

This work tackles parts of an important subject of relevance to the journal. However, it does so in such a simplistic way that the conclusions are either obvious (viruses impact plankton production) or unbelievable (results are based on a model describing only one phytoplankton type, so there is no competition between phytoplankton that are more or less impacted by their own species-specific virus and/or by the likely selection zooplankton grazing). For some reason the authors do not seem to be aware of Flynn et al. 2022, which goes into various of the matters considered here and shows the critical importance of using a multi-species model. Here, the authors have actually used a 2-phytoplankton variant of their approach, but this is mentioned rather in passing in Discussion. If the whole work had been conducted using that more complex model then the work would have been on a much firmer grounding.

We thank the reviewer for the helpful and detailed comments on our manuscript.

Regarding the design and chosen complexity of our model system:

We designed our model based on state-of-the-art descriptions of phytoplankton-virus dynamics (Talmy et al. 2019, Flynn et al., 2021). Similar to those models, we described the spring bloom phytoplankton as a single compartment. The novelty of our model lies in resolving phytoplankton-virus interaction dynamics in a 1-dimensional water column & ecosystem framework. We thank the reviewer for pointing us at the study by Flynn et al, 2022, which we clearly missed to cite in our manuscript. We see a lot of potential for future research using multi-species approaches as described in Flynn et al. 2022. However, we chose the description of phytoplankton using one “bulk” compartment to be able to compare our model with available data on the effects of viral lysis and grazing on the bulk of Baltic Sea spring bloom phytoplankton.

Since we are aware that our model description cannot fully represent the complexity of the Baltic Sea ecosystem, we tested a more complex version of the model with two phytoplankton (size) groups, their two respective viruses and two zooplankton (size) groups. We will describe the design of the complex model in more detail in the revised version.

However, by increasing the model complexity, the uncertainty in model estimates increases as well (Fulton et al., 2003). Since we lack data on species-resolved viral lysis and grazing, we cannot accurately constrain all physiological parameters for the more complex model setup. To strike a balance between complexity and a reasonable description of food web dynamics, we decided to focus our manuscript on the initial NPZD-V model design. This being said, the results of our complex model with two phytoplankton groups agree with the results of our initial model. For this reason, we think that our results are not necessarily dependent on an increase in model complexity. We will make sure to discuss potential shortcomings of our chosen model design in more detail in the revised version.

## DETAILED COMMENTS

L12 Virus-host dynamics are highly specific; the specificity of this interaction here needs to be made very clear in the abstract.

L12 We will make sure to address the specificity of virus-host dynamics in the revised version.

L16 How did this warming interaction come about?

L16 The interaction of warming and viruses is caused by the dependence of the viral burst size on the growth conditions of the host. Under nutrient-replete conditions, a higher temperature will lead to a higher growth rate (unless the optimum temperature is exceeded), causing an increase in viral progeny. This is described in L 102ff.

L22 Is there a specific reason for not referencing Flynn et al. 2022 - it seems to have rather a lot in common with this submission.

L22 We thank the reviewer for pointing us to the recent study by Flynn et al., 2022, which we missed to refer to. We will relate it to our study in the revised version.

L26 Such an increase in primary production is not assured, and depends on the timing of events; these are matters for which models can help.

L26 We will describe the viral shunt dynamics with more caution in the revised version.

L28 It is very important to indicate early on that virus induced mortality is very different to that induced by zooplankton.

L28 We will point at the difference between virus induced mortality and zooplankton grazing in the revised version.

L69 It is very important to make it clear how many phytoplankton-virus couples are considered here - from what I can see there is just the one, implying that the Baltic has only one phytoplankton species with its virus and zooplankton. That is surely too much of a simplification. When a virus attacks its host, we must expect other phytoplankton to come to dominance. Whether they are suitable prey for the zooplankton is another important matter.

L69 We would like to refer you to our explanation regarding the chosen complexity of our model above. We will make sure to state the complexity of our model more accurately here.

L83 Cell size is affected by factors other than temperature, and certainly the species composition (and thence the specificity of any virus attacks) will be affected during successions.

L83 While there are other (more-complex) factors influencing cell size, e.g., grazer presence (Flynn et al., 2022), we modelled changes in cell size based on temperature alone, since this is a well-established correlation (Atkinson et al. 2003) and we investigate the effects of temperature on the dynamics of the ecosystem.

L134 I really do not see how such runs can possibly be related to reality. What happens depends as much on how uninfected species behave as it depends on that of virus-affected species.

L134 Please see our explanation regarding the chosen complexity of our model above.

L153 Most of what is released when phytoplankton burst would contribute to the DOM pool (as per L203), not to detritus. This does not appear to have been modelled, and neither is the activity of bacteria (and their grazers) that would be stimulated by such an event.

L153 The currency of our model is nitrogen. We fully agree with the reviewer that the exudation from phytoplankton contributes to the dissolved organic matter (DOM) pool. However, studies have shown differential remineralization of dissolved inorganic carbon, nitrogen and phosphorus (DOC, DON and DOP) to their inorganic counterparts and have reported that DON is least preferentially remineralized, and thereby not contributing significantly to the pool of dissolved inorganic nitrogen (DIN) in high latitude oceans (Sigman and Casciotti 2001, Wetz et al., 2007, Letscher et al., 2015). For this reason, we do not explicitly model the release of DON by phytoplankton. We do account for microbial mediated regeneration of nutrients through remineralization of detritus. Our detritus compartment comprises both dissolved and particulate organic matter (nitrogen). We will clarify this in the revised version of the manuscript.

L213 Virus presence alone cannot lead to a regeneration of nutrients (by which I assume you mean inorganic nutrient). I do not see how, at least in the system modelled, virus attack could ever promote primary production. Can it?

L213 According to the “viral shunt” hypothesis (Poulton et al., 2021), viral lysis leads to the production of dissolved organic matter (simulated as part of the detritus in our model), which in turn becomes remineralised leading to the increase in inorganic nutrient levels. Nutrient levels can then potentially favor increased primary production. We will describe this in more detail in the revised version of this manuscript.

L220 This model really cannot support such a claim; to do so it needs to describe the biodiversity of the plankton, and the allied specificity of viruses on components of the community.

L220 We would like to refer to our statement above on the chosen complexity of our model. Based on our model results, we still believe that our statement that viruses can play an important role in the termination of the spring bloom in the Baltic Sea is valid. However, we will discuss the possible biases of our chosen model design in the revised version.

L231 What does this 'interact actively' term mean? Viruses cannot do anything alone; they rely on the success of their host, and thence on many factors. This statement seems rather exaggerated.

L231 Danovaro et al., 2011 describe that “marine viruses interact actively with the present climate change”. We describe our definition of the interaction of two stressors in the previous lines in the manuscript. We regard viruses as a stressor. For this reason, we investigated the interactive effects of two stressors (viruses and climate change). We will clarify this in the revised version.

L246 While this paragraph is interesting, and begs additional questions, I fear that the model is far too simple to make generalised claims like this.

L246 Please see our explanation regarding the chosen complexity of our model above. We discuss the biases of our model in the discussion section L258ff.

L261 How was the zooplankton configured to handle this additional prey item?

L261 In the more complex model version, we included two phytoplankton groups (diatoms and picophytoplankton), their respective viruses and zooplankton grazers. We will describe this model version in more detail in the revised version.

L268 This is incorrect. They only impact their specific host, and the ramifications from the different host-virus interactions with competition appears (from Flynn et al. 2022) to be complex and profound.

L268 We find the model simulations by Flynn et al. 2022 on the role of viruses of species dominance very compelling and are happy to discuss the ramifications for the Kill-the-winner hypothesis in the revised version.

Fig.1 That this is operated within a 1D scenario based on a real hydrodynamic scenario makes it no more representative than models operated in theoretical scenarios. The problem here is that the trophic setup is far, far, too simplistic. Viruses would only impact their own host; the idea that all phytoplankton would be impacted simultaneously in nature is not plausible. There is no bacterial activity simulated here (with or without their own viruses). Excretion of DIN by phytoplankton? What types of zooplankton are these (I assume from the 'sloppy feeding' term they are metazoan?).

Fig. 1. The aim of our study was to study ecosystem dynamics caused by viral lysis in a realistic hydrodynamic framework. Please see also our explanation regarding the chosen complexity of our model above and L153. The zooplankton grazers are described to represent copepods. We will specify this in the revised version of the manuscript. Adding more taxonomic and trophic complexity such as described in Flynn et al. 2022, is an important angle for future research efforts. We will discuss these possible future directions in the revised version.

Fig.5 These 'future' plots carry even more caveats than does the control. All of these appears rather too much like a 'first try' rather than a comprehensive attempt to explore the dynamics.

Fig. 5 We would like to refer to our explanation regarding the chosen complexity of our model above and our description in the model biases. Since there are hardly any experimental, observational or modelling data available on the potential role of viruses under climate change, we believe our study adds valuable information on this topic.