

## ***Interactive comment on “Marine viral populations detected during a nutrient induced phytoplankton bloom at elevated pCO<sub>2</sub> levels” by J. B. Larsen et al.***

### **Anonymous Referee #3**

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The role of ocean acidification has been vastly understudied is is argueably one of the biggest 'side-effects' of exponential rises in atmospheric CO<sub>2</sub> concentrations since the start of the industrial revolution. Scientists are still in the early phase of trying to work out the effects of a lower oceanic pH. The ocean biological system is driven by microbial processes and these in turn are 'lubricated' by viruses which serve to mediate horizontal gene transfer, organic nutrient release and subsequent succession of microbial populations. Consequently viruses play a hugely important role in the ocean and any major perturbation (such as ocean acidification) will influence their activity. It is refreshing to see a study that tackles this question head on. The authors chose to look purely at the response of the viruses to artificially elevated levels of CO<sub>2</sub>. Of course

in a study like this the answers are not clear cut, but nonetheless they show there is a response by the viruses to elevated CO<sub>2</sub>. It is not an easy response to explain and this is where I have a slight problem with the ms. As a stand alone paper I really would like to have seen the phytoplankton data to help illustrate if the virus response was simply caused by changes in host concentrations. This has already been covered partly by referee 2 (I love this interactive system!) and answered by the authors (also in the paper discussion) but it is not clear. The differences are not huge. Is there a better way of looking at this? Okay I agree virus numbers have dropped, could it be anything else has caused this other than CO<sub>2</sub> concentrations? If a multivariate analysis with all the other measured parameters (principally cell numbers) was done would anything else flag up? I don't doubt the data, I just need to be sure all avenues are looked at to explain the drop. Whatever the result it WILL be interesting. Minor points: P3967: lines 1-5, where did these primer sequences come from? were they developed in house? Why didn't the authors use published EhV MCP primer sequences? Did these primers amplify all phycodnaviridae in the EhV (or CeV) sized bands or just EhV (or CeV) ie. what was the specificity of the primers? L6 Degenerate Phycodnaviridae primers. There is a lot of information missing on the design, sequence alignments optimisation etc in the development of this primer set (probably worthy of supplementary information or even a separate paper), we have to take the authors at their word on this data (I have no doubts their 'word' is sincere!). For example there is no explanation for the different sized amplicons, this seemed a bit odd for a 'universal' set of primers. How do they know they are amplifying the MCP gene? P3974 L3 Actually there are 14 core genes, for more information see: Allen et al.(2006) Evolutionary history of the Coccolithoviridae. Molecular Biology and Evolution, 23(1), 86-92. P 3975 L6 Another explanation could be simply a change in host genotype which dominates in a lower pH with consequent changes in virus production. I liked the paper a lot, it was a pleasure to read it will undoubtedly be highly cited - good luck!

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