

Interactive comment on “Scaled biotic disruption during early Eocene global warming events” by S. J. Gibbs et al.

Anonymous Referee #2

Received and published: 17 October 2012

This MS is an interesting approach to an important issue, namely to understand how biotic response varies in relation to environmental perturbations of varying magnitudes.

However, I share the concerns of Referee 1, which can be boiled down to the question: how well does genus-level variation in relative abundance of nannofossils represent “marine biotic variability through . . . the early Eocene”. I find the authors’ response to the referee’s comments somewhat unsatisfactory. Regarding relative abundance vs flux: (1) assumptions regarding sedimentation rate are inherent to the analysis undertaken (binning by time interval); (2) surely relative abundance patterns will vary between sites to a similar extent as flux. Regarding genus vs species-level analysis: it is important to remind ourselves that in paleontology these are morphological subdivisions that may bear little relation to the biological concepts of genus and species. For

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this reason I would always recommend a counting group approach, and be concerned less with formal species and genus discrimination than with identification of a robust assemblage of counting groups. The authors note that 7 of their genera are essentially monospecific anyway, which means that subdividing the three remaining taxa into species or supra-specific categories would be more internally consistent and probably much more informative.

However, my primary concern with this MS is the analytical methodology. I contend that the smoothing and binning of time series data should not be used to understand biological responses to events that may occur either abruptly or at rates that are more rapid than bin duration. For the smoothed records considered here, how is it possible to confidently identify precursor assemblage changes? Smoothing is always going to make an abrupt response appear gradual. In my opinion, the authors have adopted a methodology that does not so much increase the signal to noise ratio but rather hampers useful analysis of biological response to these short-lived climate events. More time should be devoted to deciphering the biological significance of the changes (which must involve some consideration of flux) and less to interrogation of what I consider to be a questionable analytical approach to the problem.

An additional concern I have with this MS is that the authors appear to overlook the possible effect that the duration between hyperthermals may have on biological response. The authors argue that the reason the biological response is well defined for the PETM, H1 and I1 events but not for H2 and I2 is that the impacts exceed a critical threshold. They appear to ignore the fact that H1/H2 and I1/I2 are paired events separated by ~100 ky. It would seem reasonable to consider at least two alternative explanations for the apparent threshold effect: (1) ~100 ky may not be long enough for nannofossil populations to revert to pre-H1 or pre-I1 composition, (2) there may be a stronger climatic link between these paired events than is evident in current proxy data sets. These latter primarily relate to changes in benthic $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$ and so relate to changes in the deep sea rather than the surface ocean, in which the nannoplankton

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reside.

Finally, the MS is rather poorly organised and the language is often awkward. The authors need to review the order and referencing of the figures, so that they are better integrated with the text and need to strive to simplify their language. e.g. “each taxon’s downcore record of relative abundance data. . .” vs “ the relative abundance record of each genus..” e.g. “n the taxa number” vs “n being the number of taxa” e.g. “Higher abundance taxa” vs “More abundant taxa” e.g. “which parallels the recent documentation of scaled temperature change” vs “which is in line with evidence for scaled temperature change”

In acknowledgements, the current program is the Integrated Ocean Drilling Program.

Interactive comment on Biogeosciences Discuss., 9, 1237, 2012.