

Interactive comment on “Marine viral populations detected during a nutrient induced phytoplankton bloom at elevated pCO₂ levels” by J. B. Larsen et al.

Anonymous Referee #1

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The work of Larsen and coworkers examines the influence of elevated pCO₂ levels on the marine virioplankton. The study was part of a bigger experimental setup, where mesocosms were treated with double and triple amount of pCO₂ levels than present, respectively, and compared to control mesocosms with current pCO₂ level. Their approach was to follow the abundance of virioplankton populations by flow cytometric measurements and to explore the diversity by PFGE analysis and PCR amplification of specific viral genes. They could identify two viruses specific for abundant haptophytes. One of these viruses EhV and an unidentified virus indeed showed a change in abundance with rising pCO₂ levels, however the rest of the virioplankton were largely unaffected. This work is a nice one and the methods are up-to-date. The manuscript

reads nice and fluently. The results are clearly presented and the discussion is interpreting them with the necessary caution. I have only minor comments: * Material and Methods: page 3964, line 15-17: Please give data on the location (lat, long) and size of the mesocosms and when the sampling occurred (time, date). * page 3965, line 8-10: What viral standard have you used to identify the viral populations by flow cytometry? Pure cultures? Please give details. * page 3965, line 20: What is a SM buffer? * Results: page 3969, line 4-6: I do not agree, that there was a ‘significant’ effect of pCO₂ on EhV abundance - the error bars are overlapping. * Figure 2 is too small, please increase the size to improve readability. * Discussion: page 3974, line 12: What do you mean by region? Gene region = operon?

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