



Interactive comment on “Simulating the growth and distribution of planktic foraminifer using an ecophysiological multi-species model” by F. Lombard et al.

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I thank the authors for their thorough response to my comments. The authors are clearly aware of the pertinent issues and I am confident they will be able to treat these adequately in the revised version of their paper. However, I feel there remain several misunderstandings, which I feel need to be clarified:

1) Shell size and abundance From the response, I am not sure whether the authors appreciate the well known phenomenon of the correlation between shell size and maximum abundance. This has been postulated by Hecht (1976) and confirmed by Schmidt et al. (2004). The consequence is that it is not possible to convert relative abundances

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of planktonic foraminifera species to biomass abundances IN THE SAME WAY throughout their ranges. 20% of *G. ruber* in a tropical setting corresponds to a much higher biomass contribution than 20% *G. ruber* in temperate waters, simply because the shell size is different among these settings. This observation has consequences not only for the comparison between model output and sediment data, but also for the calibration of the model. It does not matter whether the model predicts biomass or growth rates - the scaling to the number of individuals (relative abundance) is clearly more complex than what the paper portrays at present.

2) Growth rate limitation The point is indeed, as the authors note, that on a population level, growth has two components - the growth of individuals and growth of the population. Although I have no data to prove or disprove it, I am quite convinced the latter is more significant at population level, especially in organisms like foraminifera, which produce enormous amounts of propagules. In such situation, population growth in terms of the number of decreased juvenile mortality, is virtually unlimited.

4) Comparison with data The authors should note that none of the MARGO calibration data from the Indopacific are affected by dissolution. All samples affected by dissolution have been removed. This has been documented clearly in the appropriate paper. Therefore, seafloor dissolution in the Pacific is not a good candidate explanation for the model misfit.

5) *Sacculifer* vs *ruber* The observation that the model predicts different adaptations for these species is really important. The reason why these are opposite to the hypothesis by Siccha et al. (2009) remain, however, unclear. The argument in that paper did not consider any local adaptations in the Red Sea and it showed indeed that neither oxygen nor salinity could possibly be responsible for the opposite behaviour of the two species in the Red Sea.

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