

***Interactive comment on “Incorporating genomic information and predicting gene expression patterns in a simplified biogeochemical model” by P. Wang et al.***

**Anonymous Referee #2**

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The manuscript describes a simple resource competition model designed to allow including genomic information in the model formulation. The simulations are performed in a chemostat-like setting intended to allow comparison with conditions in the surface ocean. Genomic information is implemented as trade-offs between resource-use abilities and maximum growth rate. The authors claim that their simulations are conceptually consistent with observations from marine plankton systems and that their approach should lead to better predictions about the response of plankton systems to environmental change.

General evaluation.

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Including genomic information in a plankton model is a novel and intriguing approach. I also liked the authors' attempt to keep the model as simple as possible. However, the model formulation is fraught with severe problems and in my eyes just plain wrong. Also, the discussion of the results is overly optimistic and this appears to show a lack of sufficient critical distance of the authors to their work. Nevertheless, I expect that the main outcomes would remain the same if the model's problems were corrected. Thus, a thoroughly revised manuscript together with a reworked model could eventually be publishable.

My main concern here is with the model formulation itself. Problems with the text are given further below. While I very much agree with the approach of keeping the model simple, where the model does a good job, the formulations should nevertheless reflect the processes they are supposed to represent, and here the model fails.

To begin with, the different nitrogen and phosphorus compounds enter a phytoplankton cell on very different routes, the main difference in the present context being that ammonium can be taken up passively by diffusion through the cell wall, whereas all the other molecules (except N<sub>2</sub>) can only be acquired via active uptake by specialised (channel) enzymes at the cell surface. The difference is very important because all phytoplankton species can use ammonium, whereas some (*Prochlorococcus*, although Martiny et al. (2009), PNAS 106:10787, find that some *Prochlorococcus* types can use nitrate) may be unable to utilise nitrate and nitrate, but not ammonium, uptake is affected by iron limitation. Thus, the ability for ammonium use should be treated differently, as common for all species.

The next problem is the treatment of nutrient uptake. Firstly, the authors state that they describe nutrient uptake as a reaction-diffusion process (p. 822, l. 17), but then the equations only describe diffusion. Secondly, and more importantly, Eqs. (5) and (6) describe a sawtooth function if the corresponding gene is present. I am ready to accept neglecting the feedback between uptake and diffusion (constant surface concentration) as a simplification. However, the sawtooth function used here does not appear to make

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any sense. Worse, because uptake switches quickly between close to zero if  $C_j$  is slightly above  $C_{0,j}$ , this introduces a positive feedback between nutrient concentration and uptake. Both this and the previous problem could be solved if the uptake was described like this (but there are probably many other ways to solve these problems): if the gene for a nutrient is present, potential uptake (diffusion) is described by Eq. (6), otherwise there is no uptake for this nutrient, and potential ammonium uptake is always described by Eq. (6). These first two concerns about the model formulation must be convincingly resolved in the revision if the manuscript is to be published.

I also find the gene regulation by extracellular nutrient concentrations somewhat questionable. Nutrient concentrations can and do change quite rapidly in the surface ocean, so that a gene regulation based thereon could often lead to a situation where the genes are constantly switched on and off as the nutrient concentration fluctuates around the critical concentration. I think the cell quota is a more useful (because integrated) quantity. Defining critical N and P cell quotas would also not make the model more complex in any way. It would, however, be less arbitrary than the choice of ammonium and phosphate for gene regulation, as it avoids the question: why not COP (for example)?

It should at least be noted in the text that phytoplankton cells usually generate only very weak gradients ( $C \sim C_0$ ) and that  $C_0$  increases with increasing C in reality.

While the text is generally well written and clear, I find the placement of the results in general biogeochemistry and the discussion with respect to observations and application to the real ocean troubling. Also, it was not clear to me how the model was actually run. Are the figures representing a steady state? If so, the steady state does not appear to hold, e.g., in Fig. 5. If not, how were the initial conditions chosen and how long was the model run? This is important information for me to judge the validity and relevance of the model results.

At the end of the model description the authors state that this study was intended as a proof of concept (p. 11, l. 25), and as such I could live with the simplistic setup

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of the simulations. But then I would suggest to remove most of the references to biogeochemistry in the discussion and section 3.3.

The comparison of the biodiversity patterns went rather wrong. For example, Pommier et al. (2007) reported higher diversity at higher latitudes whereas the present model predicts the opposite. But the authors made it sound as if the model produced a pattern similar to the observed (p. 16, ll. 13–15). Similarly, the observations of Treusch et al. (2009) indicate an inverse relationship between diversity and temperature, which is contrary to the model prediction, but the text on p. 16, ll. 2–8 alleges a good agreement between model and observations.

I think it would be best to rewrite the discussion and focus it on the proof-of-nature type of this study rather than questionable comparisons with observations and equally questionable biogeochemical implications.

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