I. General comments

This article aims to delineate feeding habits of meiobenthic organisms (copepods and nematods) from Atlantic *Zostera noltii* meadows. Using C and N stable isotope ratios, and through application of a bayesian mixing model, authors highlight considerable trophic diversity among invertebrate genera and/or species. More importantly, their findings clearly show that caution should be taken when assigning a feeding type to an organism using morphological and/or behavioral traits. Stable isotopes indeed revealed that animals belonging to the same "trophic groups" sometimes exploited different resources.

The place of meiobenthos in seagrass-associated food webs is often overlooked, and these organisms received very little attention compared to other functional groups and/or communities (e.g. macrofauna). The topic of the study is therefore quite novel, and definitely deserves attention. Use of stable isotope ratios and mixing models to describe trophic relationships is a robust, time-tested approach. One could argue that sample replication is somewhat low. However, this can be easily explained by the important number of individuals that had to be pooled for a single analysis (sometimes up to 300) and therefore the tremendous amount of work that has been put in sample preparation. Moreover, authors always have a critical eye on their own data, and refrain from drawing speculative conclusions. Overall, the methods seem sound and suited to the scientific question. Nevertheless, I do have some concerns, notably concerning modeling choices.

II. Specific comments

1. MixSIR was run without taking into account the most "extreme" food items in terms of carbon isotopic ratios. Seagrass leaves and roots (the most positive items, roughly -11 to -13 ‰) were left out based on the assumption that none of the studied organisms were able to consume living seagrass tissues. Chemoautotrophic bacteria (the most negative item, -35‰) were included for only 3 of the studied taxa. Although it is not stated explicitly, I suppose it was assumed that it could only be a major food source for the most ^{13}C-depleted animals.
A priori exclusion of sources likely has an important influence on model outputs, and is in my opinion a valid option only if authors are sure that these food sources do not contribute to the diet of any consumer, either directly or indirectly. Here, I highly doubt that it is the case. For example, examination of figure 3 reveals that some *Metachromadora* and one *Daptonema* samples had δ^{13}C values compatible with important reliance on living seagrass tissues. Moreover, results suggest that several of the studied organisms are secondary consumers. In the absence of supporting data, I don't think it is reasonable to assume that none of their prey could rely on either seagrass tissues or chemoautotrophic bacteria. Actually, the authors themselves state that some nematods could indirectly depend on the latter source (p.1290, l. 25-28 & p.1291, l. 1-2).
In this context, I don't think it is wise to exclude those "extreme" food sources. I therefore suggest that authors run the model again, including them. Of course, adding extra sources could impair model performance, but this can be taken into account by using diagnostic tools (e.g. correlation between sources in model-estimated proportions distributions).

2. Authors ran MixSIR twice: once including seagrass epiphytes as a food item, and once without epiphytes (p. 1284, l. 21-23). It is not clear to me what they were trying to achieve by doing so, but it seems like a rather arbitrary way to decrease the number of sources. In addition, it is conceptually wrong, because animals had access to seagrass epiphytes regardless of their inclusion as food items in the model.
I think that seagrass epiphytes should be included in MixSIR inputs. If authors want to lower the number of "overlapping" (i.e. isotopically similar) sources, like microphytobenthos and seagrass epiphytes in this case, I think that aggregating them (i.e. computing a single mean and SD for all values of these two sources) constitutes a more objective, and therefore more suitable approach. I don't expect it to cause a significant loss of model predictive power, because the model will not be able to efficiently discriminate between isotopically similar sources anyway.

3. Models estimates are presented by giving the median and 95th percentile, with the full distribution of solutions as electronic supplementary material. I think that presenting model outputs as credibility intervals (e.g. 95% intervals, with lower and upper limits) would be more intuitive because it would allow the reader to estimate dispersion on both sides of the solution distribution.

4. In some cases (e.g. tables 1 and 3), authors give sample numbers, but in some cases they do not (e.g. table 2 or model input data). Moreover, the pooling strategy is not described in detail, and only partial information is given on p. 1282 (l. 21-23).
I think it would add value to the manuscript if authors provided a synthetic table giving sample numbers and (if applicable) pooling strategy for each food item and studied taxon, and for each measured parameter (δ^{13}C and δ^{15}N). For example, it would help the reader to quickly and conveniently understand what is meant by "We used δ^{13}C and δ^{15}N of all replicate samples per taxon separately [...] as input data (p. 1284, l. 17-19).

5. Table 1 (seasonal variation of food items isotopic composition) and the associated results section (3.1, p. 1285) do not seem very informative to me. In some cases, inter-season comparisons are impossible (e.g. seagrass detritus that were only sampled in one season), and in other effectives are very low, questioning the validity of comparisons (e.g. epiphytes, where n=2 for one of the seasons). Regardless of the outcome of these comparisons, source values measured in both seasons were pooled for elaboration of figure 3 and for modeling purposes. Distinction between sampling events is almost never made for consumers.
In this context, I don't think that the sampling strategy was adequate to assess seasonal variation among the studied food web, and the discussion statements focusing on this issue (p. 1292, l. 27-29 and p. 1293, l. 1-6) seem rather arbitrary, as there is not enough data to either support or infirm them. I'd advocate taking these results out of the paper to focus on findings that are more relevant to this study's aims.

6. On p. 1281 (l. 1-3), authors mention that the studied system is still recovering from a major collapse that happened in 2008. I have concerns about potential impacts of meadow structure alteration on trophic relationships among the associated communities. Besides lower shoot density, are major perturbations of the ecosystem still visible? If so, this should be explicitly mentioned and discussed.

III. Technical corrections

- p. 1284 l.28 and p. 1285 l. 1-2: This sentence seems redundant with p. 1284 l.2-4.
- p. 1294 l.3: Parentheses are lacking in the unpublished citation.
- p. 1294 l.12: Use of a common name without stating the organism's scientific name first should be avoided, especially when, like "cordgrass", it can relate to several taxa.

IV. Concluding remarks

All that being said, I don't think any of these flaws should justify a rejection of the paper. All the criticisms and concerns I expressed in this review are made in a constructive way, and I hope that authors will use them as so. I believe this article is already an interesting and well-made piece of work, and I am convinced that after revision, its quality will be even improved.

Kind regards,

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