

Interactive comment on “Species variability and connectivity in the deep sea: evaluating effects of spatial heterogeneity and hydrodynamics” by Lidia Lins et al.

Lidia Lins et al.

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Dear Anonymous referee #2,

We thank you for your very useful comments and suggestions. We have taken them into account and tried to address them as detailed as possible. You can find our answers below for each mentioned comment: 1) “The title should be changed, at present it is far too general. The topic of the manuscript is free-living nematode species variability and connectivity- not species variability and connectivity.

The reviewer is right. We have changed the title accordingly to: Evaluating environmental drivers of spatial variability in free-living nematode assemblages along the Por-

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tuguese margin.

2) “Moreover, the manuscript does not study effects of hydrodynamics as no hydrodynamic variables are measured. There are a sufficient number of ways that sediment heterogeneity may be obtained that “high” hydrodynamics can not be inferred. I’m also not sure what “high” hydrodynamics means.”

Indeed. The reviewer is right. We have rewritten this section in the discussion. We have not measured hydrodynamics in the area but we have based our assumption of hydrodynamics on previously available data for the Western Iberian Margin to suggest that in our case, sediment heterogeneity could be an indirect measure of hydrodynamic effects. We do not suggest the blind use of sediment as the single measure for hydrodynamics, but rather a combination of those with other data available in the literature. For the WIM region, specifically, because it is characterized by a steep slope, alongshore transport of sediments can be very strong (Condie and Sherwood, 2006; Drago et al., 1998; Quaresma et al, 2007). In our study area, distances between the shallow and the deep station were only ~30 km, indicating that such big changes in sediment composition could be mainly derived from bottom stress derived from alongshore transport of sediments. Furthermore, in the discussion we also mention that sediment heterogeneity at the shallow transect could also be derived from fishing events occurring in the area. Thus, although we did not measure directly bottom stress effects, we find important to discuss the subject for the WIM, especially because of the amount of information already available for the area. Concerning the use of “high hydrodynamics” we have followed the suggestion of the reviewer. Thus, the term “high” was excluded from the text.

3) “Finally the degree to which connectivity is analysed in the manuscript is pretty limited- connectivity between deep and shallow only measured apparently by cluster techniques.”

The reviewer is right. Considering that the success rate of our PCR amplification was

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low, we could not increase the amount of data used. However, we intended in this paper to corroborate with the results found by Bik et al (2010) conducted with the same genus and to give an insight that connectivity is possible for certain nematode genera in the deep sea. Of course, we tried to be careful with the interpretation of our results. In this paper, we could observe that there was no evidence for the lack of connectivity between the two transects, and not that connectivity is the rule for deep-sea nematodes. Moreover, the use of cluster techniques was the only molecular method used for connectivity in this paper, together with the morphological analysis. For deep-sea nematodes, however, the use of other techniques, such as population genetics, is still in its infancy and even for 18S rDNA the results obtained cover a very small fragment of the DNA, and are mostly used to compare diversity between areas rather than more specific questions which require more refined techniques.

4) “Furthermore, if I have followed the methods correctly, there are only 3 – 4 replicates from 6 and 4 stations (shallow and deep respectively) for nematodes (and it is unstated whether there is any replication for the other measures). I would have expected a study focussed on defining and explaining variability to have more replication and stations that that.”

For the molecular analyses we have stated in the material and methods section: “One sample from each of the ‘shallow’ stations S4 and S2 and one from the ‘deep’ station D4 were preserved in DESS (Yoder et al., 2006) and used for molecular analyses.” For the environmental analyses we have included in the text that also 3-4 replicates were used according to the suggestion of the reviewer: “Three to four replicated samples for granulometric and geochemical analyses (1 g of sediment) from the first sediment layer (0–1 cm) were frozen at -80 °C.”

5) I was surprised to see no reference to the Leduc et al paper “Nematode beta diversity on the continental slope of New Zealand: spatial patterns and environmental drivers.”

The reviewer is right. We have included the paper of Leduc et al. (2012) in the discus-

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sion, since it provides important information conducted at slopes as well.

6) I would like to see a reduction in the scope of the manuscript with a focus on the variables actually measured (food availability) and the type of organism studied. Broadening the discussion to consider how different results may have been obtained if a greater mix of phyla, size and biological traits (including dispersal) had been studied would also be useful.

We have followed the suggestion of the reviewer and decreased the importance of the hydrodynamics section in the paper. We have rewritten this section. Currently, the section about disturbance and hydrodynamics focused specially on the consequences of nematode resuspension and habitat colonization rather than hydrodynamics. Considering the different phyla, we have discussed in (H4) how other groups, such as bivalves, gastropods, and crustaceans (amphipods and isopods) differentiate with increasing water depth along the slope in the following paragraph: “Processes such as deep-water formation and upwelling, potentially represent means of (passive) across-depths dispersal (Brandt, 1992; Brandt et al., 2007; Kussakin, 1973; Strugnell et al., 2008). Contrastingly, for some deep-sea taxa, such as protobranch bivalves, gastropods, and some crustaceans, depth-related diversification have been observed, indicating possible depth-related barriers to dispersal (Etter and Bower, 2015; Etter et al., 2011; Etter et al., 2005; Havermans et al., 2013; Wilson, 1983). The depth-related population differentiation observed in these studies, however, covered larger bathymetric ranges than the ones studied here, and were mostly situated at the lower bathyal and abyss (Etter and Bower, 2015; Etter et al., 2011). Just a few studies have assessed shallow-deep connectivity using a combined morphological and molecular approach (Bik et al., 2010; Riehl and Kaiser, 2012; Van Campenhout et al., 2014; Van Gaever et al., 2009). In contrast to the molluscs and crustaceans mentioned above, selected nematodes and isopods show high degrees of genetic similarity across depth, suggesting taxon-specific barriers (Bik et al., 2010; Riehl and Kaiser, 2012). “

7) I don't know that connectivity to the degree that it is analysed here is actually useful

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as there is no indication of space and time scales. The “connectivity” terminology should be dropped from the manuscript and instead merely discussed as a lack of clear depth-related population differences, depth-endemic lineages or isolation.

We have followed the suggestion of the reviewer. The term connectivity was substituted in the discussion for the lack of isolation per habitat observed in this study, whenever it dealt with phylogenetic relationships. The (H4) of the discussion was rewritten.

Yours faithfully, Lidia Lins, on behalf of all authors

Please also note the supplement to this comment:

<http://www.biogeosciences-discuss.net/bg-2016-134/bg-2016-134-AC2-supplement.pdf>

Interactive comment on Biogeosciences Discuss., doi:10.5194/bg-2016-134, 2016.