

Authors response to referee comment 3

Dear editor, dear referee, dear EGU sphere,

First we would like to thank the referee for the time invested reviewing the paper, and the constructive comments and suggestions that were made.

Here, we answer in details some of the comments. We took notes of the other suggestions regarding language, or small additions.

Comparison of the new equation of the oxygen isotope fractionation with those of Brand et al. (2019). Both equations are similar in the temperature range between 10-25°C, but differ in the low-temperature field (<10°C). Since the Brand et al brachiopod-data set is by far much better constrained by data points, the authors should provide a more in-depth discussion about causes of the offset. Further, they should strengthen their arguments why it is necessary to introduce the new equation, and why it shall be an improvement.

We will clarify this part and add elements of comparison between the different fractionation equations.

The supposed sampling procedure avoids specialized parts of the shell as umbo, edges, muscle scars, primary layers. However, Ullmann et al. (2017) observed additional significant taxon-specific ranges in their intra-specific high-resolution oxygen isotope data. How has this observation an effect for the results of this study? Is intra-specific variability smoothed by the sample size? Which degree of uncertainty introduce specimens of the suborder Terebratellidina to the fractionation equations? Please comment on this.

We assume that the sampling area, which spans at least two major growth lines, allows a smoothing of the intra-specimen variability within the collected homogenized powder. While major growth lines are commonly interpreted as annual, that is not necessarily the case, which explains the uncertainty on the time represented by the sampling area. This sampling creates mass-averaged geochemical compositions, which is mathematically different from time-averages which we use for environmental conditions, because of varying shell growth rates through time. The more variable the growth rate, the more biased this sampling will be towards periods of high growth rates (Schöne, 2008; Yamamoto et al., 2011; Takayanagi et al., 2015).

Specimens of the suborder Terebratellidina highlight clumped isotope deviations from equilibrium and trace elements compositions of their inner layer significantly different than specimens from the suborder Terebratulidina. However, deviation from thermodynamic equilibrium in oxygen isotope composition are not significantly different between the two groups, within the dataset tested. So we do not expect the fractionation equation to be biased by any of the groups.

The Jurassic example is not well executed and not the scope of this study. New and very few data points are introduced first time in the discussion. I recommend the removal of this part of the manuscript, since its focus is on modern brachiopod taxa.

As also suggested by another referee, this part will be removed from the revised version of the manuscript.

References

Schöne, B. R.: The curse of physiology—challenges and opportunities in the interpretation of geochemical data from mollusk shells, *Geo-Mar. Lett.*, 28, 269–285, <https://doi.org/10.1007/s00367-008-0114-6>, 2008.

Takayanagi, H., Asami, R., Otake, T., Abe, O., Miyajima, T., Kitagawa, H., and Iryu, Y.: Quantitative analysis of intraspecific variations in the carbon and oxygen isotope compositions of the modern cool-temperate brachiopod *Terebratulina crossei*, *Geochim. Cosmochim. Acta*, 170, 301–320, <https://doi.org/10.1016/j.gca.2015.08.006>, 2015.

Yamamoto, K., Asami, R., and Iryu, Y.: Brachiopod taxa and shell portions reliably recording past ocean environments: Toward establishing a robust paleoceanographic proxy: BRACHIOPOD OXYGEN ISOTOPE RECORDS, *Geophys. Res. Lett.*, 38, L13601, <https://doi.org/10.1029/2011GL047134>, 2011.