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Interactive comment on “Small diversity effects on ocean primary production under environmental change in a diversity-resolving ocean ecosystem model” by A. E. F. Prowe et al.

A. Ridgwell (Referee)

andy@seao2.org

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I like this – the model is a great synthetic ecological environment for exploring such a wide range of fundamental and practical (model-development) questions as the authors have already demonstrated in a variety of papers over the past few years. I am intrigued by the current approach. But I am not yet entirely convinced that what is being demonstrated in the model comparison experiments is quite what the authors intend. Anyway ...

The importance of marine biodiversity to the future global climate change sensitivity of e.g. primary production is an important assessment to make. One might expect that

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a highly diverse (emergent) ecosystem model such as the MIT Darwin model might be inherently more stable, or rather: less likely to respond abruptly to environmental change, than the more traditional discrete PFT-based models. Friederike Prowe and co-workers do not quite go this far, but do find in their modelling study that the number of phytoplankton functional types and not necessarily the total represented biological diversity per se appears to be the most important factor in controlling the sensitivity of ocean productivity to climate perturbation. This is a useful result and raises questions (or adds to the debate) about what the ‘best’ future marine ecosystem modelling strategy might be, and whether high diversity / emergent models such as the Darwin model should be the way forward or whether current PFT based models will remain perfectly adequate for assessing the main impacts of future climate change (and ocean acidification) on marine carbon and linked biogeochemical cycling. While I think the overall approach and intention is interesting and valuable, I do have some questions/criticisms about the details of the methodology employed and have some doubts as to whether the methodology is sufficient to support the interpretation (alternatively: there is room for improvement in the methodology and which would lead to a significantly improved paper):

* If I am reading Figure 4 correctly – my single most serious concern about the methodology arises from the distributions of T_{opt} . For the full $n=78$ model, almost all the ‘small’ plankton varieties cluster around the KPO_4 for *Prochlorococcus* and there are very few varieties appearing anywhere near the ca. $0.025 \text{ mmol P m}^{-3}$ value for ‘other small phytoplankton’ (the middle marked vertical line). If the ‘other small phytoplankton’ PFT (vertical line) fails to reflect the mean diversity in KPO_4 space of the ‘other small phytoplankton’ varieties in the highly resolved ($n=30$ or $n=78$) model, then the comparison between highly resolved and $n=4$ or $n=3$ PRT models does not seem valid, i.e. you are creating a PFT in $n=4$ or $n=3$ PRT configurations that has no analogue in the highly resolved model. This may not be critical to the interpretation but does rather obfuscate what would otherwise be an extremely conceptually neat and transparent approach. Secondly, the choice of which of the 4 $n=4$ PFTs to ‘remove’ (*Prochlorococcus*) in the

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$n=3$ PRT configuration creates an apparent bias in that the PFT with the very lowest KPO4 is been chosen. Surely this is always going to induce a substantially different ecosystem compared to $n=4$ and $n=30$ (and 78) particularly as something like $\sim 50\%$ of total d $n=30$ (and 78) variants seem to be clustered at the very lowest KPO4 end? For example, removing the ‘other small phytoplankton’ PFT might give a rather different result and an $n=3$ PFT model might look rather more like the higher diversity ones.

* There are potentially important complications about quite what is being compared here. The resolved ($n=30$ or $n=78$) has its phytoplankton varieties relatively clustered around the PFTs in KPO4 space (excepting whatever is going on with the ‘other small phytoplankton’). Certainly, KPO4 space is not by any means evenly populated. The varieties in each PFT cluster are then primarily differing in their value of T_{opt} (we don’t get to see how the varieties are distributed in k_{par} space – see comment below). The ‘Epply-like’ temperature response that is incorporated in traditional PFT-based models and adopted here for $n=4$ and $n=3$ configurations is implicit designed to account for a diversity of T_{opt} values. Hence, for a hypothetical PFT, would one not expect a close similarity between a PFT with an Epply-like response, and a diversity of phytoplankton varieties that differ in their explicit T_{opt} value but otherwise share similar KPO4 Properties? In other words: are the results and conclusions of the paper really at all that surprising in this respect? Is the methodology used really sufficient to provide a strong test of the hypothesis of ‘primary-production [being] largely independent of the number of coexisting phytoplankton types’? Would not having a diversity of sizes (either with a T_{opt} or Epply-like temperature response) not provide a more appropriate test? An alternative way of comparing low and high diversity modelling approaches would be to progressively sub-sample the population and have the 4 (or 3) PFTs chosen randomly (but perhaps in an ensemble of sub-sampling) – i.e. much as was done to move from $n=78$ to $n=30$ but taken to the extreme. Overall, I am not yet convinced in this study that the comparison is in reality principally between an $n=4$ model including a parameterization of (Epply) temperature response, vs. a $n=78$ (or 30) model that is unpicking the underlying diversity in temperature response whilst conforming to the Epply curve

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and hence in danger or providing only a test of whether the Epply curve 'works'.

* I was surprised that temperature diffusion/mixing were also not simultaneously reduced in the model (alongside nutrients). Why? Surely this rather spoils the attempt at creating an environmental perturbation with some future global change relevance? If, as suggested, it is to 'separate direct effects on the ecosystem from more complex responses driven by physical feedbacks' then why not carry out both possible perturbations (nutrients+phytoplankton only, and nutrients+phytoplankton and temperature) and explicitly separate out the effects. The analysis presented by Dutkiewicz et al. [2013] in GBC earlier this year is extremely relevant in this respect.

Other comments / suggestions

* General: Do prior inter-comparing ecosystem models of different complexity not exist (if only for specific ocean locations rather than global patterns of productivity)? Citing/discussing a little more literature addressing the importance/consequences of different choices in the representation of marine ecosystems would not go amiss. * General (e.g. Abstract): There is some potential for confusion between 'phytoplankton types' and 'phytoplankton functional types'. Probably 'types' is too ingrained in the Darwin model literature, but making a clearer distinction ('sub-types', 'varieties'?) would be helpful if at all possible. * Title: This could be a little simpler and clearer. * Methods: A table summarizing the different experiments would be useful. * Page 12576 / Lines 16-27: This is a really interesting and important section and analysis, but I did not find it as easy to follow as I would have liked. * Page 12582 / Lines 15-19: It would be helpful to know a little more about the transient changes induced by the change in vertical mixing coefficient (k_e) – would it be possible to have a time-series of e.g. diversity vs. PP (as presented for an annual average and zonally in Figure 2) and for each of the different diversity (n) experiments – i.e. the question of whether the rate of response differs between e.g. $n=78$ and $n=4$ and whether the degree of represented diversity might affect the time-scales of response (rather than just final magnitude). * Figure 1: It would be useful to see the corresponding global primary productivity patterns of

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the 2 default and 2 reduced mixing experiments as well as the anomalies. In addition: could not the corresponding diversity maps also be shown? I appreciate that zonal averages are given in Figure 2, but it is a short paper and I see no reason not to provide a reasonably full set of spatially-explicit results. * Figure 3: The different lines are not all sufficiently distinct from each other. * Figure 4: Please explicitly label (e.g. with arrows) which vertical line is which PFT. And also make distinct the 2 coincident lines (e.g. one thick/dashed or dashed/colored) for 'diatoms' and 'other large phytoplankton'. Is there a similar diversity in terms of light limitation? If so: it would be helpful for completeness to plot a 2nd set of 4 panels with k_{par} (?) on the y-axis rather than T_{opt} . Alternatively, the 4 panels with T_{opt} on the y-axis could be repeated, but with the colour scale representing k_{par} rather than biomass fraction.

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