

## Reply to Review 2

We would like to thank Damien Eveillard very much for his constructive comments and helpful advice on our manuscript. We would be happy to account for his points of criticism in a revised manuscript version.

- 1) As suggested, we will point out more clearly the constraints arising when applying our approach to other biological entities, such as heterotrophic bacterial populations.
- 2) Unfortunately, we didn't quite understand what the reviewer means by discussing model plasticity. Based on our understanding, the term plasticity refers to the physiological plasticity of organisms as a response to altered environmental conditions. This definition does not align with the reviewer's comment, though. However, we hope that our revised version will account for this criticism.
- 3) We will add a more extensive discussion on the potential risk of model overfitting.
- 4) We agree that our manuscript would benefit from a thorough presentation of contemporary evolutionary modeling approaches. As also suggested by Reviewer 1, we think that a text box would be appropriate to explain different state-of-the-art modeling approaches. In that box, we can further clarify the rationale behind these approaches and evolutionary ecosystem models in general (i.e., the underlying mechanisms in the form of mathematical equations and parameters). This would also allow us to explain how both new and historical data can be incorporated into these models and how changes in ecosystem structure can be simulated.
- 5) As suggested, we will make a stronger link between section 2.3.3 and the rest of the manuscript and expand lines 206-210 regarding phytoplankton traits that are of particular relevance for ecosystem modeling. We are not completely sure what the reviewer means by asking for approaches to connect GWAS analysis and identified characteristics. However, we suggest to explain that it is necessary to validate the candidate loci identified in GWAS by experiments that target the phenotypic functionality of these loci.
- 6) While we like the idea of connecting figures 1 & 2 by the same color-coding, we see major practical complications, since both figures have a different level of detail. In Fig. 1, we distinguish between different sources of sedimentary data (sedimentary ancient DNA, biomarkers, microfossils...), whereas in Fig. 2, we focus on how information from different sources can be integrated into ecosystem models. As an example, information on biodiversity can be obtained from different data sources, such as sedimentary DNA, microfossils, and biomarkers, making a simple color-coding impossible. Therefore, it will unfortunately not be possible to establish a color code for these two figures. However, we will still try to establish a better connection between

both figures through adjusting the wording (e.g., by replacing “resurrection experiments” in Fig. 2 with resurrectable resting stages).

- 7) We will further expand on how DNA sediment data may limit quantitative parameter assessments.
- 8) Finally, we agree that we should further clarify the difference between model structure and parameters. We think that the text box we proposed above would be a good opportunity for that.