is there a citation they can provide?

We have provided the references (L577-578).  
  
Line 721: the arrows in Fig 1 are very hard to see when printed in black, white and gray.

We apologize for this design flaw. It has been corrected.  
  
Line 752: Not clear where the solid lines are and what they delineate. There are solid lines at 0.50 and 0.25/0.75 but these are just grid markers…

We apologize for this design flaw. It has been corrected.

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Reviewer 2 report:  
  
In this paper, the authors use joint species distribution models to evaluate coexistence of two species of blue mussels. The dataset they have is impressive. The paper could use substantial work to improve clarity and to broaden out the topic to more general ecological principles.  
  
General comments  
  
The introduction is extremely long and unclear. The background information could be much more direct and succinct. For example, Table 1 summarizing the potential drivers that are considered in this paper could be referenced in the introduction; it wasn’t until this table was referenced in line 196 that I was able to understand the main categories relevant to this study. I think a statement that several factors (Table 1) have been hypothesized to drive distributions would suffice, and the authors could eliminate a lot of the text describing each individual driver. In Table 1, adding a literature reference or two identifying a previous study that looked at each driver would help organize the parameters tested in the context of past research. There is also a tone in the Introduction that a lot of separate drivers have been looked at in the past, but there’s no consensus, or there’s not a single driver that comes out as being more important. Yet, the findings of this paper are that many drivers are important (lines 325). So the Introduction sets up a false expectation that the single most important driver is going to be identified because of the extensive dataset used here, but it does not deliver on this expectation. The authors should also be made clear from the start (probably in the Introduction itself) that the relative influence of the different drivers is not going to be identified in this paper (as stated in line 484-485).

We are sincerely grateful for your advice that allowed us to improve both illustrations and the text.

Following your instructions, we have rewritten the Introduction shortening it wherever possible. However, we also had to expand it at some places at the request of the other reviewers. References in parentheses in our answers are to lines in the **pdf-file with labeled changes**.

To the best of our knowledge, the hypothesis that there is no single major predictor explaining M. edulis and M. trossulus species distribution in any contact zone has never been formally tested before our study.

Table 1 summarizes the predictors from our study; we could not fit into it the results of published studies.

The statement that the SDM we used does not directly assess the relative or absolute significance of factors has been moved to Materials and Methods (L270-274).

The results would benefit from some summary statements to help a reader know what the main findings were. For example, in line 273, what does this mean? That all parameters were thus retained in further analyses? Or the paragraph starting with line 275 could include a more general take home point such as: Substrate type substantially influenced distributions of Ptros. The importance of the curvilinear finding stated in line 289 is not clearly summarized.

All results of the modeling are presented in standard form (Table 2 and Fig. 2). We hope the statistical conclusions are articulated more clearly in the new version of the Results.

It is not clear how some decisions for analysis were made. For example, in line 274 all correlations are stated as being low, but the thresholds for what counts as low vs high are never defined (or citations included to justify those decisions).

When judging the multicollinearity of predictors, we focused on the variance inflation factor (VIF). This metric not only takes into account pairwise relationships, like Pearson correlation, but also estimates the dependence of a given predictor on the set of all predictors included in the model. Using VIF, we found no collinearity between predictors. Pearson correlation coefficients between continuous predictors are given only for the general characterization of their relationships. In the light of the above, low correlation coefficients could be expected.

The use of quotations is odd (especially in lines 423-440). I’d suggest just stating what you mean, rather than using quotations. Quotations imply (whether intentionally or not) that you’re using some proxy rather than saying directly what the finding is.

Thank you for the advice. Corrected.

Line by line comments  
  
Line 3: suggest making mussel singular rather than plural in the running head

Corrected. Now “Mussel species niche divergence”   
  
Line 20: suggest taking out the “no conclusion has been made” because it’s likely that individual papers have in fact drawn conclusions, even if there is no general consensus.

The sentence has been rephrased (L 20-21).

Line 29: can the authors provide some more information about what they conclude about usefulness of this outside of the White Sea, instead of saying that they are going to do that, just say what they found

The sentence has been rephrased (L 30-31).  
  
Line 33-41: The value of using SDMs to address ecological or conservation questions would help this paper broaden out to a wider audience. Why do we need to know which environmental parameters related to species occurrence more generally, and why do we need to know about species diversity more broadly?

Thank you for this valuable piece of advice. We explain it referring to the experience of studying invasive species (also following suggestions of another Reviewer) (L 35-43).

Line 42: remove quotations and the valuation statement and just say they are applied to morphologically distinct species

Corrected ( L 46)

Line 43: I’m not sure what involved means. Does that mean sampled? And level of ease is relative…most monitoring programs are actually quite difficult!

We have rephrased this sentence to make it clearer. Now: … “which are distinguished in routine biodiversity assessment studies” (L 47)

Line 46: citations about coexistence are needed here

The citations have been provided (L 48)  
  
Line 54: can more information be provided here, how many species exist, typically how many coexist

We have written six species and cited references to papers with details (L 63-66). To note, in Western Norway, mixed settlements may contain purebreds of M. edulis, M. trossulus and M. galloprovincialis as well as all the possible hybrids between them (Simon et al. 2020).

Line 59: can you provide the correlates specifically? Is salinity included in this, since it becomes important later on?

Temperature correlates are ice extent and primary production. This is now explained in the text (L 69-71)

Line 84: suggest adding “a” before the word mosaic

We have rephrased this sentence (L 96)

Line 100: definite conclusions in ecology are rare and maybe shouldn’t be expected in the first place…suggest rewording

We have removed this text to avoid confusion (L 114-117)   
  
Line 108: suggest replacing “is” with “may be” because you’re trying to suggest that using cryptic diversity might help understand these patterns better, but you don’t know for sure

We have reworked the paragraph (L 126-143).  
  
Line 119: not sure the see also above is needed, or what it specifically refers to

We have reworked the paragraph (L 126-143).

Line 126: can more information be provided on where the Ptros name comes from? Is it an acronym? I’m not able to figure out where that nomenclature is derived from. It’s even difficult to follow in the methods (line 188)

Ptros is the proportion of M. trossulus in each sample (Khaitov et al., 2021). This term and the reference were introduced in the Materials and Methods section (L 220)

Line 120-128: this reads like methods and breaks up the flow of the introduction

We have removed the technical details (L144-151)

Line 189: is this a minus sign after the PT? If not, I’d suggest replacing the dash with the word “is”

Corrected (L 224)

Line 267: the authors might mean variable here rather than mosaic

Corrected (L332)  
  
Line 273: what would be considered high in this correlation analysis? It would be worth adding thresholds to the methods section to demonstrate the level at which correlation was considered happening and subsequently some parameters thrown out.

The correlations are only needed to assess the relationship between the predictors, i.e., to assess their collinearity. When judging the multicollinearity of predictors, we focused on the variance inflation factor (VIF). This metric not only takes into account pairwise relationships, like Pearson correlation, but also estimates the dependence of a given predictor on the set of all predictors included in the model. Using VIF, we found no collinearity between predictors. Pearson correlation coefficients between continuous predictors are given only for the general characterization of their relationships. In the light of the above, low correlation coefficients could be expected. We present the correlations as an additional source of information to support our assertion about the low correlation of the predictors included in the model.

Line 288: I think In contrast would be better here than on the contrary

Corrected (L355)

Line 295: I think In addition would be better here than besides

Corrected (L363)

Line 317: “fit well” might be better here than “good”

Corrected (L395)

Line 320: The plots for Tyuva look very poorly fit. However, I think the authors are suggesting here that they fit fairly well. Could some more context be provided? What would be considered a poor fit? All of those points are far off the 1:1 line, so it’s not clear how the data are being evaluated here. There is some discussion of this in lines 409-420, but the tone of that paragraph in the discussion doesn’t match how the results are reported here.

AUC greater than or equal to 0.7 is considered acceptable discrimination (Hosmer et al., 2013). However, you may be right, and we no longer insist that Model 1 works well in the Barents Sea. We have rewritten the Discussion to reflect it. Thank goodness it works well in the White Sea.

Line 324: I think the authors mean dataset instead of material

We have rewritten the paragraph (L400-409)

Line 330-335: Instead of saying what you’re going to do in the discussion, I'd suggest stating directly what you found. This first paragraph would benefit from being rewritten to reiterate the findings just presented in the results and then a statement or two about the importance of this work more broadly.

We have shortened the introductory paragraphs of the Discussion according to your recommendations (L410 - 415).

Line 351: Needs some clarification. Which important factors? If salinity is the important factor, I don’t quite follow how it can be masked. If there’s something else masking it, isn’t that other factor the important factor then?

We have rewritten the sentence. We hope it is now clear what factors we are talking about (L432-433).

Line 351-352: provide a reasonable range for each location to emphasize the point being made

We have rewritten this paragraph, and the range of salinity in the two seas is no longer discussed (L426-438).

Line 359: Needs some clarification. Opportunistic in what sense? In feeding? In colonization? Perhaps the authors mean generalist rather than opportunistic?

We have rewritten this paragraph, and opportunism is no longer discussed. (L444-445)

Line 478-479: What are the predictors that were ignored. These should be included in Table 1 as a separate category to accurately represent the possible drivers, distinguished from the subset of drivers the authors chose to study.

The predictors unaccounted for in our study were depth, predators and temperature. We have rewritten the sentence and hope it is clearer now (L588-589). A meta-analysis of the literature would be cumbersome, and would not fit into a table from Materials and methods.

Line 486: This topic deserves broadening out. Multiple stressors, context dependency, etc. in the ecological literature more generally makes this point.

We would like to follow this suggestion, but the Editor and other reviewers say that the Discussion is too long as it is.

Table 2 doesn’t define the ref abbreviation

Corrected (L827)  
  
Line 715: suggest adding “red” box since there’s also a black box outlining the inset

The description of the box is given in the subscript section of Figure 1 A.

Figure 1: I’d suggest stating that white is ocean and grey is land. The anchors and asterisk labeling is confusing. As written it sounds like there are two separate ports identified, one by an anchor and one by an asterisk. I think the wording just needs to be adjusted to something like “Anchors with names mark ports. Asterisks identify whether the port is currently abandoned.” I’d suggest changing the color of the arrows in (c) since the yellow matches the legend. Can you also add numbers within the arrows to match to numbers in Table S1? Please add units for the metrics fetch and salinity.

We have modified Figure 1 following your instructions. We believe that numbering the river mouths in the figure would make it overcomplicated, and the other information would be difficult to understand. The coordinates of the river mouths are given in ESM.

Line 722: I think it should read by the GAM fit

We have completely redesigned this Figure and its caption.

Line 725: wiggling sounds very informal. Is there a more formal way to describe why the dotted lines are needed and what they show?

We have changed the caption and removed “wiggling”.

Line 727: I might be missing it, but I don’t see any information here on substrate (bottom vs algae)

This information is presented in the new version of the figure (L852-859)  
  
Figure 3: I don’t think the grey shading or bolding in the insets of panels b and c are defined.

We have provided explanations in the caption of the figure (L863 – 870).

Line 734: It would help to have Diff somewhere on the panel itself, maybe as an axis title

This could be confusing, since all three panels of the figure concern Diff.

Line 735: I don’t see a D panel, I think this might be a typo.

This was a indeed typo. We have completely redone this drawing and corrected it.

Figure S1: can statistics be provided here (r values?)

Statistics are provided in the main text: VIF as a measure of predictors’ collinearity.

Table S2: what is the red text?

It was used to mark samples taken from Katolikova et al., 2016. Using color was in fact unnecessary; thank you for noticing it. The text is now in black.

Table S3: the heading/table legend is cut off.

We have checked: the heading is present.

Table S4: the heading/table legend is cut off.  
  
We have checked: the heading is present.

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Reviewer 3 report:  
  
General comments  
In the context of increasing invasions by alien species, it is crucial to better understand how these species overlap with the ecological niches of endemic species, especially in the case of cryptic species. This paper investigates the ecological niche differentiation between two conspecific mussel species, Mytilus edulis (ME) and Mytilus trossulus (MT), in sympatry within a so-called contact zone using a Generalized Additive Model (GAM) approach. By applying a relative proportion index (Ptros) based on mussel morphotype abundance, the authors find that M. edulis (ME) and M. trossulus (MT) dominate in distinct environmental conditions. The authors also explore potential competition mechanisms in structuring the intertidal community by investigating whether the segregation pattern across substrate types is dependent on species abundance.  
The study was conducted rigorously well illustrated, but some methodological aspects require further clarification. A key point to address is why the authors chose to focus on the relative proportions of MT species, which provide less informative insights compared to directly analyzing morphotype abundance. For instance, examining only proportions does not indicate whether mussels of each morphotype are more abundant in certain environments relative to others, which may offer more insights on species niche differences. Additionally, in cases of low abundance, it cannot be excluded that the dominance of some mussel morphotypes may occur by chance. As a suggestion, developing morphotype/species-specific SDMs based on abundance (either with or without including the abundance of other species as an independent variable to account for potential competition effects) could provide a clearer comparison of ecological niches. The use of species abundance would also enable the use of other niche comparison methods, such as those proposed by Broennimann et al. (2012) and Guisan et al. (2014). Otherwise, the reason for using Ptros to explore niche divergence needs to be explicitly specify.  
Broennimann, O., Fitzpatrick, M. C., Pearman, P. B., Petitpierre, B., Pellissier, L., Yoccoz, N. G., et al. (2012). Measuring ecological niche overlap from occurrence and spatial environmental data: Measuring niche overlap. Global Ecology and Biogeography, 21(4), 481–497. https://doi.org/10.1111/j.1466-8238.2011.00698.x  
Guisan, A., Petitpierre, B., Broennimann, O., Daehler, C., & Kueffer, C. (2014). Unifying niche shift studies: insights from biological invasions. Trends in Ecology & Evolution, 29(5), 260–269. https://doi.org/10.1016/j.tree.2014.02.009

We are very grateful to you for your detailed and friendly review. Bellow we provide answers to your comments. References in parentheses in our answers are to lines in the **pdf-file with labeled changes**.

We focused on species proportion (Ptros) rather than morphotype abundance A) in order to make the analysis more simple and B) because the samples were collected in different ways from different substrates. But we were happy to supplement the study by morphotype abundance data analysis (Model 2).

Another point that requires clarification, as highlighted by the authors, is the potential presence of confounding variables in the models. While collinearity between continuous variables and multicollinearity have been addressed, it would be useful to examine any potential dependencies between categorical and continuous variables.

Using the variance inflation factor (VIF, calculated by function vif() from R-package 'car') as a measure of collinearity, we estimated potential collinearity for both continuous and discrete predictors. All VIF values were within the acceptable range (less than 2).

Additionally, although the authors confirm the structural impact of water temperature on mussel species distribution, the absence of this variable from the study is regrettable, especially given that no justification for its exclusion is provided.

It is known that temperature affects species distribution at the scale of thousands of kilometers but no one has checked whether this is so at a more local scale, like in our study (the maximum distance between the sites was 100 km). Unfortunately, we have not monitored temperature in the study sites and have nowhere to get it from.

While the paper is generally well-written, it contains numerous imprecisions and stylistic issues, particularly in the introduction and discussion sections, which hinder a clear understanding of the proposal (see specific comments below). For example, the introduction is somewhat confusing and should be revised to improve clarity and conciseness. Specifically, the first few paragraphs discussing jSDM in the context of cryptic species could be simplified, as this is not the central focus of your work.

We have rewritten the Introduction and Discussion following your suggestions and those of other reviewers.

Section-specific comments and suggestions

Abstract  
-line 24. The term "normal" is not appropriate. It would be better to refer to values that are consistent with the averages found in the White Sea.

Corrected (L24) and elsewhere

Introduction  
-line 38-39: jSDM is only a particular case of multispecies modelling framework which also include the correlative analysis of residuals. However, there is different way to produce community models (for instance see (Caradima et al. 2019)  
Caradima, B., Schuwirth, N., & Reichert, P. (2019). From individual to joint species distribution models: A comparison of model complexity and predictive performance. Journal of Biogeography, 46(10), 2260–2274. https://doi.org/10.1111/jbi.13668

Thanks for the useful reference! Added (L43)

-line 43: The term "Good species" is too imprecise. Please modify it

Morphologically distinct species (L46)

-line 64: "Dating back to the Pliocene" - Is there a reference for this claim?

Yes (L 76-77)

Line 85: "At the local scale" – Could you clarify what you mean by "local scale"? Are you referring to centimeters, meters, or hundreds of meters?

We have changed sentence to clarify it. Now: “….from dozens of kilometers to dozens of centimeters” (L97).

-line 93: "On the bottom" – Do you mean "bare bottom"? Please clarify this term here and consistently throughout the paper.

We have rephased the sentence, which now reads “directly on the bottom substrates such as mud, sand, stones and gravel” (L109-110). We hope it is clear now. We would rather not use the expression “bare bottom” because of its obscene connotations, though we know that it does occur in marine science, particularly in works by Scandinavian authors. Besides, we have used the term “bottom substrate” in our previous studies.

-lines 102-103: This sentence is crucial for the paper's objective. It would be better placed earlier in the manuscript, when describing the known dependencies of ME and MT distributions across different basins.

We have followed your advice (see L119-121).

-lines 111-113: The meaning here is unclear. Since SDM approaches were successfully applied, as mentioned in the following sentence, please clarify what you are trying to convey.

We have reworked the paragraph (L126-143).

-line 129: space is lacking

We do not quite understand this comment. If you mean physical space, it seems irrelevant to the discussion of gradients.

Method  
-line 148: Please remove “ppt,” as it is no longer commonly used in scientific literature.

Corrected (L25) and elsewhere in the text.

-line 149: The term "normal salinity" is still confusing here and elsewhere. Please rephrase for clarity.

We have changed “normal salinity” to “average salinity in the White Sea” (L175) and elsewhere.  
  
-line 165: Did you control for the different years of sampling in your models? This aspect must be discussed at least. Additionally, it is unclear if all sampling sessions were conducted in the same season. Please clarify.

We pointed out that all samples were taken in summer (L193). Additionally, we checked for spatial and temporal patterns in the Model 1 residuals and did not find any significant pattern associated with the sampling year (L286-287).

-lines 171-174: The methodology and surface used to estimate the abundance of mussels on bare substrate (bottom samples) and on fucoid canopy were different. Is there any justification for this? What is the potential impact on abundance estimation?

Mussel settlements on fucoids (three-dimensional substrate) and on the bottom (flat substrate) are very different. Therefore, different techniques were used to quantify mussel abundance on different substrates. Differences in sampling techniques are not fundamentally important when using Ptros as the dependent variable. However, they make it difficult to compare abundance on algae and on the bottom. Because of these difficulties, we did not attempt to compare mussel abundance on the two substrates anywhere in our models. In particular, we excluded substrate as a predictor in Model 2 (added at your suggestion), in which mussel abundance was the dependent variable.

-lines 203-204: As the authors explained, the drivers of mussel community structure vary between spatial locations. To help readers better interpret the limitations of model transferability (i.e., the relatively poor performance in new environments), I suggest indicating the different samples associated with your training and testing datasets on the map (Fig. 1).

We feel that Figure 1 is already overcomplicated and do not want to complicate it further. In Appendix 2 we now provide a map (Figure S1) showing the location of the sampling sites in the testing data the from White Sea. The testing data from the Barents Sea are described in detail in the original study from which they were taken (Marchenko et al., 2023).

-line 195: Why didn’t you include variables describing temperature, given that it plays a structural role in mussel species distribution (lines 59, 118)? In my opinion, incorporating this fundamental parameter could improve overall model performance. If not included, you should provide a justification.

Unfortunately, we do not have the data on temperature, nor are there any reliable data in external sources (see also above).

-line 169: It is unclear if the bare bottom samples (bottom samples) were collected at the same depth (parallel to the seafloor) as the corresponding algal samples. If not, the distinction between algal and bottom categories may confound the effect of depth. Please clarify.

They were collected approximately at the same depth (L202)

-line 170: Is there a specific reason for using different frames for the “algal” and “bottom” samples?

Please see the explanation above.

-line 192: From which salinity values does the formula lead to false positive identifications? Please provide more details.

“However, as studies in the Barents Sea have shown, this equation may overestimate Ptros at higher salinities, e.g. up to 20% at salinity around 30 psu (Khaitov et al. 2021, Marchenko et al. 2023)” (L231-233)

-line 226: Technically, your approach is more aligned with a generalized additive mixed model (GAMM) since you included a random effect.

You are right! We have corrected the designation for Model 1, which is indeed GAMM. Model 2 and Model 3, however, are not, and they are referred to as GAM.

-line 234: Could you clarify the thresholds you used with VIF and Pearson’s r correlation to detect collinearity?

We have included the information about threshold values for VIF (VIF=3.5) (L 281-282). We have also pointed out (see above) that the correlations between the predictors are given only for general information about their relationships.

-line 257: It is unclear why you chose to test classification performance using AUC on binarized values instead of testing regression performance on Ptros values (as shown in Fig. 4) to assess model transferability. In my opinion, using performance metrics applied to your continuous predictions (predicted Ptros values) would provide a more accurate evaluation of your model transferability.

We have added Pearson correlations to Fig. 4 to give an additional possibility to compare observed and predicted Ptros values.

We chose to test classification performance using AUC on binarized values for the following reasons. Firstly, the samples from the Barents Sea were collected using different methods, and a complete match between the model prediction and the observed data could not be expected. Unfortunately, we have no other datasets from outside the White Sea except the Tyuva dataset. Secondly, we are trying to find out what species dominates the site. This is a is scientifically sound question. Thirdly, the Tyuva Inlet is small, and the predictors vary there in a narrow range (note the very close predictions in Figure 4). In such a situation, estimates of the predictive power of the model would be crude. Moreover, this complicates the application of metrics used in machine learning for continuous predictors. Finally, ROC analysis is acceptable in assessments of this kind, and many authors recommend it (references are provided, L326).

Result  
-line 266: This sentence would be more appropriate in the Materials and Methods section and should be relocated there.

We would rather leave it where it was because these are the results of the study.

-line 273: Based on the violin plot in S1, there appears to be a difference in salinity between small and large rivers. If this is the case, the estimated effect of salinity may at least partially reflect differences between river categories, and vice versa. Additionally, have you checked for any dependencies between your categorical variables (e.g., river size and port status) or between categorical and continuous variables (e.g., distance to port and port status)? Please verify.

Relationships between all predictors were controlled using VIF (see above).

-line 279: The formulation of this sentence could be improved for better readability. Are you referring to the absence of a clear spatial pattern?

We have rewritten the paragraph (L344-347)

-line 284: Please remove the unnecessary phrase “In our opinion.”

Corrected (L 350-351)  
  
-line 294: Replace the term “normal” with “moderate.”

Corrected (L361-362)

-line 297: This point has already been mentioned and is not necessary to repeat.

Corrected (L364-365)  
  
-lines 300-305: From a methodological point of view, I question the necessity of using PCA scores instead of the mean total abundance of ME and MT on both substrates, especially since the PCA axes seem to clearly describe the mean species abundance.

Assessing the dependence of Diff on PtrosSite, we could not directly operate with densities of morphotypes because they were collinear on different substrates (VIF >> 3). In such situations, PCA based on a predictor matrix is recommended, with further use of principal components as complex features that are known to be orthogonal, i.e. not collinear (Quinn, G. P., & Keough, M. J. (2002). Experimental design and data analysis for biologists. Cambridge university press. Chapter 6.1.11). We followed these recommendations.

Discussion  
-line 350: I agree with this point, but could you specify some relevant factors that were not considered in your study?

First of all, distance to ports (L433)

-lines 374-380: Alternatively, since Fucus distribution is strongly influenced by surf levels, it could also be argued that the effect of surf on mussel distribution operates indirectly through its impact on substrate availability.

This may be true. Unfortunately we did not control either abundance or species composition of fucoids. What we know is that they are ubiquitous in the study area (L188-190).

-line 407: You are correct. As a suggestion, it would be interesting, if feasible, to exclude subtidal data (sorted by algae group) to assess the transferability of your model under comparable shore height conditions.

This is exactly what we did when we analysed data from Tyuva littoral and sublittoral separately.

-line 416: Considering the possibility that the increase in Ptros could be attributed to the failure of the morphotype test under high salinity conditions ~30), could the high rate of false positive predictions be caused by the higher salinity observed in the Barents Sea?

No. We have added the explanation that Ptros for Tyuva was predicted either by direct genotyping or from morphotype frequencies using the formula derived for local populations existing under salinities higher than in the White Sea (Marchenko et al. 2023) (L250-252).

-line 496: This sentence appears to overstate the transferability performance of your model in the Barents Sea. While there is no universally accepted standard for interpreting AUC values, scores below 0.75 are often considered indicative of poor performance. Additionally, your performance plot shows that the comparison between observed and predicted Ptros does not reveal a clear relationship, further suggesting limited transferability. Please revise this sentence accordingly.

We have rewritten this part reinforcing doubts about the transferability of the model (L495-516).

-line 420: In the context of global warming, could variations in water temperature have influenced the observed Ptros? Since temperature was not included as a parameter in your model, might this explain some of the observed patterns?

Published data from 2004-2018 can be interpreted in this way (Marchenko et al. 2023), but we continue to monitor mussels in the Kola Bay and know that Ptros has grown there since that time despite rising temperatures.

-line 425: I am unsure if two functionally similar species necessarily imply a similarity in their fundamental niches, as suggested by your statement (“and therefore”). Please modify this assertion or provide a justification.

We have modified the sentence. Now: “… may inherently have overlapping fundamental ecological niches”. (L522-523).

-lines 427-440: This section is unclear. Are you proposing that, contrary to previous assumptions, the two species have conserved their fundamental niches across zones? Please revise and clarify this part for better readability.

We have reworked this section and hope it is clearer now (L523-538).

-lines 441-448: To support your argument, you could consult global occurrence databases (e.g., MT: https://obis.org/taxon/140482 and ME: https://obis.org/taxon/140480). These databases indicate differences in salinity affinity, with the global distribution showing that MT is typically found in lower salinity ranges (0–5) compared to ME.

This database reflects the state of knowledge 30 years ago, when research on cryptic mussel species was in its infancy. It does not report MT from Greenland, Scotland, Hudson Bay, Norway, and the White Sea. This makes it useless, unfortunately.

-lines 449-450: The phrases “no non-random relationship” and “significant predictors” seem circular. Please rephrase for clarity.

Done (L547-551).

-lines 453-455: This sentence is overly complex and difficult to follow, which may hinder the reader’s understanding. It also appears to contradict your intended argument. Please clarify and simplify it.

Done (L553-558).

-lines 459-461: This point would be more appropriately placed in a conclusive section. Please consider moving it there?

Thank you for this suggestion. We have moved this point to the end of the Discussion.

-lines 466-467: Why does the morphotype test not provide a reliable estimation of species abundance in your framework? What about the values shown in Table S3? Please clarify.

The text states that the morphotype test cannot account for hybrids, which may be abundant in blue mussel contact zones (but not in the White Sea). In Table S3 we provide the abundance of morphotypes.

-lines 478-479: As a suggestion, have you considered incorporating proxies of site productivity, such as chlorophyll-a or, to a lesser extent, turbidity? These proxies, which are available at relatively fine resolutions, are known to significantly influence the distribution of filter-feeding species. Additionally, what about including temperature?

You are right but for our study area these proxies are unavailable at the required resolution.

-line 482: It is recommended to use the more commonly recognized terms “high tide” and “low tide” for better clarity.

Done. Thank you for your advice.

-line 484: As an informative comment, although it depends on the sampling strategy and data quality, methods like random forest variable importance could be used to rank the most influential factors.

Thank you for your advice. To note, additional tools for identifying significant factors might also be provided by new methods of SDM construction such as "sdm" R-package. We hope to use these methods in the analysis of data collected from other MT-ME contact zones.

-line 499: To my knowledge, including biotic effects in SDM models is currently more challenging than incorporating other important abiotic factors not considered in this study, such as water temperature, turbidity, or better control for depth.

We have excluded the mention of biotic components (L605-620)

-line 504: Please remove the additional space in this line.

Done