Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2020-194-RC2, 2020

Biogeosciences Discussions
Open Access
EGU

Interactive comment on "The haplo-diplontic life cycle expands niche space of coccolithophores" *by* Joost de Vries et al.

Anonymous Referee #2

Received and published: 2 August 2020

The study by de Vries et al. is a broad synthesis studies, which a main focus on describing environmental portioning and drivers behind differential haplo-diplontic stages of the coccolithophores. As the haploid stage is often overlooked, yet it is ecologically and biogeochemically important, this is an important review studies of the inclusion of the life stages towards an improved understanding of the coccolithophore ecology.

While the paper joins various components of coccolithophores biology/ecology, my major questions are focus on the methodological approach, which in many ways is insufficiently described/explained, with some of the resulting conclusions then also not supported. I would like the authors to address the following methodological approaches.

There are several caveats behind such synthesis approach that need to be highlighted and further elaborated. The first and most important is compilation of SEM dataset,

Printer-friendly version

Discussion paper

which strikes me as uncertain (what is the images were not taken) and difficult to present in the quantitative terms. Were both phases in the initial SEM dataset presented quantitatively or where there also just studies that took qualitative SEM approach? How did this impact how the authors proceed with the study? Where are potential biases? How can you estimate uncertainty in the quantified approach?

Second, I do follow the nice overlap and nice expansions in the hyperspace. It is not clear to me how the authors transitioned from hypervolume to the nice space and how are the two haplo-diplontic stages represented in the Eq 2 (line 15) based on the similarity metrics? How was the intersection or the union between two hypervolumes determined? Why was NE not calculated for BATS?

Third, in the section of seasonality (line 135), only a handful of environmental parameters are missing and there could be other important physical-chemical drivers. For example, In Figure 8, you also include turbulence in there, why was such parameter not included in the PCA analyses? What about pH, for example? Also, as described are large-scale patterns, what about mesoscale type events, advection and other physical parameters? In line 210, why were not the same approaches used for the Med and ATM? By using water column vs niche space approach, this excludes the possibility of comparing two regions.

Forth, where is 17% of expanding niche space coming from?

Fifth, the authors report 7.3 to 18% of the species abundance, which is a relatively wide range and needs to be better quantified with the uncertainty. Also, given the quantitative estimates presented, I wish the authors to have better addressed some of the knowledge gaps, the impact on the pump of the haploid-diploid stage, standardizing the approaches to represent different species (paired- non paired, etc),. Based in Figure 3, one could conclude that the relative abundances (f,g,h) of holococcos are only slightly lower compared to the heterococcos (c,d,e) and these figures need changes. What is the difference in shading?

Printer-friendly version

Discussion paper

Interactive comment on Biogeosciences Discuss., https://doi.org/10.5194/bg-2020-194, 2020.

Printer-friendly version

Discussion paper